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OM protein - protein search, using sw model

Run on: January 20, 2006, 18:54:14 ; Search time 52.9038 Seconds  
(without alignments)  
116.273 Million cell updates/sec

Title: US-09-662-293-1

Perfect score: 78

Sequence: 1 SIKRDNDYKNPM 14

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 880474

Minimum DB seq length: 0

Maximum DB seq length: 20

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : A\_Geneseq\_21:\*  
1: geneeqp19809:\*  
2: geneeqp19908:\*  
3: geneeqp20008:\*  
4: geneeqp20018:\*  
5: geneeqp20028:\*  
6: geneeqp20038:\*  
7: geneeqp20048:\*  
8: geneeqp20058:\*  
9: geneeqp20068:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	78	100.0	14	AA552510	AA552510 House dus
2	78	100.0	14	AAU96314	AAU96314 Der HMW-m
3	37	47.4	17	ABJ01203	ABJ01203 Human Sox
4	34	43.6	20	AA833556	AA833556 5/20 natl
5	34	43.6	20	AA833107	AA833107 Peanut wt
6	34	43.6	20	AAU04769	AAU04769 Native an
7	34	43.6	20	AAU05094	AAU05094 Anaphylac
8	33	42.3	12	AAW24076	AAW24076 PD498 alk
9	32	41.0	10	ADK08378	ADK08378 Human pap
10	32	41.0	11	AA830715	AA830715 HPV 16 E2
11	32	41.0	11	AAW30009	AAW30009 CAEV immu
12	32	41.0	11	AA866994	AA866994 HPV 16 E2
13	32	41.0	15	ADU68123	ADU68123 Human pap
14	32	41.0	15	ADU11513	ADU11513 HPV type
15	32	41.0	17	ABW02637	ABW02637 Human oes
16	32	41.0	18	AA552521	AA552521 House dus
17	32	41.0	18	AAU96325	AAU96325 Der HMW-m
18	32	41.0	9	AA815551	AA815551 Immunopap
19	31	39.7	9	ADK08339	ADK08339 Human pap
20	31	39.7	20	AAW35621	AAW35621 Immunomod
21	30	38.5	15	AAW62711	AAW62711 Streptococ
22	30	38.5	19	ABU70887	ABU70887 Human adi
23	30	38.5	20	AA833557	AA833557 5/20 natl
24	30	38.5	20	AA833108	AA833108 Peanut wt

25	30	38.5	20	AAU04770	AAU04770 Native an
26	30	38.5	20	AAU05095	AAU05095 Anaphylac
27	30	38.5	20	AAU017451	AAU017451 P fatcipa
28	30	38.5	20	ADU12247	ADU12247 PDZ ligand
29	30	38.5	20	ADW33950	ADW33950 HLA bindi
30	30	38.5	20	ADW35183	ADW35183 HLA bindi
31	30	38.5	20	ADW36547	ADW36547 HLA bindi
32	29	37.2	8	ADK08317	ADK08317 Human pap
33	29	37.2	10	AA466600	AA466600 Immunogen
34	29	37.2	10	ADK08377	ADK08377 Human pap
35	29	37.2	12	ADK08377	ADK08377 Human pap
36	29	37.2	12	ADG01812	ADG01812 Carbon bl
37	29	37.2	12	ADG01812	ADG01812 Carbon bl
38	29	37.2	13	AA946623	AA946623 Carbon bl
39	29	37.2	13	AA946623	AA946623 Carbon bl
40	29	37.2	14	ADP53453	ADP53453 Human EIV
41	29	37.2	15	AAE22995	AAE22995 MCP6 603
42	29	37.2	15	AAE22995	AAE22995 MCP6 603
43	29	37.2	15	AAE22995	AAE22995 MCP6 603
44	29	37.2	15	AAE22995	AAE22995 MCP6 603
45	29	37.2	16	AAE22995	AAE22995 MCP6 603
46	29	37.2	16	AAE22995	AAE22995 MCP6 603
47	29	37.2	16	AAE22995	AAE22995 MCP6 603
48	29	37.2	17	AAE22995	AAE22995 MCP6 603
49	28	35.9	10	AAE22995	AAE22995 MCP6 603
50	28	35.9	10	AAE22995	AAE22995 MCP6 603
51	28	35.9	11	AAE22995	AAE22995 MCP6 603
52	28	35.9	11	AAE22995	AAE22995 MCP6 603
53	28	35.9	12	AAE22995	AAE22995 MCP6 603
54	28	35.9	12	AAE22995	AAE22995 MCP6 603
55	28	35.9	14	AAE22995	AAE22995 MCP6 603
56	28	35.9	15	AAE22995	AAE22995 MCP6 603
57	28	35.9	15	AAE22995	AAE22995 MCP6 603
58	28	35.9	16	AAE22995	AAE22995 MCP6 603
59	28	35.9	16	AAE22995	AAE22995 MCP6 603
60	28	35.9	16	AAE22995	AAE22995 MCP6 603
61	28	35.9	17	AAE22995	AAE22995 MCP6 603
62	28	35.9	18	AAE22995	AAE22995 MCP6 603
63	28	35.9	19	AAE22995	AAE22995 MCP6 603
64	28	35.9	20	AAE22995	AAE22995 MCP6 603
65	28	35.9	20	AAE22995	AAE22995 MCP6 603
66	28	35.9	20	AAE22995	AAE22995 MCP6 603
67	28	35.9	20	AAE22995	AAE22995 MCP6 603
68	28	35.9	20	AAE22995	AAE22995 MCP6 603
69	28	35.9	20	AAE22995	AAE22995 MCP6 603
70	27	34.6	7	AAE22995	AAE22995 MCP6 603
71	27	34.6	7	AAE22995	AAE22995 MCP6 603
72	27	34.6	7	AAE22995	AAE22995 MCP6 603
73	27	34.6	8	AAE22995	AAE22995 MCP6 603
74	27	34.6	8	AAE22995	AAE22995 MCP6 603
75	27	34.6	11	AAE22995	AAE22995 MCP6 603
76	27	34.6	11	AAE22995	AAE22995 MCP6 603
77	27	34.6	12	AAE22995	AAE22995 MCP6 603
78	27	34.6	12	AAE22995	AAE22995 MCP6 603
79	27	34.6	12	AAE22995	AAE22995 MCP6 603
80	27	34.6	12	AAE22995	AAE22995 MCP6 603
81	27	34.6	14	AAE22995	AAE22995 MCP6 603
82	27	34.6	15	AAE22995	AAE22995 MCP6 603
83	27	34.6	15	AAE22995	AAE22995 MCP6 603
84	27	34.6	15	AAE22995	AAE22995 MCP6 603
85	27	34.6	15	AAE22995	AAE22995 MCP6 603
86	27	34.6	15	AAE22995	AAE22995 MCP6 603
87	27	34.6	15	AAE22995	AAE22995 MCP6 603
88	27	34.6	15	AAE22995	AAE22995 MCP6 603
89	27	34.6	17	AAE22995	AAE22995 MCP6 603
90	27	34.6	19	AAE22995	AAE22995 MCP6 603
91	27	34.6	20	AAE22995	AAE22995 MCP6 603
92	27	34.6	20	AAE22995	AAE22995 MCP6 603
93	27	34.6	20	AAE22995	AAE22995 MCP6 603
94	27	34.6	20	AAE22995	AAE22995 MCP6 603
95	27	34.6	20	AAE22995	AAE22995 MCP6 603
96	27	34.6	20	AAE22995	AAE22995 MCP6 603
97	27	34.6	20	AAE22995	AAE22995 MCP6 603

98	27	34.6	20	4	AAM33354	Peptide #
99	27	34.6	20	4	AAU04768	Native an
100	27	34.6	20	4	ABB24400	Protein #

## ALIGNMENTS

RESULT 1  
AAVS2510

ID AAVS2510 standard; peptide; 14 AA.

XX AAVS2510;

DT 22-FEB-2000 (first entry)

DE House dust mite allergen protein (map) A/B N-terminal fragment.

XX Mite allergen protein; map; high molecular weight; HMW-map; allergy;

KW house dust mite; IGE; immunoglobulin E; allergen; mapA; mapB;

KW hypersensitivity reaction; therapy; treatment; diagnosis; human; feline;

KW canine; veterinary; antibody; vaccine; immunisation.

XX Dermatophagoides farinae.

XX WO954349-A2.

XX 28-OCT-1999.

PF 16-APR-1999; 99WO-US008524.

XX 17-APR-1998; 98US-00062013.

PR 13-MAY-1998; 98US-0085295P.

PR 02-SEP-1998; 98US-0098909P.

XX (HESK-) HESKA CORP.

PI Mccall CA, Hunter SW, Weber ER;

DR WPI; 2000-052700/04.

XX Novel high molecular weight Dermatophagoides nucleic acid polypeptides

PT used to modify an animal's hypersensitivity to mite allergens.

XX Claim 3; Page 69; 154pp; English.

CC Sequences AAVS2510-Y5522 represent proteolytic fragments of

CC Dermatophagoides farinae high molecular weight mite allergen protein (HMW

CC -map) composition. The HMW-map composition was isolated from a D. farinae

CC homogenate by gel filtration, with each fraction being analysed for the

CC presence of proteins that bound to IGE present in mite-allergic dog

CC antiserum. The HMW-map composition comprises mapA (a 109 kD protein) and

CC mapB (98 kD). Mite allergenic proteins and peptides, and nucleic acids

CC encoding them, may be used in therapeutic compositions to modify an

CC animal's hypersensitivity reaction to mite allergens. Animals that may be

CC treated include mammals and birds, especially felines, canines, equines,

CC humans, other pets, and work or domestic animals. The proteins or

CC fragments may also be used to diagnose allergies via a skin test. The

CC proteins and peptides can also be used to raise antibodies, which have a

CC variety of potential uses. For example, they can be used as vaccines to

CC passively immunise animals against dust mite hypersensitivity, as

CC positive controls in test kits and as tools to recover desired dust mite

CC allergens from a mixture of proteins

XX Sequence 14 AA:

SQ

Query Match 100.0%; Score 78; DB 3; Length 14;

Best Local Similarity 100.0%; Pred. No. 1.3e-06;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SIKRDNDYKNPM 14

DB 1 SIKRDNDYKNPM 14

RESULT 2  
AAU96314

ID AAU96314 standard; peptide; 14 AA.

XX AAU96314;

DT 15-JUL-2002 (first entry)

DE Der HMW-map polypeptide #1.

XX Der HMW-map; American house dust mite; anti-allergic; mite; IGE;

KW mite allergenic protein; immunoglobulin E; hypersensitivity;

XX immunocomplex formation.

XX Dermatophagoides farinae.

XX WO200222807-A2.

XX 21-MAR-2002.

PF 14-SEP-2001; 2001WO-US028730.

PR 14-SEP-2000; 2000US-00662293.

XX (HESK-) HESKA CORP.

PI Mccall CA, Hunter SW, Weber ER;

DR WPI; 2002-351888/38.

XX New mite allergenic protein isolated from Dermatophagoides, designated

PT Der HMW-map protein, useful as a vaccine for treating mite allergy.

XX Claim 12; Page 70; 161pp; English.

XX The invention relates to an isolated mite allergenic protein of

CC Dermatophagoides, designated Der HMW-map protein, and its related nucleic

CC acid. The Der HMW-map protein is useful for eliciting an immune response

CC against Der HMW-map protein. The protein or a reagent comprising a non-

CC proteinaceous epitope is useful for identifying an animal (e.g., dog,

CC cat) susceptible to or having an allergic response to a mite. A

CC therapeutic composition is useful for desensitising a host animal to an

CC allergic response to a mite. The DNA and protein can be used in the

CC detection of anti-Der HMW-map antibodies in animal fluids, and inhibition

CC of immunoglobulin (Ig)E or Der HMW-map protein activity associated with a

CC disease. Antibodies that bind to Der HMW-map are useful for inhibiting

CC binding of proteins to IGE, to prevent immunocomplex formation, thus

CC reducing hypersensitivity responses to mite allergens, and as vaccines

CC against mite allergen hypersensitivity. Sequences AAU96314-AAU96342

CC represent Der HMW-map polypeptides of the invention

XX Sequence 14 AA:

SQ

Query Match 100.0%; Score 78; DB 5; Length 14;

Best Local Similarity 100.0%; Pred. No. 1.3e-06;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SIKRDNDYKNPM 14

DB 1 SIKRDNDYKNPM 14

RESULT 3

AB01203

ID AB01203 standard; peptide; 17 AA.

XX AB01203;

AC AB01203;

DT 13-SEP-2002 (first entry)

XX Human Sox-10 transcriptional regulator peptide fragment.



```

XX Human; cancer; neoplastic disease; tumour specific marker; cytostatic;
XX transcription factor.
XX
XX Homo sapiens.
XX
XX WO200240716-A2.
XX
XX 23-MAY-2002.
XX
XX
XX 13-NOV-2001; 2001WO-US043461.
XX
XX 16-NOV-2000; 2000US-0249508P.
XX
XX (CEMI-) CEMINES LLC.
XX
XX Palm K;
XX
XX WPI/ 2002-537346/57.
XX
XX Determining the presence of neoplastic molecular markers, by identifying
XX the presence of markers in host test sample using array of neoplastic
XX molecular marker specific reagents and analyzing the array of the
XX reagents.
XX
XX Example 3; Page 12; 41pp; English.
XX
XX The present invention relates to a method for determining the presence of
XX neoplastic molecular markers in a host, involving the use of neoplastic
XX molecular marker specific reagents to detect such markers and analyzing
XX the array of reagents, allowing the identification of the neoplastic
XX disease present. This can be used to determine the best treatment for
XX cancer, in particular neural cell, lung and prostate tumours. The
XX present sequence is a peptide derived from a transcription factor capable
XX of acting as a marker of the invention
XX
XX Sequence 17 AA;
XX
XX Query Match 47.4%; Score 37; DB 5; Length 17;
XX Best Local Similarity 54.5%; Pred. No. 25;
XX Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0
XX
XX 3 KRDHNDYKMP 13
XX :|:|:|
XX 1 KKDHPDYKXP 11
XX
XX
XX RESULT 4
XX AAB33556
XX ID AAB33556 standard; peptide; 20 AA.
XX
XX AAB33556;
XX
XX 12-SEP-2003 (revised)
XX DT 22-JAN-2001 (first entry)
XX
XX 5/20 native Ara h 2 peptide #10.
XX
XX Allergy; allergic reaction; allergen; anaphylactic antigen; peanut;
XX Ara h 1; Ara h 2; Ara h 3; epitope; binding; immunoglobulin E; IgE;
XX food antigen; sensitising; immune response; anti-allergic.
XX
XX Arachis hypogaea.
XX
XX WO200051647-A2.
XX
XX 08-SEP-2000.
XX
XX 03-MAR-2000; 2000WO-US005655.
XX
XX 03-MAR-1999; 99US-0122960P.
XX PR 06-DEC-1999; 99US-00455294.
XX

```

PA	(MOUN ) MOUNT SINAI SCHOOL MEDICINE.
XX	
PI	Sampson HA;
XX	
DR	WPI; 2000-611341/58.
XX	
PT	Non-human animal sensitized to an antigen, useful as an animal model for
PT	studying allergic reactions to allergens, such as those in food and in
PT	the environment.
XX	
PS	Example 5; Page 62; 124pp; English.
XX	
CC	The present invention describes an animal model which can be used for
CC	studying allergic reactions to allergens. The animal is sensitised to a
CC	selected antigen by administering the antigen itself or a nucleic acid
CC	encoding the antigen, where preferably the antigen is an anaphylactic
CC	antigen. The sensitised animal can then be used to screen for compounds
CC	which may help to prevent, ameliorate, or cure allergic conditions in
CC	humans. The animal model can be used for studying allergic reactions to
CC	allergens, such as those in food (peanuts, fruit, berry, nut, bean, milk,
CC	dairy products), or in the environment (weed pollen, grass pollen, tree
CC	pollen, mite, animal, animal dander, fungal, and insect antigens).
CC	AA833478 to AA833601 represent sequences which are used in examples from
CC	the present invention to specifically examine the peanut allergy, and the
CC	peanut anaphylactic antigens Ara h 1 to 3. (Updated on 12-SEP-2003 to
CC	standardise OS field)
XX	
SQ	Sequence 20 AA;
XX	
Query Match	43.6%; Score 34; DB 3; Length 20;
Best Local Similarity	41.7%; Pred. No. 99;
Matches 5;	Conservative 4; Mismatches 3; Indels 0; Gaps 0;
Oy	2 IKRDNDYSKNP 13
	:: : ::
Db	5 IQRDEDSYBRDP 16
XX	
RESULT 5	
AA823107	
ID	AA823107 standard; peptide; 20 AA.
XX	
AC	AA823107;
XX	
DT	29-JAN-2001 (first entry)
XX	
DE	Peanut wild-type Ara h 2 20 residue peptide #10.
XX	
KW	Ara h 2 protein; peanut; epitope; antigen; allergy; anaphylaxis; asthma;
XX	immunomodulation; unmethyated CpG oligonucleotide; anti-allergic.
XX	
OS	Arachis hypogaea.
XX	
PN	WO200054803-A2.
XX	
PD	21-SEP-2000.
XX	
PE	16-MAR-2000; 2000MO-US007213.
XX	
PR	16-MAR-1999; 99US-0124595P.
XX	
PR	17-MAR-1999; 99US-0125071P.
XX	
PA	(PANA-) PANACEA PHARM LLC.
XX	
PI	Sosin HB, Caplan MJ;
XX	
DR	WPI; 2000-628168/60.
XX	
PT	Immunostimulatory composition for treating or preventing an allergic
PT	reaction leading to conditions such as asthma or anaphylaxis, comprises
PT	oligonucleotides with unmethylated CpG sequences and antigens derived
PT	from allergens.
XX	

PS Example 3; Page 67; 103pp; English.

XX The invention relates to an immunomodulatory composition comprising a Cpg

CC oligonucleotide of the sequence 5' purine-purine-C-g-pyrimidine-

CC pyrimidine 3', where C and G are unethylyated, and at least one antigen

CC derived from an allergen that causes anaphylaxis. The composition is

CC useful for treating allergy in an individual. The composition prevents or

CC modulates an individual's immune response to an antigen which leads to

CC asthma and/or anaphylaxis. Individuals susceptible to anaphylactic shock

CC upon exposure to allergens from foods (e.g., peanut), venom or rubber may

CC be treated using the composition. Sequences ABB23098-B23125 represent a

CC series of 20-residue peptides from wild-type peanut Ara h 2 protein used

CC in an exemplification of the invention

XX

SQ Sequence 20 AA;

Query Match 43.6%; Score 34; DB 3; Length 20;

Best Local Similarity 41.7%; Pred. No. 99;

Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 2 IKRDHNDYSKNP 13

DB 5 IQRDEDSYERDP 16

RESULT 6

AAU04769

ID AAU04769 standard; peptide; 20 AA.

XX

AC AAU04769;

XX

DT 23-OCT-2001 (first entry)

XX

DE Native anaphylactic antigen Ara h 2 peptide #10.

XX

KW Ara h 2; anaphylactic antigen; immunoglobulin E; IgE; immunogenic;

KW allergy; mast cell; basophil; mouse; epitope.

XX

OS Mus sp.

XX

PN WO200140264-A2.

XX

PD 07-JUN-2001.

XX

PF 06-DEC-2000; 2000WO-US033124.

XX

PR 06-DEC-1999; 99US-00455294.

PR 23-JUN-2000; 2000US-0213765P.

PR 27-SEP-2000; 2000US-0235797P.

XX

PA (PANA-) PANACEA PHARM LLC.

PA (UYAR-) UNIV ARKANSAS.

PA (MOUN) MOUNT SINAI SCHOOL MEDICINE NEW YORK.

PI Bannon GA, Burks WA, Caplan MJ, Sampson H, Sosin H;

XX

DR WPI; 2001-381378/40.

XX

PT Antigenic fragments useful for reducing anaphylactic risk and reducing

PT the severity and/or number of allergic symptoms in individuals sensitive

PT to antigens, have reduced ability to bind Immunoglobulin E.

XX

PS Claim 40; Page 52; 100pp; English.

XX

CC The sequence represents the amino acid sequence of native anaphylactic

CC antigen Ara h 2 peptide #10. Ara h 2 is an anaphylactic antigen (A) which

CC was used to design antigenic peptides having a reduced ability to bind

CC IGE as compared with the intact (A), or having a sequence substantially

CC identical to a portion of sequence of an antigen that includes at least

CC one IGE binding site, where at least one IGE binding site of the peptide

CC is altered. The antigenic peptides are used in a composition which is

CC useful for reducing risk or severity of allergic reaction to an antigen.

CC This is done by identifying an individual at risk of allergic reaction to

CC an antigen by identifying prior display of allergic symptoms when exposed

CC to the antigen, or a familial relationship with an individual who

CC previously displayed allergic symptoms when exposed to the antigen.

CC Following this an antigen-specific IGE present on one or more mast cells

CC or basophils in the individual's serum is identified. The individual is

CC then contacted with a peptide corresponding to a portion of the antigen,

CC which is selected, formulated, and delivered so that binding of the

CC peptide to antigen-specific IGE is reduced as compared with IGE binding

CC of intact antigen. The composition is also useful for treating and

CC preventing allergic reactions

XX

SQ Sequence 20 AA;

Query Match 43.6%; Score 34; DB 4; Length 20;

Best Local Similarity 41.7%; Pred. No. 99;

Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 2 IKRDHNDYSKNP 13

DB 5 IQRDEDSYERDP 16

RESULT 7

AAU05094

ID AAU05094 standard; peptide; 20 AA.

XX

AC AAU05094;

XX

DT 24-OCT-2001 (first entry)

XX

DE Anaphylactic peanut antigen Ara h 2, native peptide #10.

XX

KW Anaphylactic antigen; Ara h 2; peanut; desensitisation; antigen; allergy;

KW immunotherapy; rush immunotherapy; anaphylaxis; asthma; food allergen;

KW milk allergen; shellfish allergen; latex; drug; environmental allergen;

KW grass pollen; ovalbumin; insect venom; peanut oil; immunoglobulin E; IGE.

XX

OS Arachis sp.

XX

PN WO200139799-A2.

XX

PD 07-JUN-2001.

XX

PF 06-DEC-2000; 2000WO-US033125.

XX

PR 06-DEC-1999; 99US-00455294.

PR 23-JUN-2000; 2000US-0213765P.

PR 27-SEP-2000; 2000US-0235797P.

XX

PA (PANA-) PANACEA PHARM LLC.

PA Caplan M;

PI

XX

DR WPI; 2001-408258/43.

XX

PT Preventing allergic response against antigens, e.g. food and

PT environmental allergens such as peanut allergen or grass pollen, latex or

PT drug, comprises administering agent, e.g. a peptide, that blocks antigen

PT binding sites on offending IGE.

XX

PS Example 2; Page 46; 76pp; English.

XX

CC The sequence represents the amino acid sequence of anaphylactic peanut

CC antigen Ara h 2, native peptide #10. The peptide is used in active or

CC passive desensitisation of an individual to an antigen; for alleviating

CC or preventing allergic reactions and for decreasing the risk of allergic

CC reactions during immunotherapy or rush immunotherapy, anaphylaxis and

CC asthma. The antigen may be a food allergen (e.g. peanut or milk

CC allergen), shellfish allergen, environmental allergen (e.g. grass pollen

CC or tree pollen), latex, drug, pollen, ovalbumin, an insect venom antigen

CC or predominantly linear epitopes. The protein is useful for protecting an

CC individual against subsequent inadvertent or intentional exposure to

CC antigen, e.g. receiving blocking agent before eating a chocolate bar

CC which may inadvertently contain peanut components or before eating foods  
CC prepared using peanut oil. Administration of the blocking agent does not  
CC result in cross-linking of anti-antigenic IgE. After exposure to the  
CC agent, the individual's antigen sensitivity is at least temporarily  
CC reduced. Only those IgE molecules that bind the offending antigen and  
CC contribute to the risk of an allergic response are blocked

XX Sequence 20 AA;

Query Match 43.6%; Score 34; DB 4; Length 20;  
Best Local Similarity 41.7%; Pred. No. 99;  
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;  
QY 2 IKRDNDYSKNP 13  
|:|:|:|:|:  
Db 5 IQRDSDSYERDP 16

## RESULT 8

AAW24076 standard; peptide; 12 AA.

AC AAW24076;  
DT 16-OCT-2003 (revised)  
DT 25-MAR-2003 (revised)  
DT 17-NOV-1997 (first entry)  
XX PD498 alkaline protease peptide fragment B.  
DE PD498 alkaline protease; heterologous protein production; detergent;  
KM vector; promoter; signal sequence; primer; amplification.

XX Bacillus sp; strain PD498.

PN MO9634963-AA.

XX 07-NOV-1996.

PP 01-MAY-1996; 96MO-US006097.

PR 03-MAY-1995; 95US-00434255.

PA (NOVO ) NOVO NORDISK BIOTECH INC.  
(NOVO ) NOVO-NORDISK AS.

PI Sloma AP, Outtrup H, Dammann CHG, Aaslyng DA;

XX WPI; 1996-506165/50.

PT Alkaline protease nucleic acid coding sequence - used to develop prods  
PT for use in detergents and for the recombinant expression of  
PT polypeptide(s).

PS Example 6.2; Page 35; 67pp; English.

XX AAW24075-76 are peptide fragments of a protease, used to design  
CC degenerate primers (AAW185623-24) for the amplification of a 180 bp gene  
CC fragment. The gene fragment can be used to isolate a full length gene  
CC encoding the protease, which was isolated from Bacillus sp. PD498. The  
CC protease has the properties: (a) a molecular weight of about 34 kD as  
CC determined by SDS-PAGE; (b) pI of about 9.3; (c) pH optimum in the range  
CC of pH 9-11 at about 25 degrees C and with casein as substrate; (d)  
CC temperature optimum in the range of about 40-55 degrees C at a pH of  
CC about 9.5 and with casein as substrate; and (e) obtainable from Bacillus  
CC sp. Group I. This alkaline protease is useful in detergent compositions.  
CC The promoter and signal sequences of the protease gene and its encoded  
CC product, can be used for the recombinant expression of heterologous  
CC polypeptides. In particular nucleic acid constructs and vectors for this  
CC purpose are also claimed. NB. The specification is unclear as to the  
CC numbering of the sequences in the sequence ID listing. (Updated on 25-MAR  
CC -2003 to correct PI field.) (Updated on 16-OCT-2003 to standardise OS  
CC field)

XX Sequence 12 AA;

Query Match 42.3%; Score 33; DB 2; Length 12;  
Best Local Similarity 60.0%; Pred. No. 81;  
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 DHRDYSKNPM 14  
|:|:|:|:|:  
Db 2 DFRDYDNNPM 11

## RESULT 9

ADK08378 standard; peptide; 10 AA.

AC ADK08378;

DT 06-MAY-2004 (first entry)

DE Human papillomavirus peptide #433.

XX pathogenic virus; alternative reading frame; antigenic determinant;  
KM viricide; vaccine; therapeutic agent; infection; HPV.

OS Human papillomavirus.

PN WO2004011650-A2.

PP 05-FEB-2004.

PR 24-JUL-2003; 2003MO-EP008112.

PR 24-JUL-2002; 2002AT-00001124.

PR 11-JUL-2003; 2003EP-00450171.

PA (INTE-) INTERCELL AG.

PI Matner F, Schmidt W, Habel A;

DR WPI; 2004-169243/16.

PT New polypeptide encoded by an alternative reading frame of a pathogenic  
PT virus comprising an antigenic determinant, useful for treating or  
PT preventing an infection with the pathogenic virus.

PS Claim 18; Page 178; 220pp; English.

XX This invention relates to a novel polypeptide encoded by an alternative  
CC reading frame of a pathogenic virus, where the polypeptide starts with a  
CC methionine amino acid residue, which comprises an antigenic determinant  
CC and more than 7 amino acid residues. The invention may be useful for the  
CC production of compounds with a viricide activity or the development of a  
CC vaccine. The polypeptide or its fragments may be useful as a therapeutic  
CC agent. It is also useful for the manufacture of a medicament for treating  
CC or preventing an infection with the pathogenic virus. The present  
CC sequence is that of a human papillomavirus (HPV) epitope peptide of the  
CC invention.

XX Sequence 10 AA;

Query Match 41.0%; Score 32; DB 8; Length 10;  
Best Local Similarity 66.7%; Pred. No. 98;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 RDNDYSKN 12  
|:|:|:|:|:  
Db 2 RDHDYWKH 10

## RESULT 10

AAW30715 standard; peptide; 11 AA.

```
XX AC AAR30715;
XX XX
XX DT 27-AUG-2003 (revised)
XX DT 25-MAR-2003 (revised)
XX DT 19-MAY-1993 (first entry)
XX DE HPV 16 E2-1170 peptide (amino acids 25-35) .
XX XX
XX KM HPV; E1; E2; ELISA; diagnosis; vaccine; antibody.
XX OS Human papillomavirus.
XX PN BP523395-A2.
XX PD 20-JAN-1993.
XX PF 20-JUN-1992; 92EP-00110430.
XX PR 18-JUL-1991; 91DE-04123760.
XX PA (BEHV ) BEHRINGMERKE AG.
XX PI Mueller M, Giesmann L;
XX DR WPI; 1993-019476/03.
XX PT Peptide(s) corresp. to regions of HPV 16 E1 and E2 proteins - useful for
XX PT prevention, diagnosis and treatment of cervical tumours.
XX PS Claim 2; Page 13; 20pp; German.
XX CC The sero-reactive region is useful in the prevention, diagnosis and
XX CC therapy of HPV16-derived tumours and in the development of an ELISA
XX CC (Updated on 25-MAR-2003 to correct PN field.) (Updated on 27-AUG-2003 to
XX CC correct OS field.)
XX SQ Sequence 11 AA;

Query Match          41.0%; Score 32; DB 2; Length 11;
Best Local Similarity 66.7%; Pred. No. 1.1e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 RDHNDYSKN 12
   |||||
Db 3 RDHIDYMKH 11

RESULT 11
AAW30009
ID AAW30009 standard; peptide; 11 AA.
XX
XX AC AAW30009;
XX
XX DT 17-OCT-2003 (revised)
XX DT 07-APR-1998 (first entry)
XX DE CAEV immunogen pol 1033.
XX XX
XX KM Immunogen; CAEV; caprine arthritis encephalomyelitis virus; HIV vaccine;
XX KM protective immune response; human; HIV-1; B-lymphocyte; T-lymphocyte;
XX KM diagnosis.
XX OS Caprine arthritis-encephalitis virus.
XX PN WO9733615-A2.
XX PD 18-SEP-1997.
XX PF 14-MAR-1997; 97WO-US004020.
XX PR 15-MAR-1996; 96US-00616854.
XX PR 15-MAR-1996; 96US-00616855.
```

```
XX XX
XX PA (UYSC-) UNTV SOUTHERN CALIFORNIA.
XX PI Douvas A, Ehresmann G;
XX DR WPI; 1997-470647/43.
XX XX
XX PT Vaccine containing caprine arthritis-encephalomyelitis virus immunogen -
XX PT used to generate immune response against CAEV that is cross-reactive with
XX PT human immunodeficiency virus.
XX PS Claim 4; Page 8; 71pp; English.
XX XX
XX CC This sequence represents a caprine arthritis encephalomyelitis virus
XX CC (CAEV) immunogen. This sequence, along with a carrier, can be used as a
XX CC vaccine of the invention. The immunogen is used to stimulate protective
XX CC immune responses against CAEV which, in humans, are cross-reactive with
XX CC human immunodeficiency virus (HIV-1), i.e. it protects against HIV-1
XX CC infection or reduces severity of existing infections. An immune response
XX CC can also be induced by exposure, particularly in vitro, of T- or B-
XX CC lymphocytes to the immunogen, followed by expansion of the stimulated
XX CC cells and return to the patient. Assays using CAEV specific antibodies
XX CC recognising this sequence are used for diagnosis, to screen blood for
XX CC contamination by CAEV and to monitor the effect of vaccination. CAEV-
XX CC based vaccines can protect against HIV without the risks attendant on
XX CC using HIV-based vaccines. The assays are simple, inexpensive and suitable
XX CC for large scale screening. (Updated on 17-OCT-2003 to standardise OS
XX CC field)
XX SQ Sequence 11 AA;

Query Match          41.0%; Score 32; DB 2; Length 11;
Best Local Similarity 60.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 KRDNHYSKN 12
   |||||
Db 1 KRINKYKNKN 10

RESULT 12
AAB86994
ID AAB86994 standard; peptide; 11 AA.
XX
XX AC AAB86994;
XX
XX DT 09-JAN-2002 (first entry)
XX DE HPV 16 E2 protein fragment SEQ ID 3.
XX XX
XX KM Sero-reactive; E2 protein; antiviral; antitumor; vaccine; infection;
XX KM cancer; detection.
XX OS Human papillomavirus.
XX PN EP136500-A2.
XX PD 26-SEP-2001.
XX PF 20-JUN-1992; 2001EP-00102056.
XX PR 18-JUL-1991; 91DE-04123760.
XX PR 20-JUN-1992; 92EP-00110430.
XX PA (DADE-) DADE BEHRING MARBURG GMBH.
XX PI Mueller M, Giesmann L;
XX DR WPI; 2001-591567/67.
XX PT Sero-reactive regions of human papilloma virus 16 E2 protein, and the
XX PT specific antibodies, useful in vaccines and diagnosis.
```

PS Claim 1, Page 10, 17pp; German.  
XX  
CC This invention describes novel seroreactive regions (A) from the E2  
CC protein of human papilloma virus 16 (HPV 16). The products of the  
CC invention have antiviral and antitumor activity. Peptides (I) that  
CC include at least one (A) are used (i) to prepare vaccines against HPV 16  
CC infection (and associated cancers) and (ii) for diagnosis (detection of  
CC E2-specific antibodies). Monoclonal antibodies raised against (I) are  
CC useful for diagnosis, by detecting HPV 16-specific E2 protein. This  
CC sequence represents a fragment of the human papillomavirus E2 protein  
CC which is used in the method of the invention  
CC  
SQ Sequence 11 AA;  
XX  
Query Match 41.0%; Score 32; DB 4; Length 11;  
Best Local Similarity 66.7%; Pred. No. 1.1e+02;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 4 RDHNDVSKN 12  
DB 3 RDHIDYWKH 11  
XX  
RESULT 13  
ADU68123  
ID ADU68123 standard; peptide; 15 AA.  
XX  
AC ADU68123;  
XX  
DT 10-FEB-2005 (first entry)  
XX  
DE Human papillomavirus-derived epitope peptide SeqID82.  
XX  
KM epitope mapping; T-cell; antiviral; cytostatic; vaccine;  
KM vaccine, antiviral; benign tumor; tumor.  
XX  
OS Human papillomavirus.  
XX  
PN WO2004098497-A2.  
XX  
PD 18-NOV-2004.  
XX  
PF 23-APR-2004; 2004WO-US012652.  
XX  
PR 28-APR-2003; 2003US-0466235P.  
XX  
PA (GSMV ) GENENCOR INT INC.  
XX  
PI Babe LM, De Young LM, Harding FA, Huang MTF, Power SD;  
PI Stickler M;  
XX  
DR WPI; 2004-813965/80.  
XX  
XX  
PT Identifying CD4+ human papillomavirus (HPV) epitopes or determining T-  
PT cell epitope of HPV strain, useful in prophylactic/therapeutic vaccines,  
PT by combining dendritic cells, CD4+ and/or CD8+ T-cells with pepset of  
PT peptides from HPV.  
XX  
PS Claim 4; SEQ ID NO 82; 56pp; English.  
XX  
CC This invention relates to a novel method of identifying CD4+ human  
CC papillomavirus (HPV) epitopes or determining a T-cell epitope of a HPV  
CC strain. The method comprises combining a solution of differentiated  
CC dendritic cells and naive CD4+ and/or CD8+ T-cells with a set of peptides  
CC from the HPV (which comprises the T-cell epitope) and measuring T-cell  
CC proliferation. The invention may be useful for the production of T-cell  
CC compounds with an antiviral or cytostatic activity. The method or the  
CC modified epitopes are useful in prophylactic and/or therapeutic vaccines,  
CC as means for the development of HPV vaccines for the prevention of  
CC infection with high-risk HPV strains, or as means for the development of  
CC therapeutic vaccines against high-risk HPV types for use in the  
CC prevention of the development of benign and/or malignant tumors in  
CC infected individuals. The present sequence is that of a human

CC papillomavirus-derived epitope peptide which was identified using the  
CC method of the invention.  
XX  
SQ Sequence 15 AA;  
XX  
Query Match 41.0%; Score 32; DB 8; Length 15;  
Best Local Similarity 66.7%; Pred. No. 1.6e+02;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 4 RDHNDVSKN 12  
DB 6 RDHIDYWKH 14  
XX  
RESULT 14  
ADV11513  
ID ADV11513 standard; peptide; 15 AA.  
XX  
AC ADV11513;  
XX  
DT 24-FEB-2005 (first entry)  
XX  
DE HPV type 16 E2 protein CD4+ T-cell epitope, SEQ ID No:82.  
XX  
KM Papillomavirus infection; CD4+ T-cell; T-lymphocyte; E2;  
KM immune modulation; vaccine; tumor suppressor; infection; virucide.  
XX  
OS Human papillomavirus type 16.  
XX  
PN WO2004105681-A2.  
XX  
PD 09-DEC-2004.  
XX  
PF 23-APR-2004; 2004WO-US012650.  
XX  
PR 28-APR-2003; 2003US-0466235P.  
XX  
PA (INNO-) INNOGENETICS NV.  
XX  
PI Babe LM, De Young LM, Harding FA, Huang MTF, Power SD;  
PI Stickler M;  
XX  
DR WPI; 2005-021230/02.  
XX  
XX  
PT Novel isolated human papillomavirus epitope (HPV) e.g., HPV B6.16 or HPV  
PT E7.16 epitope, useful for producing medicament for inducing immune  
PT response against HPV.  
XX  
PS Claim 1; SEQ ID NO 82; 56pp; English.  
XX  
XX  
CC The invention relates to isolated human papillomavirus (HPV) epitopes  
CC given as SEQ ID Nos 1-109 in the specification. The epitopes are CD4+ T-  
CC cell epitopes in B6, B7 and B2 proteins isolated from various strains of  
CC HPV. Also claimed are: a polynucleotide comprising one or more of the  
CC nucleic acid sequences encoding an epitope of the invention, a vector  
CC comprising the above polynucleotide, a polypeptide encoded by the above  
CC polynucleotide, a cell comprising the above polynucleotide, a composition  
CC comprising the above polypeptide, one or more peptide that has a HPV  
CC epitope or one or more nucleic acid that encodes the HPV epitope, and a  
CC vaccine composition comprising a HPV epitope or one or more nucleic acid  
CC that encodes a HPV epitope. The HPV epitopes of the invention are useful  
CC for producing a medicament for inducing an immune response (e.g. an  
CC antibody-mediated response or cell-mediated response) directed against  
CC one or more strain of HPV. The epitopes are useful in the development of  
CC HPV vaccines (particularly multivalent vaccines) for the prevention of  
CC infection with high-risk HPV strains. The HPV epitopes are useful in  
CC prophylactic and therapeutic vaccines against HPV. The therapeutic  
CC vaccines can be used to prevent the development of benign and/or  
CC malignant tumors in HPV infected individuals. This sequence represents a  
CC HPV epitope of the invention.  
XX  
SQ Sequence 15 AA;

Query Match 41.0%; Score 32; DB 9; Length 15;  
 Best Local Similarity 66.7%; Pred. No. 1.6e+02;  
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 RDHNDYSKN 12  
 ||| |||  
 DB 6 RDHIDYWKH 14

## RESULT 15

ABW02637  
 ID ABW02637 standard; peptide; 17 AA.

AC ABW02637;

DT 12-FEB-2004 (first entry)

DE Human oestrogen receptor (ER) alpha mutant peptide, ER50.1.

KM Tamoxifen activated system; TAS; 4-hydroxytamoxifen; OHT; gene therapy;

KM oestrogen receptor; ER; fundamental research; transgenic; biomedical;

OS Homo sapiens.

OS Synthetic.

Key Location/Qualifiers

FT Misc-difference 16..17 /note="Encoded by GAC"

PN US003199022-A1.

PD 23-OCT-2003.

PF 11-MAR-2002; 2002US-00095373.

PR 11-MAR-2002; 2002US-00095373.

PA (UNIT ) UNIV ILLINOIS FOUND.

PI Mao C, Shapiro DJ;

DR WPI; 2003-852787/79.

PS N-PSDB; AAD64546.

PT New isolated polynucleotide useful for gene therapy applications (e.g. in

PT treating breast cancer), in vivo and in vitro gene expression, in

PT producing bioactive or toxic polypeptides, in research, or in producing

PT transgenic animals.

XX Claim 12; SEQ ID NO 22; 0bp; English.

CC The invention relates to tamoxifen activated system (TAS) and 4-  
 CC hydroxytamoxifen (OHT) activated system for regulated production of  
 CC proteins in eukaryotic cells. TAS includes mutant oestrogen receptors  
 CC (ERs) and chimeras thereof. The invention is useful in gene therapy (e.g.  
 CC in treating breast cancer) or in vivo and in vitro gene expression, in  
 CC producing bioactive, toxic, recombinant polypeptides in mammalian cells,  
 CC in biomedical and fundamental research, or in producing transgenic  
 CC animals. The transgenic animals may be used as disease models, in  
 CC studying the function and/or activity of a polypeptide, or in identifying  
 CC and/or evaluating modulators of a polypeptide activity. The present  
 CC sequence is human ERalpha mutant peptide used in TAS

XX Sequence 17 AA;

QY Query Match 41.0%; Score 32; DB 7; Length 17;  
 Best Local Similarity 71.4%; Pred. No. 1.8e+02;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 KRDNNDY 9  
 ||: ||||  
 DB 11 KOGHNDY 17

## RESULT 16

AAV52521  
 ID AAV52521 standard; peptide; 18 AA.

AC AAV52521;

DT 22-FEB-2000 (first entry)

DE House dust mite allergen protein (map) A/B fragment map(11).

KM Mite allergen protein; map; high molecular weight; HMW-map; allergy;

KM house dust mite; IGE; immunoglobulin E; allergen; mapA; mapB;

KM hypersensitivity reaction; therapy; treatment; diagnosis; human; feline;

OS canine; veterinary; antibody; vaccine; immunisation.

OS Dermatophagoides farinae.

PN MO9954349-A2.

PD 28-OCT-1999.

PF 16-APR-1999; 99WO-US008524.

PR 17-APR-1998; 98US-00062013.

PR 13-MAY-1998; 98US-0085295P.

PR 02-SEP-1998; 98US-0098909P.

PA (HESK-) HESKA CORP.

PI McCall CA, Hunter SW, Weber ER;

DR WPI; 2000-052700/04.

PS Novel high molecular weight Dermatophagoides nucleic acid polypeptides

PT used to modify an animals' hypersensitivity to mite allergens.

XX Claim 3; Page 70; 154bp; English.

CC Sequences AAV52510-Y52522 represent proteolytic fragments of  
 CC Dermatophagoides farinae high molecular weight mite allergen protein (HMW  
 CC map) composition. The HMW-map composition was isolated from a D. farinae  
 CC homogenate by gel filtration, with each fraction being analysed for the  
 CC presence of proteins that bound to IGE present in mite-allergic dog  
 CC antisera. The HMW-map composition comprises mapA (a 109 kD protein) and  
 CC mapB (98 kD). Mite allergen proteins and peptides, and nucleic acids  
 CC encoding them, may be used in therapeutic compositions to modify an  
 CC animal's hypersensitivity reaction to mite allergens. Animals that may be  
 CC treated include mammals and birds, especially felines, canines, equines,  
 CC humans, other pets, and work or domestic animals. The proteins or  
 CC fragments may also be used to diagnose allergies via a skin test. The  
 CC proteins and peptides can also be used to raise antibodies, which have a  
 CC variety of potential uses. For example, they can be used as vaccines to  
 CC passively immunise animals against dust mite hypersensitivity, as  
 CC positive controls in test kits and as tools to recover desired dust mite  
 CC allergens from a mixture of proteins

XX Sequence 18 AA;

QY Query Match 41.0%; Score 32; DB 3; Length 18;  
 Best Local Similarity 83.3%; Pred. No. 2e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 DYSKNP 13  
 ||: ||||  
 DB 1 DYAKNP 6

RESULT 17  
 AAU96325  
 ID AAU96325 standard; peptide; 18 AA.



PS Claim 18; Page 177; 220pp; English.

XX This invention relates to a novel polypeptide encoded by an alternative  
CC reading frame of a pathogenic virus, where the polypeptide starts with a  
CC methionine amino acid residue, which comprises an antigenic determinant  
CC and more than 7 amino acid residues. The invention may be useful for the  
CC production of compounds with a virucide activity or the development of a  
CC vaccine. The polypeptide or its fragments may be useful as a therapeutic  
CC agent. It is also useful for the manufacture of a medicament for treating  
CC or preventing an infection with the pathogenic virus. The present  
CC sequence is that of a human papillomavirus (HPV) epitope peptide of the  
CC invention.

XX Sequence 9 AA;

Query Match 39.7%; Score 31; DB 8; Length 9;

Best Local Similarity 75.0%; Pred. No. 2e+06; Mismatches 2; Indels 0; Gaps 0;

Matches 6; Conservative 0; Indels 0; Gaps 0;  
Qy 4 RDHNDYSK 11  
Db 2 RDHIDYWK 9

RESULT 20

AAW35621 standard; peptide; 20 AA.

XX AAW35621;

XX 13-MAY-1998 (first entry)

DE Immunomodulatory peptide #12 of vespid antigen 5.

KM Immunomodulatory peptide; vespid antigen 5; immunogenic; allergy;  
KW vespid venom; white face hornet wasp.

OS Dolichovespula maculata.

OS Synthetic.

PN WO9733910-A1.

PD 18-SEP-1997.

PF 11-MAR-1997; 97WO-US003753.

PR 11-MAR-1996; 96US-00614935.

PA (UYRQ ) UNIV ROCKEFELLER.

PI Kling TP;

DR WPI, 1997-470817/43.

PT Vespid venom antigen 5 peptide fragments - useful to treat or diagnose  
PT vespid venom sensitivity.

PS Claim 2; Page 50; 73pp; English.

XX This sequence represents a specifically claimed peptide which is derived  
CC from vespid venom antigen 5 (VVS) and is antigenic for T cell  
CC proliferation in mice immunised with VVS. The peptide can be used to  
CC treat or diagnose vespid venom sensitivity e.g. to Dolichovespula  
CC maculate (white face hornet), Vespa vulgaris (yellowjacket), V.  
CC maculifrons (yellowjacket), D. areolaris (yellow hornet), Polistes  
CC annularis (wasp), P. exclamans (wasp), V. circo (European hornet), V.  
CC flavopilosa (yellowjacket), V. germanica (yellowjacket), V. pennsylvanica  
CC (yellowjacket), V. squamosa (yellowjacket), V. vidua (yellowjacket) and  
CC P. fuscatus (paperwasp)

XX Sequence 20 AA;

Query Match 39.7%; Score 31; DB 2; Length 20;

Best Local Similarity 45.5%; Pred. No. 3.3e+02;  
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 2 IKRDNDYSKN 12  
Db 4 IKRDNDYRQN 14

RESULT 21

AAW62711 standard; protein; 15 AA.

XX AAW62711;

DT 09-NOV-1998 (first entry)

DE Streptococcus pneumoniae polypeptide.

KM Polypeptide; ORF, open reading frame; infection; bacterial;

KW streptococcal; bacteremia; diagnosis; prophylaxis.

OS Streptococcus pneumoniae.

PN WO9823631-A1.

PD 04-JUN-1998.

PF 24-NOV-1997; 97WO-US021976.

PR 27-NOV-1996; 96US-0031879P.

PA (SMIK ) SMITHKLINE BEECHAM CORP.

PA (SMIK ) SMITHKLINE BEECHAM PLC.

PI Black MT, Hodgson JE, Knowles DC, Lonetto MA, Nicholas RO;  
PI Reid RH, Zarlos PN;

DR WPI, 1998-322654/28.

PT Streptococcus pneumoniae polynucleotides - useful for developing products  
PT for diagnosis, prevention and treatment of infections e.g. pneumonia,  
PT bacteremia, meningitis or endocarditis.

PS Claim 5; Page 32; 181pp; English.

XX The sequence is that of a Streptococcal polypeptide. The polypeptide can  
CC potentially be used for the diagnosis and prevention of bacterial  
CC infections, especially sp infection. It may be used for the treatment of  
CC diseases such as otitis media, conjunctivitis, pneumonia, bacteremia,  
CC meningitis, sinusitis, pleural empyema, endocarditis or infection of the  
CC cerebrospinal fluid

XX Sequence 15 AA;

Query Match 38.5%; Score 30; DB 2; Length 15;  
Best Local Similarity 55.6%; Pred. No. 3.5e+02;

Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 SIKRDNDY 9  
Db 2 AINRFHNDP 10

RESULT 22

ABU70887 standard; protein; 19 AA.

XX ABU70887;

DT 10-JUN-2003 (first entry)

DE Human adipocyte selected interacting domain, SID, #518.



KM Human; prey; adipocyte; SID; selected interacting domain; anorectic;  
 KM antidiabetic; protein-protein interaction; diabetes;  
 KM yeast 2-hybrid assay; metabolic disorder; obesity.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200286122-A2.  
 XX  
 PD 31-OCT-2002.  
 XX  
 PF 14-MAR-2002; 2002WO-BP003768.  
 XX  
 PR 14-MAR-2001; 2001US-0275734P.  
 XX  
 PA (HYBR-) HYBRGENICS.  
 XX  
 PI Legrain P, Davlet L;  
 DR WPI; 2003-103412/09.  
 DR N-PSDB; ACA57431.  
 XX  
 PT New complex between two interacting proteins in adipocyte cells, useful  
 PT for identifying selected interacting domains that modulate protein  
 PT interactions, or for preventing or treating metabolic disorders such as  
 PT obesity or diabetes.  
 XX  
 PS Claim 6, Page 279, 382pp; English.  
 XX  
 CC The invention relates to a complex between two interacting proteins in  
 CC adipocyte cells, given in the specification. The proteins are identified  
 CC by selecting a bait protein from a known adipocyte marker and then  
 CC performing a yeast 2-hybrid selection to isolate prey proteins encoded by  
 CC members of an adipocyte cDNA library. The proteins are designated SID  
 CC (RWM) (selected interacting domains) proteins. Also included are a  
 CC polynucleotide encoding a polypeptide in the adipocyte cells, a  
 CC recombinant host cell expressing at least one of the interacting  
 CC polypeptides of the complex, selecting a modulating compound in adipocyte  
 CC cells, a SID (RWM) polypeptide comprising any of the 738 amino acid  
 CC sequences given in the specification (including its fragment or variant),  
 CC a SID (RWM) polynucleotide comprising any of the 738 nucleotide sequences  
 CC given in the specification (including its fragment or variant), a vector  
 CC comprising the SID (RWM) polynucleotide, a recombinant host cell  
 CC comprising the vector, a protein chip comprising the polypeptides and a  
 CC record comprising all or part of the data, listed in the specification.  
 CC The complex, polypeptides, polynucleotides and compounds are useful for  
 CC preventing or treating metabolic disorders such as obesity or diabetes.  
 CC The polynucleotides are useful as probes or primers. The complex is  
 CC particularly useful for identifying selected interacting domains (SID  
 CC (RWM)) for screening drugs that modulate the protein interaction, thus  
 CC exhibiting the therapeutic effect. The present sequence represents a SID  
 CC (prey) protein of the invention  
 XX  
 SQ Sequence 19 AA;  
 XX  
 XX  
 Query Match 38.5%; Score 30; DB 6; Length 19;  
 Best Local Similarity 55.6%; Pred. No. 4.7e+02;  
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
 QY 4 RDHNDYSKN 12  
 :|||:|:  
 Db 9 RDHNDYRKS 17  
 :|||:|:  
 RESULT 23  
 AAB33557  
 ID AAB33557 standard; peptide; 20 AA.  
 XX  
 AC AAB33557;  
 XX  
 XX 12-SEP-2003 (revised)  
 DT 22-JAN-2001 (first entry)  
 XX  
 DE 5/20 native Ara h 2 peptide #11.

XX  
 KM allergy; allergic reaction; allergen; anaphylactic antigen; peanut;  
 KM Ara h 1; Ara h 2; Ara h 3; epitope; binding; immunoglobulin E; IgE;  
 KM food antigen; sensitizing; immune response; anti-allergic.  
 XX  
 OS Arachis hypogaea.  
 XX  
 PN WO200051647-A2.  
 XX  
 PD 08-SEP-2000.  
 XX  
 PF 03-MAR-2000; 2000WO-US005655.  
 XX  
 PR 03-MAR-1999; 99US-0122960P.  
 PR 06-DEC-1999; 99US-00455294.  
 XX  
 PA (MOUN ) MOUNT SINAI SCHOOL MEDICINE.  
 PA  
 PI Sampson HA;  
 DR WPI; 2000-611341/58.  
 DR  
 XX  
 PT Non-human animal sensitized to an antigen, useful as an animal model for  
 PT studying allergic reactions to allergens, such as those in food and in  
 PT the environment.  
 XX  
 PS Example 5, Page 62, 124pp; English.  
 XX  
 CC The present invention describes an animal model which can be used for  
 CC studying allergic reactions to allergens. The animal is sensitized to a  
 CC selected antigen by administering the antigen itself or a nucleic acid  
 CC encoding the antigen, where preferably the antigen is an anaphylactic  
 CC antigen. The sensitized animal can then be used to screen for compounds  
 CC which may help to prevent, ameliorate, or cure allergic conditions in  
 CC humans. The animal model can be used for studying allergic reactions to  
 CC allergens, such as those in food (peanuts, fruit, berry, nut, bean, milk,  
 CC dairy products), or in the environment (weed pollen, grass pollen, tree  
 CC pollen, mite, animal, animal dander, fungal, and insect antigens).  
 CC AAB33478 to AAB33601 represent sequences which are used in examples from  
 CC the present invention to specifically examine the peanut allergy, and the  
 CC peanut anaphylactic antigens Ara h 1 to 3. (Updated on 12-SEP-2003 to  
 CC standardise OS field)  
 XX  
 SQ Sequence 20 AA;  
 XX  
 XX  
 Query Match 38.5%; Score 30; DB 3; Length 20;  
 Best Local Similarity 36.4%; Pred. No. 5e+02;  
 Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;  
 QY 3 KRDNDSKNP 13  
 :|||:|:  
 Db 1 QRDSDSYERDP 11  
 :|||:|:  
 RESULT 24  
 AAB23108  
 ID AAB23108 standard; peptide; 20 AA.  
 XX  
 AC AAB23108;  
 XX  
 DT 29-JAN-2001 (first entry)  
 XX  
 XX Peanut wild-type Ara h 2 20 residue peptide #11.  
 DE  
 XX  
 KM Ara h 2 protein; peanut; epitope; antigen; allergy; anaphylaxis; asthma;  
 KM immunomodulation; unmethylated CpG oligonucleotide; anti-allergic.  
 XX  
 OS Arachis hypogaea.  
 XX  
 PN WO200054803-A2.  
 XX  
 PD 21-SEP-2000.  
 XX

PF 16-MAR-2000; 2000WO-US007213.  
XX  
PT 16-MAR-1999; 99US-0124595P.  
PR 17-MAR-1999; 99US-0125071P.  
XX  
XX (PANA-) PANACEA PHARM LLC.  
XX  
PI Sosin HB, Caplan MJ;  
XX  
DR WPI, 2000-628168/60.  
XX  
XX Immunostimulatory composition for treating or preventing an allergic  
PT reaction leading to conditions such as asthma or anaphylaxis, comprises  
PT oligonucleotides with unmethylated CpG sequences and antigens derived  
PT from allergens.  
XX  
XX Example 3; Page 67; 103pp; English.  
XX  
XX The invention relates to an immunomodulatory composition comprising a CpG  
CC oligonucleotide of the sequence 5' purine-purine-C-G-pyrimidine-  
CC pyrimidine 3', where C and G are unmethylated, and at least one antigen  
CC derived from an allergen that causes anaphylaxis. The composition is  
CC useful for treating allergy in an individual. The composition prevents or  
CC modulates an individual's immune response to an antigen which leads to  
CC asthma and/or anaphylaxis. Individuals susceptible to anaphylactic shock  
CC upon exposure to allergens from foods (e.g., peanut), venom or rubber may  
CC be treated using the composition. Sequences AA832098-AA833125 represent a  
CC series of 20-residue peptides from wild-type peanut Ara h 2 protein used  
CC in an exemplification of the invention  
XX  
SQ Sequence 20 AA;  
XX  
XX  
Query Match 38.5%; Score 30; DB 3; Length 20;  
Best Local Similarity 36.4%; Pred. No. 5e+02;  
Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;  
QY 3 KRDNDYSKNP 13  
: || : | : : |  
Db 1 QRDEDSYERDP 11  
XX  
RESULT 25  
AAU04770  
ID AAU04770 standard; peptide; 20 AA.  
XX  
AC AAU04770;  
XX  
DT 23-OCT-2001 (first entry)  
XX  
DE Native anaphylactic antigen Ara h 2 peptide #11.  
XX  
KW Ara h 2; anaphylactic antigen; immunoglobulin E; IGE; immunogenic;  
KW allergy; mast cell; basophil; mouse; epitope.  
XX  
OS Mus sp.  
XX  
XX  
PN WO200140264-A2.  
PD 07-JUN-2001.  
XX  
PF 06-DEC-2000; 2000WO-US033124.  
XX  
PR 06-DEC-1999; 99US-00455294.  
PR 23-JUN-2000; 2000US-0213765P.  
PR 27-SEP-2000; 2000US-0235797P.  
XX  
XX (PANA-) PANACEA PHARM LLC.  
PA (UYAR-) UNIV ARKANSAS.  
PA (MOUN) MOUNT SINAI SCHOOL MEDICINE NEW YORK.  
XX  
PI Bannon GA, Burks WA, Caplan MJ, Sampson H, Sosin H;  
XX  
DR WPI; 2001-381378/40.

XX  
XX Antigenic fragments useful for reducing anaphylactic risk and reducing  
PT the severity and/or number of allergic symptoms in individuals sensitive  
PT to antigens, have reduced ability to bind Immunoglobulin E.  
XX  
XX Claim 40; Page 52; 100pp; English.  
XX  
XX The sequence represents the amino acid sequence of native anaphylactic  
CC antigen Ara h 2 peptide #11. Ara h 2 is an anaphylactic antigen (A) which  
CC was used to design antigenic peptides having a reduced ability to bind  
CC IGE as compared with the intact (A), or having a sequence substantially  
CC identical to a portion of sequence of an antigen that includes at least  
CC one IGE binding site, where at least one IGE binding site of the peptide  
CC is altered. The antigenic peptides are used in a composition which is  
CC useful for reducing risk or severity of allergic reaction to an antigen.  
CC This is done by identifying an individual at risk of allergic reaction to  
CC an antigen by identifying prior display of allergic symptoms when exposed  
CC to the antigen, or a familial relationship with an individual who  
CC previously displayed allergic symptoms when exposed to the antigen.  
CC Following this an antigen-specific IGE present on one or more mast cells  
CC or basophils in the individual's serum is identified. The individual is  
CC then contacted with a peptide corresponding to a portion of the antigen,  
CC which is selected, formulated, and delivered so that binding of the  
CC peptide to antigen-specific IGE is reduced as compared with IGE binding  
CC of intact antigen. The composition is also useful for treating and  
XX preventing allergic reactions  
XX  
SQ Sequence 20 AA;  
XX  
XX  
Query Match 38.5%; Score 30; DB 4; Length 20;  
Best Local Similarity 36.4%; Pred. No. 5e+02;  
Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;  
QY 3 KRDNDYSKNP 13  
: || : | : : |  
Db 1 QRDEDSYERDP 11  
XX  
RESULT 26  
AAU05095  
ID AAU05095 standard; peptide; 20 AA.  
XX  
AC AAU05095;  
XX  
DT 24-OCT-2001 (first entry)  
XX  
DE Anaphylactic peanut antigen Ara h 2, native peptide #11.  
XX  
XX  
KW Anaphylactic antigen; Ara h 2; peanut; desensitisation; antigen; allergy;  
KW immunotherapy; rush immunotherapy; anaphylaxis; asthma; food allergen;  
KW milk allergen; shellfish allergen; latex; drug; environmental allergen;  
KW grass pollen; ovalbumin; insect venom; peanut oil; immunoglobulin E; IGE.  
XX  
OS Arachis sp.  
XX  
XX  
PN WO200139799-A2.  
PD 07-JUN-2001.  
XX  
PF 06-DEC-2000; 2000WO-US033125.  
XX  
PR 06-DEC-1999; 99US-00455294.  
PR 23-JUN-2000; 2000US-0213765P.  
PR 27-SEP-2000; 2000US-0235797P.  
XX  
XX (PANA-) PANACEA PHARM LLC.  
PA Caplan M;  
XX  
PI WPI; 2001-408258/43.  
XX  
DR Preventing allergic response against antigens, e.g. food and  
XX environmental allergens such as peanut allergen or grass pollen, latex or  
PT

PT drug, comprises administering agent, e.g. a peptide, that blocks antigen  
 binding sites on offending IGE.  
 XX Example 2, Page 46, 76pp, English.  
 CC The sequence represents the amino acid sequence of anaphylactic peanut  
 CC antigen Ara h 2, native peptide #11. The peptide is used in active or  
 CC passive desensitization of an individual to an antigen, for alleviating  
 CC or preventing allergic reactions and for decreasing the risk of allergic  
 CC reactions during immunotherapy or rush immunotherapy, anaphylaxis and  
 CC asthma. The antigen may be a food allergen (e.g. peanut or milk  
 CC allergen), shellfish allergen, environmental allergen (e.g. grass pollen  
 CC or tree pollen), latex, drug, pollen, ovalbumin, an insect venom antigen  
 CC or predominantly linear epitopes. The protein is useful for protecting an  
 CC individual against subsequent inadvertent or intentional exposure to  
 CC antigen, e.g. receiving blocking agent before eating a chocolate bar  
 CC which may inadvertently contain peanut components or before eating foods  
 CC prepared using peanut oil. Administration of the blocking agent does not  
 CC result in cross-linking of anti-antigenic IGE. After exposure to the  
 CC agent, the individual's antigen sensitivity is at least temporarily  
 CC reduced. Only those IGE molecules that bind the offending antigen and  
 CC contribute to the risk of an allergic response are blocked  
 CC XX  
 SQ Sequence 20 AA;  
 Query Match 38.5%; Score 30; DB 4; Length 20;  
 Best Local Similarity 36.4%; Pred. No. 5e+02; 3; Indels 0; Gaps 0;  
 Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;  
 QY 3 KRDNHNSKNP 13  
 :||:|:|:  
 Db 1 GRDEDSYERDP 11  
 RESULT 27  
 ID AAO17451 standard; peptide; 20 AA.  
 AC AAO17451;  
 XX  
 DT 11-JUL-2002 (first entry)  
 XX  
 DE P falciparum TRAP CD4+ T cell epitope #10.  
 KM Tuberculosis; TB; vaccination; vaccine; CD4+ T cell immune response;  
 KM poxvirus vector; HIV; malaria; Helicobacter pylori; influenza; hepatitis;  
 KM viral infection; leprosy; protozoan parasite; cancer; tuberculosis;  
 KM anti-HIV; proteoasidic; antibacterial; virucide; hepatotropic;  
 KM antiinflammatory; antileptotic; cytostatic; epitope.  
 OS Plasmodium falciparum.  
 XX  
 XX WO200224224-A2.  
 XX  
 PD 28-MAR-2002.  
 XX  
 PF 13-SEP-2001; 2001WO-GB004116.  
 XX  
 PR 21-SEP-2000; 2000GB-00023203.  
 XX  
 PA (OXO-) OXON PHARMACEUTICALS LTD.  
 XX  
 PI Hill AVS, Meshane H, Gilbert S, Reece W, Schneider J;  
 XX  
 DR WPI; 2002-394098/42.  
 XX  
 PT Inducing CD4+ T-cell response against target antigen by administering a  
 PT recombinant comprising a source of CD4+ epitopes which is a non-  
 PT replicating or replicating impaired recombinant poxvirus vector.  
 XX  
 PS Example 2, Page 33, 50pp, English.  
 CC The present invention relates to a method of inducing a CD4+ T-cell

CC response against a target antigen, by administering two different  
 CC compositions comprising a source of CD4+ T-cell epitope(s) of the target  
 CC antigen, where the second composition further includes an epitope which  
 CC is same as the epitope of the first composition, where the source of the  
 CC epitopes for the compositions is a non-replicating or replication  
 CC impaired recombinant poxvirus vector. The methods are useful for inducing  
 CC CD4+ T-cell immune responses against diseases such as tuberculosis, human  
 CC immunodeficiency virus (HIV) (persistent viral infection), malaria,  
 CC Helicobacter pylori, influenza, hepatitis (chronic hepatitis B and C),  
 CC cytomegalovirus (CMV), viral infection, herpes virus-induced disease,  
 CC leprosy and diseases caused by non-malarial protozoan parasite such as  
 CC toxoplasma and cancer. The present sequence is an epitope from Plasmodium  
 CC falciparum useful in the method of the invention  
 CC XX  
 SQ Sequence 20 AA;  
 Query Match 38.5%; Score 30; DB 5; Length 20;  
 Best Local Similarity 63.6%; Pred. No. 5e+02; 3; Indels 0; Gaps 0;  
 Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
 QY 2 IKRDHNSKNP 12  
 :||:|:|:  
 Db 10 IIRHSDASKN 20  
 RESULT 28  
 ID ADD12247 standard; peptide; 20 AA.  
 AC ADD12247;  
 XX  
 DT 01-JAN-2004 (first entry)  
 XX  
 DE PDZ ligand (PL) peptide #9.  
 XX  
 KM modulator; PDZ; post-synaptic density protein 95; PSD95;  
 KM Drosophila large disc protein; Zonula Occludin 1 protein; ZO-1;  
 KM PDZ ligand; PL; antiinflammatory; antiallergic; antitumor; antidiabetic;  
 KM antiasthmatic; dermatological; neuroprotective; virucide; antidiabetic;  
 KM osteopathic; antiarthritic; immunosuppressive; antiatherosclerotic;  
 KM cytostatic; anti-HIV; vasotropic; immunomodulator; neurological disease;  
 KM immune response disease; muscular disease; cancer;  
 KM modulating vesicular trafficking; tumor suppression;  
 KM signal transduction; protein sorting; membrane polarity; apoptosis;  
 KM synapse formation; multi-protein complex; leukocyte activation inhibitor.  
 OS Unidentified.  
 XX  
 XX WO2003014303-A2.  
 XX  
 PD 20-FEB-2003.  
 XX  
 PF 02-AUG-2002; 2002WO-US024655.  
 XX  
 PR 03-AUG-2001; 2001US-0309841P.  
 XX  
 PR 25-FEB-2002; 2002US-0360061P.  
 XX  
 PA (ARBO-) ARBOR VITA CORP.  
 XX  
 PI Lu PS, Rabinowitz JD, Schweizer J, Carrick DM,  
 XX  
 DR WPI; 2003-268193/26.  
 XX  
 PT Modulator of binding between discs-large homology repeat protein, PDZ and  
 PT PDZ ligand protein, is a peptide having few residues of C-terminal  
 PT sequence of PDZ ligand protein.  
 XX  
 PS Example 7, Page 150, 172pp, English.  
 CC The invention relates to a novel modulator of binding between a PDZ  
 CC protein (post-synaptic density protein 95 (PSD95), Drosophila large disc  
 CC protein and zonula Occludin 1 protein (ZO-1)) and a PDZ ligand (PL)  
 CC protein. The modulator is a peptide having 3 residues of a C-terminal

CC sequence of a PL protein. PDZ and PL proteins are a binding pair given in  
 CC specification, or a peptide mimetic of the 3 residue PL protein, or a  
 CC small molecule having similar functional activity as the 3 residue PL  
 CC protein. The reagents of the invention have the following activities:  
 CC antiinflammatory, antiallergic, antitumor, antidiabetic, antiasthmatic,  
 CC dermatological, neuroprotective, virucide, antidiabetic, osteopathic,  
 CC antiautistic, immunosuppressive, antiatherosclerotic, cystostatic, anti-  
 CC HIV, vasotropic, and immunomodulator. The novel modulator is useful for  
 CC treating a disease correlated with binding between a PDZ protein and PL  
 CC protein. The disease can be a neurological disease, immune response  
 CC disease, muscular disease or cancer. The modulator is useful for  
 CC modulating vesicular trafficking, tumour suppression, signal  
 CC transduction, protein sorting, establishment of membrane polarity,  
 CC apoptosis, regulation of immune response and organization of synapse  
 CC formation. The modulator is useful for facilitating the assembly of multi-  
 CC -protein complexes, often serving as a bridge between several proteins,  
 CC or regulating the function of other proteins, and to inhibit leukocyte  
 CC activation. The modulator is useful for treating diseases characterised  
 CC by inflammatory and humoral immune responses e.g., inflammation, allergy,  
 CC inflammatory bowel diseases, ulcerative colitis, psoriasis, asthma,  
 CC allergic rhinitis, atopic dermatitis, arthritis, multiple sclerosis,  
 CC diabetes, osteoarthritis, graft-versus-host diseases, atherosclerosis,  
 CC leukemia, infectious diseases (viral infection such as human  
 CC immunodeficiency virus (HIV)), and ischaemia. This sequence represents a  
 CC PDZ ligand (PL) peptide of the invention.

XX  
 SQ Sequence 20 AA;

Query Match 38.5%; Score 30; DB 7; Length 20;  
 Best Local Similarity 57.1%; Pred. No. 5e+02;  
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 7 NDYSKNP 13  
 DB 9 NDFTQNP 15

#### RESULT 29

ADW33950  
 ID ADM33950 standard; peptide; 20 AA.

XX ADW33950;

XX 10-MAR-2005 (first entry)

XX HLA binding epitope #4700.

XX Virucide; cytostatic; gene therapy; vaccine; epitope; cytotoxic T cell;

KW MHC class I; CTL; HTL; A2-restricted cytotoxic lymphocyte; HLA;

KW viral disease; cancer.

XX Unidentified.

XX WO2003040165-A2.

XX 15-MAY-2003.

XX 18-OCT-2001; 2001WO-US051650.

XX 19-OCT-2000; 2000US-0242350P.

XX 20-APR-2001; 2001US-0285624P.

XX (EPIM-) EPIMMUNE INC.

XX Sette A, Sidney J, Southwood S;

XX WPI; 2003-441519/41.

XX New composition comprising at least one peptide having allele-specific  
 PT binding motifs for HLA, useful for preventing, treating or diagnosing  
 PT viral diseases and cancer.  
 XX Claim 1; Page 52-379; 382pp; English.

XX The invention relates to a composition comprising at least one peptide  
 CC having an isolated, prepared epitope selected from any of the sequences  
 CC from 30 lists given in the specification. Also disclosed is a method for  
 CC inducing a cytotoxic T cell response against a pre-selected antigen in a  
 CC patient expressing a specific MHC class I allele by contacting cytotoxic  
 CC T cells from the patient with the composition cited above. The  
 CC composition comprises an epitope that is joined by an amino acid linker.  
 CC The epitope is admixed or joined to a CTL or HTL epitope. The epitope is  
 CC bound to an HLA molecule on the antigen-presenting cell, where when an A2  
 CC -restricted cytotoxic lymphocyte (CTL) is present, a receptor of the CTL  
 CC binds to a complex of the HLA molecule and the epitope. Specifically  
 CC claimed are peptides having allele-specific binding motifs for HLA. The  
 CC compositions and methods are useful for preventing, treating or  
 CC diagnosing viral diseases and cancer. The peptide epitopes are useful as  
 CC diagnostic agents for evaluating immune responses, for making antibodies  
 CC and for evaluating efficacy of a vaccine. Sequences given in ADW29251-  
 CC ADW37745 represent epitopes of the invention as given in Tables 2-31.

XX  
 SQ Sequence 20 AA;

Query Match 38.5%; Score 30; DB 7; Length 20;  
 Best Local Similarity 63.6%; Pred. No. 5e+02;  
 Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 IKRDNDYSKN 12  
 DB 5 IIRLHSDASKN 15

#### RESULT 30

ADW35183  
 ID ADM35183 standard; peptide; 20 AA.

XX ADW35183;

XX 10-MAR-2005 (first entry)

XX HLA binding epitope #5933.

XX Virucide; cytostatic; gene therapy; vaccine; epitope; cytotoxic T cell;

KW MHC class I; CTL; HTL; A2-restricted cytotoxic lymphocyte; HLA;

KW viral disease; cancer.

XX Unidentified.

XX WO2003040165-A2.

XX 15-MAY-2003.

XX 18-OCT-2001; 2001WO-US051650.

XX 19-OCT-2000; 2000US-0242350P.

XX 20-APR-2001; 2001US-0285624P.

XX (EPIM-) EPIMMUNE INC.

XX Sette A, Sidney J, Southwood S;

XX WPI; 2003-441519/41.

XX New composition comprising at least one peptide having allele-specific  
 PT binding motifs for HLA, useful for preventing, treating or diagnosing  
 PT viral diseases and cancer.  
 XX Claim 1; Page 52-379; 382pp; English.

XX The invention relates to a composition comprising at least one peptide  
 CC having an isolated, prepared epitope selected from any of the sequences  
 CC from 30 lists given in the specification. Also disclosed is a method for  
 CC inducing a cytotoxic T cell response against a pre-selected antigen in a  
 CC patient expressing a specific MHC class I allele by contacting cytotoxic  
 CC T cells from the patient with the composition cited above. The

CC composition comprises an epitope that is joined by an amino acid linker.  
 CC The epitope is admixed or joined to a CTL or HTL epitope. The epitope is  
 CC bound to an HLA molecule on the antigen-presenting cell, where when an A2  
 CC restricted cytotoxic lymphocyte (CTL) is present, a receptor of the CTL  
 CC binds to a complex of the HLA molecule and the epitope. Specifically  
 CC claimed are peptides having allele-specific binding motifs for HLA. The  
 CC compositions and methods are useful for preventing, treating or  
 CC diagnosing viral diseases and cancer. The peptide epitopes are useful as  
 CC diagnostic agents for evaluating immune responses, for making antibodies  
 CC and for evaluating efficacy of a vaccine. Sequences given in ADW29251-  
 CC ADW37745 represent epitopes of the invention as given in Tables 2-31.  
 CC  
 SQ Sequence 20 AA;  
 XX  
 SQ  
 Query Match 38.5%; Score 30; DB 7; Length 20;  
 Best Local Similarity 63.6%; Pred. No. 5e+02;  
 Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
 QY 2 IKRDHNDYSKN 12  
 DB 5 IIRLHSDASKN 15  
 DB  
 RESULT 31  
 ADW36547  
 ID ADW36547 standard; peptide; 20 AA.  
 AC  
 AC ADW36547;  
 XX  
 DT 10-MAR-2005 (first entry)  
 XX  
 DE HLA binding epitope #7297.  
 XX  
 KW virucide; cytostatic; gene therapy; vaccine; epitope; cytotoxic T cell;  
 KM MHC class I; CTL; HTL; A2-restricted cytotoxic lymphocyte; HLA;  
 KM viral disease; cancer.  
 XX  
 OS unidentified.  
 XX  
 PN WO2003040165-A2.  
 PD  
 PD 15-MAY-2003.  
 XX  
 PF 18-OCT-2001; 2001WO-US051650.  
 XX  
 PR 19-OCT-2000; 2000US-0242350P.  
 PR 20-APR-2001; 2001US-0285624P.  
 XX  
 PA (EPIM-) EPIMUNE INC.  
 XX  
 PI Sette A, Sidney J, Southwood S;  
 XX  
 DR WPI; 2003-441519/41.  
 XX  
 PT New composition comprising at least one peptide having allele-specific  
 PT binding motifs for HLA, useful for preventing, treating or diagnosing  
 PT viral diseases and cancer.  
 XX  
 PS Claim 1; Page 52-379; 382pp; English.  
 XX  
 CC The invention relates to a composition comprising at least one peptide  
 CC having an isolated, prepared epitope selected from any of the sequences  
 CC from 30 lists given in the specification. Also disclosed is a method for  
 CC inducing a cytotoxic T cell response against a pre-selected antigen in a  
 CC patient expressing a specific MHC class I allele by contacting cytotoxic  
 CC T cells from the patient with the composition cited above. The  
 CC composition comprises an epitope that is joined by an amino acid linker.  
 CC The epitope is admixed or joined to a CTL or HTL epitope. The epitope is  
 CC bound to an HLA molecule on the antigen-presenting cell, where when an A2  
 CC -restricted cytotoxic lymphocyte (CTL) is present, a receptor of the CTL  
 CC binds to a complex of the HLA molecule and the epitope. Specifically  
 CC claimed are peptides having allele-specific binding motifs for HLA. The  
 CC compositions and methods are useful for preventing, treating or

CC diagnosing viral diseases and cancer. The peptide epitopes are useful as  
 CC diagnostic agents for evaluating immune responses, for making antibodies  
 CC and for evaluating efficacy of a vaccine. Sequences given in ADW29251-  
 CC ADW37745 represent epitopes of the invention as given in Tables 2-31.  
 CC  
 SQ Sequence 20 AA;  
 XX  
 SQ  
 Query Match 38.5%; Score 30; DB 7; Length 20;  
 Best Local Similarity 63.6%; Pred. No. 5e+02;  
 Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
 QY 2 IKRDHNDYSKN 12  
 DB 5 IIRLHSDASKN 15  
 DB  
 RESULT 32  
 ADK08317  
 ID ADK08317 standard; peptide; 8 AA.  
 AC  
 AC ADK08317;  
 XX  
 DT 06-MAY-2004 (first entry)  
 XX  
 DE Human papillomavirus peptide #372.  
 XX  
 KW pathogenic virus; alternative reading frame; antigenic determinant;  
 KM virucide; vaccine; therapeutic agent; infection; HPV.  
 KM Human papillomavirus.  
 OS  
 OS WO2004011650-A2.  
 PN  
 PD 05-FEB-2004.  
 PD  
 PD 24-JUL-2003; 2003WO-EP008112.  
 XX  
 PF 24-JUL-2002; 2002AT-00001124.  
 PR 11-JUL-2003; 2003EP-00450171.  
 XX  
 PA (INTE-) INTERCELL AG.  
 XX  
 PI Mettner F, Schmidt W, Habel A;  
 XX  
 DR WPI; 2004-169243/16.  
 XX  
 PT New polypeptide encoded by an alternative reading frame of a pathogenic  
 PT virus comprising an antigenic determinant, useful for treating or  
 PT preventing an infection with the pathogenic virus.  
 XX  
 PS Claim 16; Page 177; 220pp; English.  
 XX  
 CC This invention relates to a novel polypeptide encoded by an alternative  
 CC reading frame of a pathogenic virus, where the polypeptide starts with a  
 CC methionine amino acid residue, which comprises an antigenic determinant  
 CC and more than 7 amino acid residues. The invention may be useful for the  
 CC production of compounds with a virucide activity or the development of a  
 CC vaccine. The polypeptide or its fragments may be useful as a therapeutic  
 CC agent. It is also useful for the manufacture of a medicament for treating  
 CC or preventing an infection with the pathogenic virus. The present  
 CC sequence is that of a human papillomavirus (HPV) epitope peptide of the  
 CC invention.  
 CC  
 SQ Sequence 8 AA;  
 XX  
 SQ  
 Query Match 37.2%; Score 29; DB 8; Length 8;  
 Best Local Similarity 83.3%; Pred. No. 2e+06;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 4 RDHNDY 9  
 DB 2 RDHNDY 7  
 DB

```
RESULT 33
AAV46600
ID AAV46600 standard; peptide; 10 AA.
XX
AC AAV46600;
XX
DT 01-DEC-1999 (first entry)
XX
DE Immunogenic peptide having a human leukocyte antigen binding motif #1211.
XX
KW Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA;
KW Immune response; T cell activation; major histocompatibility complex;
KW cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer;
KW prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;
KW vaccine; immunisation.
XX
OS Synthetic.
XX Homo sapiens.
XX
PN MO9945954-A1.
XX
PD 16-SEP-1999.
XX
PF 13-MAR-1998; 98WO-US005039.
XX
PR 13-MAR-1998; 98WO-US005039.
XX
PA (EPIM-) EPIMONE INC.
XX
PI Sette A, Kubo RT, Sidney J, Cells E, Grey HM, Southwood S;
XX
DR WPI; 1999-551214/46.
XX
PT New immunogenic peptides with HLA binding motif, useful in treatment and
PT diagnosis of cancers and viral diseases.
XX
PS Claim 1; Page 78; 150pp; English.
XX
CC AAV45390 to AAV48214 represent specifically claimed immunogenic peptides
CC having a human major histocompatibility complex (MHC) Class I (also known
CC as human leukocyte antigen (HLA)) binding motif. The immunogenic peptides
CC can bind to a specific HLA allele (i.e. HLA-A subtypes HLA-A2.1, A1, A3.2
CC or A24.1 or HLA-B or C) and induce a cytotoxic T cell response against
CC the antigen from which the peptide is derived. Cytotoxic T lymphocytes
CC (CTLs) which destroy antigen-bearing cells are normally induced by an
CC antigen in the form of a peptide fragment bound to a HLA molecule, rather
CC than the intact foreign antigen itself, and are particularly important in
CC tumour rejection and in fighting viral infections. The peptides are
CC therefore useful therapeutically to treat or prevent viral infections and
CC cancers in mammals (especially humans) e.g. prostate cancer, hepatitis B
CC and C, AIDS, and renal carcinoma. They can be administered as vaccines to
CC elicit an immune response in individuals susceptible or otherwise at risk
CC of viral infection or cancer, or used to treat chronic or acute
CC conditions. They are also useful diagnostically, and can be used to
CC induce a cytotoxic T cell response, by contacting a cytotoxic T cell with
CC the peptide e.g. to produce CTLs ex vivo for infusion back into a
CC patient. The polynucleotides encoding the immunogenic peptides are also
CC useful therapeutically and for immunisation as above
XX
SQ Sequence 10 AA;
XX
Query Match 37.2%; Score 29; DB 2; Length 10;
Best Local Similarity 66.7%; Pred. No. 3.3e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
ID ADK08377 standard; peptide; 10 AA.
XX
AC ADK08377;
XX
DT 06-MAY-2004 (first entry)
XX
DE Human papillomavirus peptide #432.
XX
KW pathogenic virus; alternative reading frame; antigenic determinant;
KW virucide; vaccine; therapeutic agent; infection; HPV.
XX
OS Human papillomavirus.
XX
PN WO2004011650-A2.
XX
PD 05-FEB-2004.
XX
PF 24-JUL-2003; 2003WO-EP008112.
XX
PR 24-JUL-2002; 2002AT-00001124.
XX
PR 11-JUL-2003; 2003EP-00450171.
XX
PA (INTE-) INTERCELL AG.
XX
PI Mattnex F, Schmidt W, Habel A;
XX
DR WPI; 2004-169243/16.
XX
PT New polypeptide encoded by an alternative reading frame of a pathogenic
PT virus comprising an antigenic determinant, useful for treating or
PT preventing an infection with the pathogenic virus.
XX
PS Claim 18; Page 178; 220pp; English.
XX
CC This invention relates to a novel polypeptide encoded by an alternative
CC reading frame of a pathogenic virus, where the polypeptide starts with a
CC methionine amino acid residue, which comprises an antigenic determinant
CC and more than 7 amino acid residues. The invention may be useful for the
CC production of compounds with a virucide activity or the development of a
CC vaccine. The polypeptide or its fragments may be useful as a therapeutic
CC agent. It is also useful for the manufacture of a medicament for treating
CC or preventing an infection with the pathogenic virus. The present
CC sequence is that of a human papillomavirus (HPV) epitope peptide of the
CC invention.
XX
SQ Sequence 10 AA;
XX
Query Match 37.2%; Score 29; DB 8; Length 10;
Best Local Similarity 83.3%; Pred. No. 3.3e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 4 RDHNDY 9
   |||||
DB 5 RDHIDY 10

RESULT 35
ADK64049
ID ADK64049 standard; peptide; 12 AA.
XX
AC ADK64049;
XX
DT 18-DEC-2003 (first entry)
XX
DE Carbon black-binding peptide #11.
XX
KW polyhydroxyalkanoate-containing structure; PHA-containing structure;
KW PHA synthase; polyhydroxyalkanoate synthase; 3-hydroxyacyl coenzyme A;
KW pigment dispersant; electrophotography toner; laminated structure;
KW OHP film; microcapsule pigment ink; electrophoretic particle;
KW electrophoresis display; colour filter; enzyme;
KW carbon black-binding peptide.
XX
```

OS Unidentified.  
 XX  
 PN EPI275728-A1.  
 XX  
 PD 15-JAN-2003.  
 XX  
 PF 10-JUL-2002; 2002EP-00015374.  
 XX  
 PR 10-JUL-2001; 2001JP-00210052.  
 XX  
 PR 13-JUN-2002; 2002JP-00172978.  
 XX  
 PA (CANO ) CANON KK.  
 XX  
 PI Nomoto T, Yano T, Kozaki S, Honma T,  
 DR WPI; 2003-459566/44.  
 XX  
 XX Manufacturing polyhydroxyalkanoate-containing structure useful as toner  
 PT for electrophotography, by immobilizing polyhydroxyalkanoate synthase on  
 PT base material and synthesizing polyhydroxyalkanoate on base material.  
 PS  
 PS Claim 49, SEQ ID NO 48; 277pp; English.  
 XX  
 CC The invention comprises a method for producing a polyhydroxyalkanoate  
 CC (PHA)-containing structure. The method involves immobilizing a PHA  
 CC synthase enzyme on a base material surface and then synthesizing PHA  
 CC using 3-hydroxyacyl coenzyme A as a substrate. The method of the  
 CC invention is useful for manufacturing a PHA-containing structure. The PHA  
 CC -containing structure has a wide range of applications as a variety of  
 CC functional structures, such as: a pigment dispersant of excellent  
 CC dispersion stability; a toner for electrophotography of excellent  
 CC electrostatic property; and the laminated structure as an OHP film. The  
 CC structure is also useful for microcapsule pigment ink of excellent  
 CC dispersion stability, an electrophoretic particle for electrophoresis  
 CC display, and colouring composition for a colour filter. The present amino  
 CC acid sequence represents a carbon black-binding peptide.  
 XX  
 SQ Sequence 12 AA;  
 Query Match 37.2%; Score 29; DB 7; Length 12;  
 Best Local Similarity 62.5%; Pred. No. 4.1e+02;  
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 QY 6 HNDYSKRP 13  
 Db 3 NNDWSKAP 10

## RESULT 36

ADG01812  
 ID ADG01812 standard; peptide; 12 AA.  
 XX  
 AC ADG01812;  
 XX  
 DT 26-FEB-2004 (first entry)  
 XX  
 DE Carbon black pigment binding peptide SEQ ID NO:25.  
 XX  
 KW target antibody; target antigen; carrier; assay reagent; determination;  
 KM detection; clinical laboratory test; environmental analysis;  
 XX  
 OS Synthetic.  
 XX  
 PN EPI371983-A1.  
 XX  
 PD 17-DEC-2003.  
 XX  
 PF 06-JUN-2003; 2003EP-00012945.  
 XX  
 PR 13-JUN-2002; 2002JP-00173027.  
 XX  
 PR 02-MAY-2003; 2003JP-00127099.  
 XX

PA (CANO ) CANON KK.  
 XX  
 PI Honma T, Yano T, Nomoto T, Kozaki S;  
 DR WPI; 2004-073347/08.  
 XX  
 PT Detecting presence or amount of target antibody/antigen comprises  
 PT preparing carrier having immobilized antigen/antibody corresponding to  
 PT antibody/antigen in specimen, mixing carrier and specimen and assaying  
 PT agglutination.  
 XX  
 PS Claim 11; SEQ ID NO 25; 63pp; English.  
 XX  
 CC The present invention describes an assay (M1) for determining the  
 CC presence or an amount of a target antibody or antigen in a specimen. M1  
 CC comprises: (a) preparing a carrier on which an antigen or antibody  
 CC corresponding to the target antibody or antigen in the specimen  
 CC respectively is immobilized; and (b) mixing the carrier with the specimen  
 CC and assaying the level of the immunological agglutination reaction caused  
 CC by the mixing step, where the antigen or antibody immobilized on the  
 CC carrier is bound to the carrier through an amino acid sequence capable of  
 CC binding to the carrier. Also described: (1) an assay reagent (I), for  
 CC (M1), where an antigen or antibody corresponding to the antibody or  
 CC antigen is immobilized on a carrier and the antigen or antibody  
 CC immobilised on a carrier is bound to the carrier through an amino acid  
 CC sequence capable of binding to the carrier; (2) producing (M2) (I)  
 CC comprising immobilising an antigen or antibody corresponding to the  
 CC antibody or antigen immobilised on a carrier and the antigen or antibody  
 CC immobilised on a carrier is bound to the carrier through an amino acid  
 CC sequence capable of binding to the carrier; (3) a peptide (II) comprising  
 CC one or more amino acid sequence (SEQ ID NO:1-SEQ ID NO:40); and (4) an  
 CC antigen protein or antibody protein comprising one or more sequences  
 CC chosen from (SEQ ID NO:1-SEQ ID NO:40). (M1) is useful for determining  
 CC the presence or an amount of a target antibody or antigen. (II) can be  
 CC used as an assay reagent for clinical laboratory tests or environmental  
 CC or food analysis. The present sequence is used in the exemplification of  
 CC the present invention.  
 XX  
 SQ Sequence 12 AA;  
 Query Match 37.2%; Score 29; DB 8; Length 12;  
 Best Local Similarity 62.5%; Pred. No. 4.1e+02;  
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 QY 6 HNDYSKRP 13  
 Db 3 NNDWSKAP 10

## RESULT 37

ADQ90327  
 ID ADQ90327 standard; peptide; 12 AA.  
 XX  
 AC ADQ90327;  
 XX  
 DT 21-OCT-2004 (first entry)  
 XX  
 DE Carbon black binding peptide, SEQ ID 19.  
 XX  
 KW Substrate; organic; carbon layer; affinity region 15a; biosensor;  
 KM bioreactor; detector.  
 XX  
 OS Unidentified.  
 XX  
 PN JP2004215514-A.  
 XX  
 PD 05-AUG-2004.  
 XX  
 PF 09-JAN-2003; 2003JP-00003554.  
 XX  
 PR 09-JAN-2003; 2003JP-00003554.  
 XX  
 PA (CANO ) CANON KK.

XX WPI; 2004-575105/56.  
XX  
XX Substrate useful in detector, bioreactor or biosensor, has organic  
PT substance that binds to carbon layer present on substrate.  
XX  
XX Clain 9; SEQ ID NO 19; 84bp; Japanese.  
XX  
CC The invention relates to a novel substrate (11) which has an organic  
CC substance that binds to the carbon layer (12) present on the substrate.  
CC The joint domain of the organic substance binds to one or more portions  
CC of the carbon layer which has an affinity region (15a). The invention  
CC further comprises a detector comprising the substrate; a method for  
CC producing the substrate, which involves fixing the organic substance on  
CC the carbon layer that is present on the substrate having numerous pores;  
CC and a biosensor or bioreactor, comprising the substrate as a module. The  
CC substrate is useful in a detector, bioreactor or biosensor. This sequence  
CC represents a carbon black binding peptide of the invention.  
XX  
XX Sequence 12 AA;  
SQ

Query Match 37.2%; Score 29; DB 8; Length 12;  
Best Local Similarity 62.5%; Pred. No. 4.1e+02;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 6 HNDYSKNP 13  
DB 3 NNDWSKAP 10  
:|:|:|:|  
|

RESULT 38  
AA94623  
ID AA94623 standard; peptide; 13 AA.  
XX  
XX AA94623;  
AC  
XX  
DT 15-AUG-2000 (first entry)  
XX  
XX Peptide used to generate polyclonal antibodies directed against ELVIS.  
DE  
XX  
XX Epidermal growth factor-like variant in skin-1; ELVIS; cyostatic;  
XX Chromosome 4q12-13; antiporiatic; vulnery; dermatological; chemotaxis;  
XX antiinflammatory; antiallergic; cell proliferation; differentiation;  
XX angiogenesis; psoriasis; cancer; hair loss; wound healing; gene therapy;  
XX contact dermatitis; burn; bipolar affective disorder; antibody.  
XX  
OS Synthetic.  
XX  
XX WO200029438-A1.  
XX  
XX 25-MAY-2000.  
PD  
XX  
XX 19-NOV-1999; 99WO-US027576.  
XX  
XX 19-NOV-1998; 98US-00196269.  
XX  
XX (MILL-) MILENNIUM PHARM INC.  
XX  
XX Busfield S, Gearing DP;  
XX  
XX WPI; 2000-387744/33.  
XX  
XX New nucleic acid molecules encoding epidermal growth factor-like variant  
PT in skin proteins (ELVIS), useful for treating psoriasis and cancer.  
XX  
XX Disclosure; Page 15; 99pp; English.  
XX  
XX This sequence represents a peptide used to generate polyclonal antibodies  
CC against human epidermal growth factor-like variant in skin (ELVIS)  
CC proteins. The ELVIS gene is located on chromosome 4q12-13. The invention  
CC relates to a family of ELVIS proteins (ELVIS-1, 2, and 3). ELVIS-1 is a  
CC membrane protein, while ELVIS-2 and ELVIS-3 are secreted proteins. These  
CC proteins show considerable identity to transforming growth factor alpha

CC (TGF-alpha). The nucleotide sequences encoding the ELVIS proteins of the  
CC invention have antiporiatic, cyostatic, vulnerary, dermatological,  
CC antiinflammatory, and antiallergic activity. ELVIS encoding nucleotide  
CC sequences are useful as modulating agents in regulating a variety of  
CC cellular processes such as cell proliferation, cell migration and  
CC chemotaxis, cellular differentiation and/or angiogenesis and also in  
CC screening and detection assays and as predictive medicines. Elvis  
CC nucleotide sequences are useful in gene therapy techniques and to express  
CC ELVIS proteins. The ELVIS proteins are useful for treating proliferative  
CC disorders such as psoriasis and cancer, and to promote hair growth and  
CC wound healing. Modulators of ELVIS are useful in the treatment of contact  
CC dermatitis and burns, for treating bipolar affective disorder. The  
CC proteins can also be used to modulate epithelial cell growth and in the  
CC treatment of hair loss  
XX  
XX Sequence 13 AA;  
SQ

Query Match 37.2%; Score 29; DB 3; Length 13;  
Best Local Similarity 62.5%; Pred. No. 4.5e+02;  
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 DNDYSKN 12  
DB 5 DNDYSKIN 12  
:|:|:|:|  
|

RESULT 39  
ABW02379  
ID ABW02379 standard; protein; 13 AA.  
XX  
XX ABW02379;  
AC  
XX  
XX 12-FEB-2004 (first entry)  
DT  
XX  
XX Human ELVIS peptide #1 used to generate polyclonal antibody.  
DE  
XX  
XX ELVIS; epidermal growth factor-like variant in skin; wound; hair loss;  
XX burn; gene therapy; dermatological; vulnerary; human.  
XX  
XX Homo sapiens.  
OS  
XX  
XX US2003338912-A1.  
XX  
XX 24-JUL-2003.  
PD  
XX  
XX 16-JAN-2003; 2003US-00345764.  
XX  
XX 19-NOV-1998; 98US-00196269.  
XX  
XX 19-NOV-1999; 99US-00443959.  
XX  
XX (MILL-) MILENNIUM PHARM INC.  
XX  
XX Busfield S, Gearing DP;  
XX  
XX WPI; 2003-851733/79.  
XX  
XX New epidermal growth factor-like variant in skin (ELVIS) nucleic acid,  
PT for treating a disorder characterized by the aberrant expression/activity  
PT of the polypeptide or nucleic acid e.g. wounds, burns, hair loss or  
PT unwanted hair growth.  
XX  
XX Disclosure; SEQ ID NO 23; 50pp; English.  
XX  
XX The present invention relates to isolated nucleic acid molecules,  
CC designated ELVIS-1, ELVIS-2, ELVIS-3 (epidermal growth factor-like  
CC variant in skin-1, 2, 3). The invention is useful for treating a disorder  
CC characterised by the aberrant activity of the polypeptide or nucleic acid  
CC molecule, e.g. skin conditions such as wounds, burns, hair loss or  
CC unwanted hair growth. The invention is also useful in gene therapy. The  
CC present sequence is human ELVIS peptide used to generate polyclonal  
CC antibody  
XX  
XX Sequence 13 AA;  
SQ



Query Match 37.2%; Score 29; DB 7; Length 13;  
 Best Local Similarity 62.5%; Pred. No. 4.5e+02;  
 Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 5 DHNDYSRN 12  
 |||||  
 DB 5 DHNGYCIN 12

RESULT 40  
 ADF53453  
 ID ADF53453 standard; peptide; 14 AA.

XX ADF53453;  
 AC  
 DT 12-FBB-2004 (first entry)  
 XX  
 DE MCPC 603 antibody CDR2 mutant peptide amino acid sequence 14.

KW walk-through mutagenesis; prototype amino acid; prototype nucleotide;  
 KW mutant polypeptide production; MCPC 603;  
 KW complementarity determining region; CDR; heavy chain; CDR2; mutant;  
 KW mutain.

XX Unidentified.  
 OS Synthetic.

XX WO2003089671-A1.

XX 30-OCT-2003.

XX 16-APR-2003; 2003WO-US011935.

XX 17-APR-2002; 2002US-0373686P.

XX (CREA/) CREA R.

XX (CAPP/) CAPPUCILLI G.

XX Crea R, Cappuccilli G;

XX WPI; 2003-854132/79.

XX Walk-through mutagenesis of a nucleic acid encoding a polypeptide, useful  
 PT for producing mutant polypeptides comprising synthesizing oligonucleotides  
 PT comprising a nucleotide sequence for each target region of a prototype  
 PT amino acid.

XX Example; Fig 6; 40pp; English.

XX This invention relates to a novel method of walk-through mutagenesis of a  
 CC nucleic acid encoding a polypeptide which comprises synthesizing a  
 CC mixture of oligonucleotides comprising a nucleotide sequence for each  
 CC target region of a prototype amino acid, where each oligonucleotide  
 CC contains, at each sequence position in the target region, a prototype  
 CC nucleotide for synthesis of the prototype amino acid, or a predetermined  
 CC nucleotide that is required for synthesis of the predetermined amino  
 CC acid. The method is useful in producing mutant polypeptides in which the  
 CC overall presence of the predetermined amino acid is limited to one or two  
 CC positions per mutated polypeptide, leaving the remaining amino acids in  
 CC the targeted region intact or as close as possible to the prototype  
 CC sequence. The invention was exemplified using the three complementarity  
 CC determining regions (CDRs) of the heavy chain of the monoclonal antibody  
 CC MCPC 603.

XX Sequence 14 AA;

Query Match 37.2%; Score 29; DB 7; Length 14;  
 Best Local Similarity 50.0%; Pred. No. 4.9e+02;  
 Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 5 DHNDYSRN 12  
 |||||

DB 7 DHNDHGH 14

RESULT 41  
 ID AAM48458  
 ID AAM48458 standard; peptide; 15 AA.

XX AAM48458;

XX 24-MAY-2002 (first entry)

DE Oestrogenic effect B pyridate protein 30.69 peptide fragment.

KW Oestrogenic effect B pyridate protein 30.69;

KW female reproduction organ maldevelopment;

KW female sexual character abnormality; female reproduction system tumour;  
 KW oestrogenic related metabolism abnormality.

XX Unidentified.

XX CN1326966-A.

XX 19-DEC-2001.

PF 05-JUN-2000; 2000CN-00116340.

XX 05-JUN-2000; 2000CN-00116340.

PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.

XX Mao Y, Xie Y;

XX WPI; 2002-206975/27.

XX New polypeptide-oestrogenic effect B pyridate protein 30.69 for treating  
 PT female reproduction organ maldevelopment, female sexual character  
 PT abnormality, female reproduction system tumor, or estrogenic related  
 PT metabolism abnormality.

XX Example 5; Page 19 (Disclosure); 33pp; Chinese.

XX The present invention relates to oestrogenic effect B pyridate protein  
 CC 30.69 (AAM48457). The protein and its coding sequence are useful in  
 CC treating various diseases, such as female reproduction organ  
 CC maldevelopment, female sexual character abnormality, female reproduction  
 CC system tumour and oestrogenic related metabolism abnormality. The present  
 CC sequence is an N-terminal peptide fragment of the protein, which was used  
 CC in an example from the invention

XX Sequence 15 AA;

Query Match 37.2%; Score 29; DB 5; Length 15;  
 Best Local Similarity 83.3%; Pred. No. 5.3e+02;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 8 DYSKNP 13  
 |||||  
 DB 8 DYSKNP 13

RESULT 42

AAB22995  
 ID AAB22995 standard; protein; 15 AA.

XX AAB22995;

XX 29-AUG-2003 (revised)

DT 21-AUG-2002 (first entry)

DE Infectious salmon anemia virus (ISAV) 9AI antigenic peptide #3.

KW Infectious salmon anemia virus; ISAV; infectious salmon anaemia;  
 KW M1 protein; M2 protein; vaccine; antigen.

XX Infectious salmon anemia virus.  
OS  
XX  
PN WO200226784-A2.  
XX  
XX  
PD 04-APR-2002.  
XX  
XX  
PF 25-SEP-2001; 2001WO-BP011129.  
XX  
XX  
PR 28-SEP-2000; 2000EP-00203358.  
XX  
XX (ALKU) AKZO NOBEL NV.  
PA  
XX Blerling E, Kirosoy B;  
PI  
XX WPI; 2002-416474/44.  
DR  
XX  
XX New infectious salmon anemia virus polynucleotide for use in diagnostics  
PT and vaccines to protect fish against the infectious salmon anemia caused  
PT by the virus.  
XX  
XX Example 2; Page 17; 33pp; English.  
PS  
XX The invention relates to polynucleotides encoding proteins M1 and M2 of  
CC infectious salmon anemia virus (ISAV). Sequences of the invention are  
CC useful in diagnostics e.g. to detect the presence of ISAV or anti-ISAV  
CC antibodies in fish, in vaccines to protect fish against the infectious  
CC salmon anaemia caused by the virus and in a marker vaccine to distinguish  
CC vaccination from field infections with the virus. Polynucleotides of the  
CC invention are used for the manufacture of DNA vaccines or vector vaccines  
CC to protect fish against the anaemia. The present sequence is an antigenic  
CC peptide of ISAV M1 and M2 protein from clone 9A1. (Updated on 29-AUG-2003  
CC to standardise OS field)  
SQ  
XX Sequence 15 AA;  
SQ  
XX  
XX Query Match 37.2%; Score 29; DB 5; Length 15;  
Best Local Similarity 66.7%; Pred. No. 5.3e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 3 KRDNND 8  
AC :||||:  
DB 5 RRDHNE 10  
DB  
XX  
XX RESULT 43  
ADU68122  
XX ID ADU68122 standard; peptide; 15 AA.  
XX  
XX AC ADU68122;  
XX  
XX DT 10-FEB-2005 (first entry)  
XX  
XX DE Human papillomavirus-derived epitope peptide SegID81.  
XX  
XX KM epitope mapping; T-cell; antiviral; cytostatic; vaccine;  
XX KM vaccine, antiviral; benign tumor; tumor.  
XX  
XX OS Human papillomavirus.  
XX  
XX PN WO2004098497-A2.  
XX  
XX PD 18-NOV-2004.  
XX  
XX PF 23-APR-2004; 2004WO-US012652.  
XX  
XX PR 28-APR-2003; 2003US-0466235P.  
XX  
XX PA (GENEV) GENENCOR INT INC.  
XX  
XX PI Babe LM, De Young LM, Harding FA, Huang MTF, Power SD,  
PI Stickler M;  
XX

DR WPI; 2004-813965/80.  
XX  
XX PT Identifying CD4+ human papillomavirus (HPV) epitopes or determining T-  
PT cell epitope of HPV strain, useful in prophylactic/therapeutic vaccines,  
PT by combining dendritic cells, CD4+ and/or CD8+ T-cells with pepset of  
PT peptides from HPV.  
XX  
XX Claim 4; SEQ ID NO 81; 56pp; English.  
PS  
XX This invention relates to a novel method of identifying CD4+ human  
CC papillomavirus (HPV) epitopes or determining a T-cell epitope of a HPV  
CC strain. The method comprises combining a solution of differentiated  
CC dendritic cells and naive CD4+ and/or CD8+ T-cells with a set of peptides  
CC from the HPV (which comprises the T-cell epitope) and measuring T-cell  
CC proliferation. The invention may be useful for the production of  
CC compounds with an antiviral or cytostatic activity. The method or the  
CC modified epitopes are useful in prophylactic and/or therapeutic vaccines,  
CC as means for the development of HPV vaccines for the prevention of  
CC infection with high-risk HPV strains, or as means for the development of  
CC therapeutic vaccines against high-risk HPV types for use in the  
CC prevention of the development of benign and/or malignant tumors in  
CC infected individuals. The present sequence is that of a Human  
CC papillomavirus-derived epitope peptide which was identified using the  
CC method of the invention.  
SQ  
XX Sequence 15 AA;  
SQ  
XX  
XX Query Match 37.2%; Score 29; DB 8; Length 15;  
Best Local Similarity 83.3%; Pred. No. 5.3e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 4 RDHNDY 9  
AC :||||:  
DB 9 RDRHDY 14  
DB  
XX  
XX RESULT 44  
ADV11512  
XX ID ADV11512 standard; peptide; 15 AA.  
XX  
XX AC ADV11512;  
XX  
XX DT 24-FEB-2005 (first entry)  
XX  
XX DE HPV type 16 E2 protein CD4+ T-cell epitope, SEQ ID NO:81.  
XX  
XX KM Papillomavirus infection; CD4+ T-cell; T-lymphocyte; E2;  
XX KM immune modulation; vaccine; tumor suppressor; infection; virucide.  
XX  
XX OS Human papillomavirus type 16.  
XX  
XX PN WO2004105681-A2.  
XX  
XX PD 09-DEC-2004.  
XX  
XX PF 23-APR-2004; 2004WO-US012650.  
XX  
XX PR 28-APR-2003; 2003US-0466235P.  
XX  
XX PA (INNO-) INNOGENETICS NV.  
XX  
XX PI Babe LM, De Young LM, Harding FA, Huang MTF, Power SD,  
PI Stickler M;  
XX  
XX DR WPI; 2005-021230/02.  
XX  
XX PT Novel isolated human papillomavirus epitope (HPV) e.g., HPV E6.16 or HPV  
PT E7.16 epitope, useful for producing medicament for inducing immune  
PT response against HPV.  
XX  
XX PS Claim 1; SEQ ID NO 81; 58pp; English.  
XX  
XX The invention relates to isolated human papillomavirus (HPV) epitopes

CC given as SEQ ID Nos 1-109 in the specification. The epitopes are CD4+ T-  
 CC cell epitopes in B6, E7 and E2 proteins isolated from various strains of  
 CC HPV. Also claimed are: a polynucleotide comprising one or more of the  
 CC nucleic acid sequences encoding an epitope of the invention, a vector  
 CC comprising the above polynucleotide, a polypeptide encoded by the above  
 CC polynucleotide, a cell comprising the above polynucleotide, a composition  
 CC comprising the above polypeptide, one or more peptide that has a HPV  
 CC epitope or one or more nucleic acid that encodes the HPV epitope, and a  
 CC vaccine composition comprising a HPV epitope or one or more nucleic acid  
 CC that encodes a HPV epitope. The HPV epitopes of the invention are useful  
 CC for producing a medicament for inducing an immune response (e.g., an  
 CC antibody-mediated response or cell-mediated response) directed against  
 CC one or more strain of HPV. The epitopes are useful in the development of  
 CC HPV vaccines (particularly multivalent vaccines) for the prevention of  
 CC infection with high-risk HPV strains. The HPV epitopes are useful in  
 CC prophylactic and therapeutic vaccines against HPV. The therapeutic  
 CC vaccines can be used to prevent the development of benign and/or  
 CC malignant tumors in HPV infected individuals. This sequence represents a  
 CC HPV epitope of the invention.

XX  
 CC Sequence 15 AA;

Query Match 37.2%; Score 29; DB 9; Length 15;  
 Best Local Similarity 83.3%; Pred. No. 5.3e+02;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 RDHNDY 9  
 |||||  
 Db 9 RDHIDY 14

RESULT 45

AEA53797  
 ID AEA53797 standard; peptide; 16 AA.

XX AEA53797;

XX 11-AUG-2005 (first entry)

XX Novel human MMP26-binding antibody-related CDR3 peptide #594.

XX antibody engineering; cytostatic; antiinflammatory; osteopathic;  
 KM antiarthritic; gene therapy; cancer; breast tumor; prostate tumor;  
 KM lung tumor; inflammation; rheumatoid arthritis; restenosis;  
 KM graft versus host disease; multiple sclerosis; gingivitis;  
 KM osteoarthritis.

XX Unidentified.

XX WO2005051299-A2.

XX 09-JUN-2005.

XX 19-NOV-2004; 2004WO-US039052.

XX 19-NOV-2003; 2003US-0523745P.

XX (DYAX-) DYAX CORP.

XX Dransfield DT, Rookey K, Ladner RC;

XX WPI, 2005-417817/42.

XX New protein comprising heavy and light chain immunoglobulin variable  
 PT domain sequences, useful in preparing a composition for treating or  
 PT preventing neoplastic or inflammatory disorders.

XX Example, Page 132, 192pp; English.

XX This invention relates to novel proteins, comprising a heavy chain  
 CC immunoglobulin variable domain sequence and a light chain immunoglobulin  
 CC variable domain sequence, which bind to matrix metalloproteinase (MMP)-26  
 CC and comprise at least one human complementarity determining region or

CC framework region. The invention may be useful for the development of  
 CC compounds with a cytostatic, antiinflammatory, osteopathic or  
 CC antiarthritic activity whilst the disclosed sequences may prove useful  
 CC for gene therapy. The protein is useful in preparing a composition for  
 CC treating or preventing neoplastic disorders, for example breast,  
 CC prostate, or lung cancer or inflammatory disorders, for example  
 CC rheumatoid arthritis, lupus, restenosis, graft versus host response or  
 CC multiple sclerosis or a disorder characterized by excessive or undesired  
 CC MMP-26 activity, for example periodontitis, rheumatoid arthritis or  
 CC osteoarthritis. The present sequence is that of a CDR peptide which was  
 CC used during the development of the novel MMP26-binding antibodies of the  
 CC invention.

XX  
 CC Sequence 16 AA;

Query Match 37.2%; Score 29; DB 9; Length 16;  
 Best Local Similarity 55.6%; Pred. No. 5.7e+02;  
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 5 DHNDYKRP 13  
 |||||  
 Db 5 DSSDYPPNP 13

RESULT 46

AEA53491  
 ID AEA53491 standard; peptide; 16 AA.

XX AEA53491;

XX 11-AUG-2005 (first entry)

XX Novel human MMP26-binding antibody-related CDR3 peptide #288.

XX antibody engineering; cytostatic; antiinflammatory; osteopathic;  
 KM antiarthritic; gene therapy; cancer; breast tumor; prostate tumor;  
 KM lung tumor; inflammation; rheumatoid arthritis; restenosis;  
 KM graft versus host disease; multiple sclerosis; gingivitis;  
 KM osteoarthritis.

XX Unidentified.

XX WO2005051299-A2.

XX 09-JUN-2005.

XX 19-NOV-2004; 2004WO-US039052.

XX 19-NOV-2003; 2003US-0523745P.

XX (DYAX-) DYAX CORP.

XX Dransfield DT, Rookey K, Ladner RC;

XX WPI, 2005-417817/42.

XX New protein comprising heavy and light chain immunoglobulin variable  
 PT domain sequences, useful in preparing a composition for treating or  
 PT preventing neoplastic or inflammatory disorders.

XX Example, Page 124, 192pp; English.

XX This invention relates to novel proteins, comprising a heavy chain  
 CC immunoglobulin variable domain sequence and a light chain immunoglobulin  
 CC variable domain sequence, which bind to matrix metalloproteinase (MMP)-26  
 CC and comprise at least one human complementarity determining region or  
 CC framework region. The invention may be useful for the development of  
 CC compounds with a cytostatic, antiinflammatory, osteopathic or  
 CC antiarthritic activity whilst the disclosed sequences may prove useful  
 CC for gene therapy. The protein is useful in preparing a composition for  
 CC treating or preventing neoplastic disorders, for example breast,  
 CC prostate, or lung cancer or inflammatory disorders, for example  
 CC rheumatoid arthritis, lupus, restenosis, graft versus host response or

CC multiple sclerosis or a disorder characterized by excessive or undesired  
CC MMP-26 activity, for example periodontitis, rheumatoid arthritis or  
CC osteoarthritis. The present sequence is that of a CDR peptide which was  
CC used during the development of the novel MMP26-binding antibodies of the  
CC invention.  
XX  
SQ Sequence 16 AA;  
  
Query Match 37.2%; Score 29; DB 9; Length 16;  
Best Local Similarity 55.6%; Pred. No. 5.7e+02;  
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
  
QY 5 DHNDYSKNP 13  
| : | | |  
Db 5 DSSDYFNP 13  
  
RESULT 47  
ADU79009  
ID ADU79009 standard; peptide; 20 AA.  
XX  
AC ADU79009;  
XX  
DT 27-JAN-2005 (first entry)  
XX  
DE Human peptide fragment, SEQ ID 382.  
XX  
KW Neuroprotective; Antidepressant; Neuroleptic; Tranquillizer;  
KW Antiparkinsonian; Nootropic; Antidiabetic; Anorectic;  
KW Cardiovascular-Gen.; Antiartherosclerotic; Antilipemic;  
KW Alzheimer's disease; neurological disorder; phosphatase; enzyme.  
XX  
OS Homo sapiens.  
XX  
PN US2004226056-A1.  
XX  
PD 11-NOV-2004.  
XX  
PF 09-FEB-2004; 2004US-00776013.  
XX  
PR 22-DEC-1998; 98US-0113534P.  
PR 12-MAR-1999; 99US-0124120P.  
PR 30-JUN-1999; 99US-0141243P.  
PR 21-DEC-1999; 99US-00466139.  
PR 17-OCT-2000; 2000US-0240790P.  
PR 13-JUL-2001; 2001US-0304775P.  
PR 10-SEP-2001; 2001US-00948904.  
PR 12-OCT-2001; 2001US-00975072.  
PR 15-JUL-2002; 2002US-00194967.  
XX  
PA (MYRI-) MYRIAD GENETICS INC.  
XX  
PI Roch J, Bartel P, Heichman K;  
XX  
DR MPI; 2004-794772/78.  
XX  
PT Selecting agents useful for treating Alzheimer's disease comprises  
PT contacting focal adhesion kinase 2 with a test agent and measuring a  
PT biological activity related to focal adhesion kinase 2 function with or  
PT without the test agent.  
XX  
PS Disclosure; SEQ ID NO 382; 247pp; English.  
XX  
CC The present invention relates to a method for selecting agents that are  
CC potentially useful for the treatment of Alzheimer's disease. The method  
CC comprises contacting focal Adhesion Kinase 2 (FAK2) with a test agent and  
CC measuring a biological activity related to FAK2 function in the presence  
CC and absence of the test agent. The method is useful for screening  
CC compounds or agents that can be used to treat neurological disorders,  
CC ailments and diseases including mild cognitive impairment, depression,  
CC schizophrenia, obsessive-compulsive disorder, bipolar disorder, and  
CC neurodegenerative diseases and disorders and motor neuron diseases and  
CC disorders such as Alzheimer's disease, Parkinson's disease, dementia with

CC Lewy bodies, amyotrophic lateral sclerosis or Lou Gehrig's disease,  
CC Alpers' disease, Leigh's disease, Pelizaeus-Werthecker disease,  
CC Olivopontocerebellar atrophy, Friedreich's ataxia, leukodystrophies, Rett  
CC syndrome, Ramsay Hunt syndrome type II, and Down's syndrome, as well as  
CC for treating or preventing other diseases such as dislipidemia, diabetes,  
CC obesity, cardiovascular diseases such as atherosclerosis and coronary  
CC heart disease. Also disclosed is the coding sequence for a novel human  
CC phosphatase called PN7740 (ADU78628 and ADU78629). PN7740 contains a  
CC protein phosphatase 2C domain, which likely acts to dephosphorylate  
CC specific phospho-serine or phospho-threonine residues on particular  
CC protein substrates. Although the precise role played by protein  
CC phosphatase 2C8 in Alzheimer's disease pathogenesis has yet to be  
CC defined, the inventors have discovered that fragments of PN7740 interact  
CC with the first phosphorylation binding domain (PTB) domain of Pe65 (also  
CC known as ABB3 (710) or amyloid beta (A4) precursor protein-binding,  
CC family B, member 1, isoform B9 (710)), suggesting that PN7740 may well be  
CC involved somehow. Pe65 is known to interact with the cytosolic C-terminal  
CC region of Amyloid beta (A4) precursor protein (APP) and APP metabolism is  
CC critical to the pathogenesis of Alzheimer's disease, because it leads to  
CC the release of either toxic Abeta or trophic secreted APP (sAPP)  
CC metabolites. The present sequence is a potentially useful agent for  
CC Alzheimer's disease.  
XX  
SQ Sequence 20 AA;  
  
Query Match 37.2%; Score 29; DB 8; Length 20;  
Best Local Similarity 50.0%; Pred. No. 7.4e+02;  
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
  
QY 6 HNDYSKNP 13  
| : | | |  
Db 3 HNDYRNP 10  
  
RESULT 48  
ABW02632  
ID ABW02632 standard; peptide; 17 AA.  
XX  
AC ABW02632;  
XX  
DT 12-FEB-2004 (first entry)  
XX  
DE Human oestrogen receptor (ER) alpha mutant peptide, ER2.  
XX  
KW Tamoxifen activated system; TAS; 4-hydroxytamoxifen; OHT; gene therapy;  
KW oestrogen receptor; ER; fundamental research; transgenic; biomedical;  
KW disease model; breast cancer; human; mutant; mutlein.  
XX  
OS Homo sapiens.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 16..17  
FT /note= "Encoded by GAC"  
XX  
PN US2003199022-A1.  
XX  
PD 23-OCT-2003.  
XX  
PF 11-MAR-2002; 2002US-00095373.  
XX  
PR 11-MAR-2002; 2002US-00095373.  
XX  
PA (UNIT ) UNITV ILLINOIS FOUNO.  
XX  
PI Mao C, Shapiro DJ;  
XX  
DR MPI; 2003-852787/79.  
XX  
DR N-PSDB; AAD64541.  
XX  
PT New isolated polynucleotide useful for gene therapy applications (e.g. in  
PT treating breast cancer), in vivo and in vitro gene expression, in  
PT producing bioactive or toxic polypeptides, in research, or in producing

PT transgenic animals.  
 XX  
 PS Claim 12, SEQ ID NO 12, Opp; English.  
 CC  
 CC The invention relates to tamoxifen activated system (TAS) and 4-  
 CC hydroxytamoxifen (OHT) activated system for regulated production of  
 CC proteins in eukaryotic cells. TAS includes mutant oestrogen receptors  
 CC (BRs) and chimeras thereof. The invention is useful in gene therapy (e.g.  
 CC in treating breast cancer) or in vivo and in vitro gene expression, in  
 CC producing bioactive, toxic, recombinant polypeptides in mammalian cells,  
 CC in biomedical and fundamental research, or in producing transgenic  
 CC animals. The transgenic animals may be used as disease models, in  
 CC studying the function and/or activity of a polypeptide, or in identifying  
 CC and/or evaluating modulators of a polypeptide activity. The present  
 CC sequence is human ERalpha mutant peptide used in TAS  
 CC  
 SQ Sequence 17 AA;  
 Query Match 36.5%; Score 28.5; DB 7; Length 17;  
 Best Local Similarity 77.8%; Pred. No. 7.5e+02;  
 Matches 7; Conservative 0; Mismatches 1; Indels 1; Gaps 1;  
 QY 1 SIKRDHNDY 9  
 Db 10 SIAR-HNDY 17  
 RESULT 49  
 AAY55315  
 ID AAY55315 standard; peptide; 10 AA.  
 XX  
 AC AAY55315;  
 XX  
 DT 07-JAN-2000 (first entry)  
 XX  
 DE CD34 antigen antigenic peak peptide SEQ ID NO:209.  
 XX  
 KM Antibody releasing peptide; CD34; hybridoma; binding; antigen;  
 KM cell surface antigen; identification; haematopoietic stem cell; tumour;  
 KM cancer; immune system; therapy; displacement.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 XX  
 PN US5968753-A.  
 XX  
 PD 19-OCT-1999.  
 XX  
 PF 07-JUN-1995; 95US-00482228.  
 XX  
 PR 14-JUN-1994; 94US-00259427.  
 XX  
 PA (NEXE-) NEXELL THERAPEUTICS INC.  
 XX  
 PI Guillermo R. Helgeson SL, Deans RJ, Tseng-Law J, Kobori JA;  
 PI Al-Abdaly FA;  
 XX  
 DR WPI; 1999-590399/50.  
 XX  
 PT Short peptides useful for displacing antibodies from cell surface  
 PT antigens.  
 XX  
 PS Example 11, Col 38, 81pp; English.  
 XX  
 CC The present invention describes peptides of 4-17 amino acids which  
 CC displace either the anti-CD34 monoclonal antibody designated 561, the  
 CC anti-CD34 mouse monoclonal antibody produced by the hybridoma ATCC HB-  
 CC 11646 (designated 9063), the anti-CD34 antibody produced by hybridoma  
 CC ATCC HB-11885 (9079), or the anti-human breast cancer antibody produced  
 CC by hybridoma ATCC HB-11884 (9187), from a cell surface antigen on a  
 CC target cell. The peptides are useful for displacing antibodies bound to  
 CC cell surfaces to release cells that have been positively selected by  
 CC antibody-mediated binding to beads or other solid support. AAY5107 to

CC AAY55319 represent peptides used in the exemplification of the present  
 CC invention  
 CC  
 SQ Sequence 10 AA;  
 Query Match 35.3%; Score 28; DB 2; Length 10;  
 Best Local Similarity 50.0%; Pred. No. 4.9e+02;  
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
 QY 4 RDHNDYSK 11  
 Db 1 KDHSYSQ 8  
 RESULT 50  
 AAY87061  
 ID AAY87061 standard; peptide; 10 AA.  
 XX  
 AC AAY87061;  
 XX  
 DT 09-MAY-2000 (first entry)  
 XX  
 DE Human haematopoietic CD34+ cell binding peptide SEQ ID #209.  
 XX  
 KM Human; haematopoietic CD34+ cell; binding peptide; monoclonal antibody;  
 KM non-enzymatic cell selection method; haematopoietic stem cell;  
 KM haematopoietic progenitor cell; antibody 561; breast cancer cell;  
 KM antibody 9187; cell surface determinant; diagnostic cell based assay.  
 XX  
 OS Homo sapiens.  
 OS  
 PN US6017719-A.  
 XX  
 PD 25-JAN-2000.  
 XX  
 PF 07-JUN-1995; 95US-00482528.  
 XX  
 PR 14-JUN-1994; 94US-00259427.  
 XX  
 PA (NEXE-) NEXELL THERAPEUTICS INC.  
 XX  
 PI Guillermo R. Helgeson SL, Deans RJ, Tseng-Law J, Kobori JA;  
 PI Al-Abdaly FA;  
 XX  
 DR WPI; 2000-136676/12.  
 XX  
 PT Non-enzymatic method for the positive selection of target cells from a  
 PT heterogeneous cell suspension, useful for selecting human breast cancer  
 PT cells from a patient's blood or bone marrow.  
 XX  
 PS Example 11; Col 43; 82pp; English.  
 XX  
 CC This sequence represents a human haematopoietic CD34+ cell binding  
 CC peptide, and was used to test the method of the invention. The method is  
 CC a non-enzymatic method for the positive selection of one or more target  
 CC cells from a heterogeneous cell suspension, by using specific peptides  
 CC which effect the displacement and release of a specific target cell from  
 CC a specific monoclonal antibody. The method is useful for positive  
 CC selection and specific release of target human haematopoietic  
 CC stem/progenitor cells bound by the monoclonal anti-CD34 antibodies and  
 CC the antibody 561. The method is also useful for positive selection and  
 CC specific release of target human breast cancer cells, bound by the  
 CC monoclonal anti-breast cancer antibody 9187, from a patient's blood or  
 CC bone marrow. Identification of peptide epitopes for antibodies which  
 CC recognize cell surface determinants also allows construction of  
 CC diagnostic cell based assays. The peptide mediated release is enzyme free  
 CC and thus leaves the cell surface proteins intact. Moreover, peptide  
 CC mediated release leaves the target cell free of bound antibody or  
 CC antibody fragments. The method also produces a high yield of functional  
 CC target cells and is relatively inexpensive to carry out  
 CC  
 SQ Sequence 10 AA;

Query Match 35.9%; Score 28; DB 3; Length 10;  
 Best Local Similarity 50.0%; Pred. No. 4.9e+02;  
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 4 RDNDYYSK 11  
 :|||:  
 Db 1 KDHQSYSQ 8

## RESULT 51

ABJ36893  
 ID ABJ36893 standard; peptide; 11 AA.

AC ABJ36893;

DT 01-MAY-2003 (first entry)

DE G protein coupled receptor related peptide SEQ ID NO 247.

XX Nootropic; cardiast; antiarteriosclerotic; hypotensive; cytoastric;  
 XX antibacterial; analgesic; antiallergic; antisthmatic; antiinflammatory;  
 XX osteoparactic; neuroprotective; anxiolytic; anorectic; lead compound;  
 XX G protein coupled receptor signaling inhibitor; GPCR; library;  
 XX high throughput screening assay; stroke; myocardial infarction;  
 XX restenosis; atherosclerosis; hypotension; cancer; infection; asthma;  
 XX septic shock; pain; allergic disorder; inflammatory bowel disease;  
 XX osteoporosis; obesity; psychotic; neurological disorder; anxiety;  
 XX schizophrenia; Alzheimer's disease.

OS Unidentified.

PN WO200272778-A2.

PD 19-SEP-2002.

PF 14-MAR-2002; 2002WO-US007561.

XX 14-MAR-2001; 2001US-0275472P.

PR 11-MAY-2001; 2001US-00852910.

XX (CUBB-) CUB BIOTECH.

PI Gilchrist A, Hamm HE;

DR WPI; 2003-247841/24.

XX Identifying G protein coupled receptor (GPCR) signaling inhibitors,  
 PT useful in screening drugs for treating stroke, cancers or pain, by  
 PT identifying compounds that block GPCR mediated signaling with high  
 PT affinity and specificity.

PS Claim 94; Page 69; 94pp; English.

XX The invention relates to a novel method for identifying a G protein  
 CC coupled receptor (GPCR) signaling inhibitor. The novel method comprises  
 CC selecting or identifying a member of a library of peptides and/or  
 CC candidate compounds, having binding to a GPCR of higher affinity than  
 CC that of the native peptide. The peptide library is based on a native GPCR  
 CC binding peptide. The method is useful for identifying inhibitors of a G  
 CC protein coupled receptor (GPCR) signaling. The method is particularly  
 CC useful for identifying drugs that antagonise the binding between a GPCR  
 CC and its extracellular ligand(s). The method is especially useful in  
 CC modern high throughput screening assays for identifying potent lead  
 CC compounds. The compounds, peptides or inhibitors identified by the method  
 CC are useful for preventing, ameliorating or treating diseases in which  
 CC GPCR signaling is a causative factor or in which a specific class of G  
 CC protein is relevant, e.g. stroke, myocardial infarction, restenosis,  
 CC atherosclerosis, hypotension, cancers, infections, septic shock, pain,  
 CC allergic disorders, asthma, inflammatory bowel disease, osteoporosis,  
 CC obesity, or psychotic and neurological disorders (e.g. anxiety,  
 CC schizophrenia or Alzheimer's disease). This sequence represents a peptide  
 CC relating to the G protein coupled receptors of the invention

SQ Sequence 11 AA;

Query Match 35.9%; Score 28; DB 6; Length 11;  
 Best Local Similarity 50.0%; Pred. No. 5.5e+02;  
 Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 2 IRDNDY 9  
 :|||:  
 Db 1 LQRDHYEY 8

## RESULT 52

ADT51321  
 ID ADT51321 standard; peptide; 11 AA.

AC ADT51321;

DT 13-JAN-2005 (first entry)

DE G protein coupled receptor signalling modifying peptide #222.

XX cerebroprotective; vasotropic; cardiast; antiarteriosclerotic;  
 XX hypotensive; cytoastric; antibacterial; fungicide; virucide; analgesic;  
 XX antiallergic; antisthmatic; antiinflammatory; antiparkinsonian;  
 XX neuroprotective; nootropic; gene therapy; G protein coupled receptor;  
 XX GPC.

OS Synthetic.

PN WO2004092199-A2.

PD 28-OCT-2004.

PF 12-APR-2004; 2004WO-US011167.

XX 11-APR-2003; 2003US-00411336.

PA (CUBB-) CUB BIOTECH INC.

PI Gilchrist A, Hamm HM;

DR WPI; 2004-766826/75.

XX Identifying modulators of G protein coupled receptor (GPCR) signaling,  
 PT useful for treating diseases associated with altered GPCR signaling (e.g.  
 PT stroke), comprises screening a peptide library for high affinity binding  
 PT to the GPCR.

PS Disclosure; SEQ ID NO 247; 264pp; English.

XX The invention relates to a method of identifying a G protein coupled  
 CC receptor (GPCR) signaling modifying peptide by providing a peptide  
 CC library based on a native GPCR binding peptide, screening the peptide  
 CC library for high affinity binding to the GPCR, and selecting a member of  
 CC the peptide library having binding to the GPCR of higher affinity than  
 CC that of the native peptide. The composition and methods are useful for  
 CC identifying modulators of GPCR signaling, for modulating the activity of  
 CC GPCR or for drug designing. These may be used for diagnosing, preventing  
 CC or treating diseases associated with altered GPCR signaling, such as  
 CC stroke, myocardial infarction, atherosclerosis, hypertension, cancer,  
 CC infections (e.g. bacterial, fungal or viral), pain, allergies, asthma,  
 CC inflammation, Parkinson's disease and Alzheimer's disease. This sequence  
 CC corresponds to a peptide of the invention.

XX Sequence 11 AA;

Query Match 35.9%; Score 28; DB 8; Length 11;  
 Best Local Similarity 50.0%; Pred. No. 5.5e+02;  
 Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 2 IRDNDY 9  
 :|||:  
 Db 1 LQRDHYEY 8

RESULT 53  
 AAB39702 standard; peptide; 12 AA.  
 ID AAB39702;  
 AC AAB39702;  
 XX  
 DT 05-FEB-2001 (first entry)  
 DE Anti-IL12 antibody L chain CDR3 related amino acid sequence SEQ ID 218.  
 XX  
 KM Human; neutralizing antibody; interleukin-12; IL-12; antiinflammatory;  
 KM complementarity determining region; CDR; antineumatic; antiarthritic;  
 KM antileptotic; neuroprotective; antipsoriatic; antiaesthetic; cardiant;  
 KM antiparasitic; antibacterial; immunosuppressive; Crohn's disease;  
 KM multiple sclerosis; rheumatoid arthritis.  
 XX  
 OS Homo sapiens.  
 OS  
 PN WO200056772-A1.  
 XX  
 PD 28-SEP-2000.  
 XX  
 PF 24-MAR-2000; 2000WO-US007946.  
 XX  
 PR 25-MAR-1999; 99US-0126603P.  
 XX  
 PA (BADI ) BASP AG.  
 PA (GEMY ) GENETICS INST INC.  
 XX  
 PI Salfield JG, Roguska M, Paskind M, Banerjee S, Tracey DE, White M;  
 PI Kaymakcalan Z, Labovsky B, Sakorafas P, Friedrich S, Myles A;  
 PI Veidman GM, Venturini A, Warner NW, Widom A, Elvin JG, Duncan AR;  
 PI Derbyshire EJ, Carmen S, Smith S, Holter TL, Du Fou SL;  
 XX  
 DR WPI; 2000-638250/61.  
 XX  
 PT New human antibody specific for human interleukin-12 (IL-12) used to  
 PT treat disorders characterized by aberrant IL-12 expression e.g. Crohn's  
 PT disease and multiple sclerosis.  
 PT  
 PS Example 1; Page 129; 377pp; English.  
 XX  
 CC This invention relates to a new human antibody specific for human  
 CC interleukin-12 (IL-12). The invention also includes antigen binding  
 CC portions that bind to IL-12. Sequences AAB39485-B39516 represent human  
 CC anti-IL-12 antibody heavy and light chain complementarity determining  
 CC region (CDR) amino acid sequences, and also includes variable region  
 CC amino acid sequences. Other variable region amino acid sequences are  
 CC given in AAB39517-B39560 and AAB40068-B40149. Sequences AAB39561-B39771  
 CC represent anti-IL-12 CDR3 related amino acid sequences, AAB39772-B40063  
 CC represent other CDR sequences. Light chain CDR3 consensus sequences are  
 CC given in AAB40064-B40067. Primers used in the identification and  
 CC construction of the antibodies of the invention are given in AAC61062-  
 CC C61071. The antibody of the invention is a neutralizing antibody and has  
 CC antineumatic; antiarthritic; antileptotic; antiinflammatory;  
 CC neuroprotective; antipsoriatic; antiaesthetic; cardiant; antiparasitic;  
 CC antibacterial and immunosuppressive activity. The antibodies or antigen-  
 CC binding fragments are useful in the treatment of disorders associated  
 CC with detrimental release of human IL-12, especially Crohn's disease,  
 CC multiple sclerosis and rheumatoid arthritis. They can also be used in the  
 CC manufacture of a pharmaceutical composition to treat human IL-12  
 CC disorders.  
 CC  
 SQ Sequence 12 AA;  
 XX  
 Query Match 35.9%; Score 28; DB 3; Length 12;  
 Best Local Similarity 50.0%; Pred. No. 6.1e+02;  
 Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 SIKRDHNDYS 10  
 | | | | |

DB 2 SYDRGHNNPS 11  
 RESULT 54  
 ADF53455  
 ID ADF53455 standard; peptide; 14 AA.  
 XX  
 AC ADF53455;  
 XX  
 DT 12-FEB-2004 (first entry)  
 DE MCP6 603 antibody CDR2 mutant peptide amino acid sequence 16.  
 XX  
 KM walk-through mutagenesis; prototype amino acid; prototype nucleotide;  
 KM mutant polypeptide production; MCP6 603;  
 KM complementarity determining region; CDR; heavy chain; CDR2; mutant;  
 KM meteln.  
 XX  
 OS Unidentified.  
 OS Synthetic.  
 OS  
 PN WO2003089671-A1.  
 XX  
 PD 30-OCT-2003.  
 XX  
 PF 16-APR-2003; 2003WO-US011935.  
 XX  
 PR 17-APR-2002; 2002US-0373686P.  
 XX  
 PA (CREA/) CREA R.  
 PA (CAP/) CAPPUCCILLI G.  
 XX  
 PI Crea R, Cappuccilli G;  
 PI  
 DR WPI; 2003-854132/79.  
 XX  
 PT Walk-through mutagenesis of a nucleic acid encoding a polypeptide, useful  
 PT for producing mutant polypeptides comprising synthesizing oligonucleotides  
 PT comprising a nucleotide sequence for each target region of a prototype  
 PT amino acid.  
 PT  
 PS Example; Fig 6; 40pp; English.  
 XX  
 CC This invention relates to a novel method of walk-through mutagenesis of a  
 CC nucleic acid encoding a polypeptide which comprises synthesizing a  
 CC mixture of oligonucleotides comprising a nucleotide sequence for each  
 CC target region of a prototype amino acid, where each oligonucleotide  
 CC contains at each sequence position in the target region, a prototype  
 CC nucleotide for synthesis of the prototype amino acid, or a predetermined  
 CC nucleotide that is required for synthesis of the predetermined amino  
 CC acid. The method is useful in producing mutant polypeptides in which the  
 CC overall presence of the predetermined amino acid is limited to one or two  
 CC positions per mutated polypeptide, leaving the remaining amino acids in  
 CC the targeted region intact or as close as possible to the prototype  
 CC sequence. The invention was exemplified using the three complementarity  
 CC determining regions (CDRs) of the heavy chain of the monoclonal antibody  
 CC MCP6 603.  
 CC  
 SQ Sequence 14 AA;  
 XX  
 Query Match 35.9%; Score 28; DB 7; Length 14;  
 Best Local Similarity 57.1%; Pred. No. 7.3e+02;  
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 QY 5 DHNDYSK 11  
 | | | | |  
 DB 7 DHSDHDK 13  
 | | | | |  
 RESULT 55  
 ADU00097  
 ID ADU00097 standard; peptide; 14 AA.  
 XX

```

AC ADU00097;
XX
XX 13-JAN-2005 (first entry)
XX
XX Amino acid sequence of the Chk2 phosphorylation site of Cdc25A.
XX
XX Chk2; E2F-1; DNA damage; DNA damage signalling pathway;
XX checkpoint control; tumour suppressor; drug discovery; checkpoint kinase;
XX Cdc25A.
XX
XX Unidentified.
XX
XX WO2004092738-A2.
XX
XX 28-OCT-2004.
XX
XX 15-APR-2004; 2004WO-GB001631.
XX
XX 15-APR-2003; 2003GB-00008711.
XX
XX (UNITU ) UNIV GLASGOW.
XX
XX La Thangue NB, Stevens C;
XX
XX WPI; 2004-758394/74.
XX
XX
XX Determining the activity of a Chk2 polypeptide, useful in drug discovery
XX industry, comprises contacting a Chk2 polypeptide and an E2F-1
XX polypeptide comprising residue Ser 364 and determining whether Ser 364
XX has been phosphorylated.
XX
XX Example; Fig 2b; 41pp; English.
XX
XX The specification describes a method for determining the activity of
XX checkpoint kinase Chk2. The method comprises contacting a Chk2
XX polypeptide and an E2F-1 polypeptide comprising residue Ser 364 under
XX conditions in which Chk2 is able to phosphorylate the E2F-1 polypeptide,
XX and determining whether the Ser 364 residue of E2F-1 polypeptide has been
XX phosphorylated. Chk2 functions as a key effector of E2F-1 induction
XX during DNA damage. The regulation of E2F-1 activity through the DNA
XX damage signalling pathway and specifically by Chk2 implies a role for E2F
XX -1 in checkpoint control. Such a role for E2F-1 may contribute to the
XX tumour suppressor activity of E2F-1. Antibodies which bind preferentially
XX to the phosphorylated form of E2F-1 protein are useful for prognosing
XX or determining whether Ser 364 of E2F-1 in samples obtained from patients
XX is in a phosphorylated or unphosphorylated form, thus useful for
XX determining appropriate treatments for patients. The method is useful in
XX the drug discovery industry. ADU00097-ADU00102 represent Chk2
XX phosphorylation sites, which were compared to derive a consensus
XX
XX
XX Sequence 14 AA;
SQ
Query Match 35.9%; Score 28; DB 8; Length 14;
Best Local Similarity 50.0%; Pred. No. 7.3e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 1 SIKRDND 8
Db 2 ALKSHSD 9

```

```

XX
XX Modified phage library; screening; cell-surface associated protein;
XX therapeutic; diagnostic; disease; ligand; drug; toxin; fractionation;
XX noise elimination; bacteriophage.
XX
XX Enterobacteria phage M13.
XX
XX WO9906542-A1.
XX
XX 11-FEB-1999.
XX
XX 29-JUL-1998; 98WO-GB002269.
XX
XX 30-JUL-1997; 97GB-00016094.
XX
XX (UNITU ) UNIV GLASGOW.
XX
XX Allen JM, Lavery B;
XX
XX WPI; 1999-153772/13.
XX
XX
XX Modified phage display library depleted in phage that react with native
XX cellular proteins - provides reduced noise and higher signal-to-noise
XX ratio when screened against cells transfected to express a specific
XX heterologous protein, used to identify potential therapeutic and
XX diagnostic agents.
XX
XX Example 1; Page 29; 49pp; English.
XX
XX The invention relates to a modified phage library for use with a selected
XX strain of cells that have been transformed to express a heterologous
XX protein (I) in a screening procedure, to detect specific binding between
XX individual phage and a recognition site on the heterologous protein. The
XX modified library is produced as follows. The initial phage library is
XX fractionated by contact with strain of cells that do not express (I) to
XX bind any phage that bind to cellular proteins other than the (I). Bound
XX and unbound phages are separated to produce the modified library,
XX depleted in components that bind proteins other than (I). The library is
XX used to identify phage that bind to cell-surface associated (I)
XX specifically receptors. Peptides identified by screening with the
XX modified library are potentially useful as therapeutic and diagnostic
XX agents, for diseases involving (I) or its ligands (including as carriers
XX for delivering drugs, toxins or antibodies to cells), and their amino
XX acid sequences can be used to design other agents for the same uses. The
XX initial fractionation eliminates much of the noise caused by binding to
XX other cell-surface proteins, and the use of transfected cells for
XX screening (these express a far greater number of (I) than wild-type
XX cells) improves the signal-to-noise ratio. The number of rounds of
XX screening may thus be reduced. (Updated on 27-AUG-2003 to correct OS
XX field.) (Updated on 17-OCT-2003 to standardise OS field)
XX
XX
XX Sequence 15 AA;
SQ
Query Match 35.9%; Score 28; DB 2; Length 15;
Best Local Similarity 50.0%; Pred. No. 7.9e+02;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 5 DNDYSKPM 14
Db 6 DNDPEQIPPL 15

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RESULT 56
AAW95137
ID AAW95137 standard; peptide; 15 AA.
XX
XX AAW95137;
XX
XX 17-OCT-2003 (revised)
XX 27-AUG-2003 (revised)
XX 24-MAY-1999 (first entry)
XX
XX Peptide X8 expressed by a modified bacteriophage library.
DE

```

```

RESULT 57
ADH62398
ID ADH62398 standard; peptide; 15 AA.
XX
XX ADH62398;
XX
XX 25-MAR-2004 (first entry)
XX
XX Arabidopsis thaliana EDS1 peptide.
XX
XX PAD4; resistance; microbial disease; crop improvement; ornamental;
XX
XX

```



KW	gene therapy; plant protectant; mouse-ear crabs; enzyme; mouse-ear crabs
XX	
OS	Arabidopsis thaliana.
XX	
PN	US6620985-B1.
XX	
XX	16-SEP-2003.
PD	
XX	
PF	04-NOV-1999; 99US-00434840.
XX	
PR	12-NOV-1998; 98US-0183020P.
XX	
PA	(UYMA-) UNIV MARYLAND BIOTECHNOLOGY INST.
PA	(PLAN-) PLANT BIOSCIENCE LTD.
PI	Glazebrook J, Jirage D, Tootle TL, Zhou N, Feyes BJF;
DR	WPI, 2003-895430/82.
XX	
PT	New PAD4 proteins and nucleic acids from Arabidopsis, useful for
PT	enhancing the resistance of a plant to disease such as those caused by
PR	virus, bacteria, fungi, oomycetes, nematodes or insects.
XX	
PS	Example 3; SEQ ID NO 81; 105bp, English.
XX	
CC	The present invention provides PAD4 compositions and methods for using
CC	PAD4 compositions for enhancing disease resistance of a plant. The
CC	invention is useful for enhancing the resistance of a plant to disease
CC	such as those caused by virus, bacteria, fungi, oomycetes, nematodes and
CC	insects. The invention is also useful in producing plants having enhanced
CC	disease resistance and in-plant protection against diseases which
CC	consequently reduces or minimizes the need for traditional chemical
CC	practices, increases production efficiency, improves crop and ornamental
CC	quality. The invention is also useful in gene therapy. The present
CC	sequence is Arabidopsis thaliana EDS1 peptide.
XX	
SQ	Sequence 15 AA;
Query Match	35.9%; Score 28; DB 7; Length 15;
Best Local Similarity	50.0%; Pred. No. 7.9e+02;
Matches	4; Conservative 2; Mismatches 2; Indels 0; Gaps 0
QY	4 RDHNDYSK 11
	: :
DB	8 RDHHSYEE 15
RESULT 58	
ADU15281	
ID	ADU15281 standard; peptide; 16 AA.
XX	
AC	ADU15281;
XX	
DT	27-JAN-2005 (first entry)
XX	
DE	Clostridium difficile-specific human antibody CDR-H3 peptide - SEQ ID 27.
XX	
KM	vaccine; antibody; antigen binding fragment; infection; CDR-H3.
XX	
OS	Homo sapiens.
XX	
PN	WO2004094474-A1.
XX	
PD	04-NOV-2004.
XX	
PF	14-APR-2004; 2004WO-GB001619.
XX	
PR	17-APR-2003; 2003GB-00009126.
XX	
PA	(NEUT-) NEUTECH PHARMA PLC.
XX	
PI	Burnle JP, Matthews RC;
XX	

DR WP1; 2004-795532/78.  
XX  
XX New Clostridium difficile focused antibodies for diagnosing, preventing  
PT or treating infections caused by C. difficile, comprises the  
PT complementarity determining region (CDR-H3 and/or CDR-L3 sequences.  
XX  
XX  
PS Claim 1; SEQ ID NO 27, 91PP; English.  
XX  
XX The invention comprises antibodies/antigen binding fragments that target  
CC Clostridium difficile. The antibodies and antigen binding fragments of  
CC the invention are useful for diagnosing, preventing (vaccine), and  
CC treating infections caused by Clostridium difficile. The present amino  
CC acid sequence represents a Clostridium difficile-specific human antibody  
CC CDR-H3 peptide of the invention.  
XX  
XX  
SQ Sequence 16 AA;  
  
Query Match 35.9%; Score 28; DB 8; Length 16;  
Best Local Similarity 66.7%; Pred. No. 8.5e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
  
QY 5 DHNDYS 10  
|||:  
db 6 DHNDPS 11

RESULT 59	
ADU15291	
ID ADU15291 standard; peptide; 16 AA.	
XX	
AC ADU15291;	
XX	
DT 27-JAN-2005 (first entry)	
DE Clostridium difficile-specific human antibody VH CDR3 peptide SEQ ID 37.	
XX vaccine; antibody; antigen binding fragment; infection; VH CDR3.	
XX Homo sapiens.	
OS	
PN WO2004094474-A1.	
XX	
PD 04-NOV-2004.	
XX	
PF 14-APR-2004; 2004WO-GB001619.	
XX	
PR 17-APR-2003; 2003GB-00009126.	
XX	
PA (NEUT-) NEUTEC PHARMA PLC.	
PI	
PI Burnie JP, Matthews RC;	
XX	
DR WPI; 2004-795532/78.	
XX	
PT New Clostridium difficile focused antibodies for diagnosing, preventing	
PT or treating infections caused by C. difficile, comprises the	
PT complementarily determining region (CDR-H3 and/or CDR-L3 sequences.	
XX	
PS Disclosure; SEQ ID NO 37; 91pp; English.	
CC	
CC The invention comprises antibodies/antigen binding fragments that target	
CC Clostridium difficile. The antibodies and antigen binding fragments of	
CC the invention are useful for diagnosing, preventing (vaccine), and	
CC treating infections caused by Clostridium difficile. The present amino	
CC acid sequence represents a Clostridium difficile-specific human antibody	
CC VH CDR3 peptide of the invention.	
XX	
SO Sequence 16 AA;	
Query Match	35.9%; Score 28; DB 8; Length 16;
Best Local Similarity	66.7%; Pred. No. 8.5e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;	

QY 5 DHNDYS 10  
 ||:|:  
 DB 6 DHRHDFS 11

RESULT 60  
 ADU15292  
 ID ADU15292 standard; peptide; 16 AA.

XX ADU15292;

XX 27-JAN-2005 (first entry)

XX Clostridium difficile-specific human antibody VH CDR3 peptide SEQ ID 38.

XX vaccine; antibody; antigen binding fragment; infection; VH CDR3.

OS Homo sapiens.

XX MO2004094474-A1.

XX 04-NOV-2004.

XX 14-APR-2004; 2004MO-GB001619.

XX 17-APR-2003; 2003GB-00009126.

XX (NEUT-) NEUTEC PHARMA PLC.

XX Burnie JP, Matthews RC;

XX WPI; 2004-795532/78.

PT New Clostridium difficile focused antibodies for diagnosing, preventing or treating infections caused by C. difficile, comprises the complementarity determining region (CDR)-H3 and/or CDR-L3 sequences.

XX Disclosure; SEQ ID NO 38; 91pp; English.

CC The invention comprises antibodies/antigen binding fragments that target Clostridium difficile. The antibodies and antigen binding fragments of the invention are useful for diagnosing, preventing (vaccine), and treating infections caused by Clostridium difficile. The present amino acid sequence represents a Clostridium difficile-specific human antibody VH CDR3 peptide of the invention.

XX Sequence 16 AA;

Query Match 35.9%; Score 28; DB 8; Length 16;  
 Best Local Similarity 66.7%; Pred. No. 8.5e+02;  
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 DHNDYS 10  
 ||:|:  
 DB 6 DHRHDFS 11

RESULT 61  
 AAU08976  
 ID AAU08976 standard; peptide; 17 AA.

XX AAU08976;

XX 18-DEC-2001 (first entry)

XX Human CDC25A inhibitory peptide #2.

XX Human; CDC25A; Ser123; cancer; hyperproliferative disorder; cytostatic;  
 KW antiproliferative; antineoplastic; antineoplastic; arteriogenesis; inflammation;  
 KW checkpoint kinase; Chk1, Chk2.

XX Homo sapiens.

FH Key Location/Qualifiers  
 FT Region 7  
 FT /note= "Serine corresponding Serine 123 of full length  
 FT CDC25A which is phosphorylated by checkpoint kinase 1 or  
 FT 2"

XX MO200166708-A2.

XX 13-SEP-2001.

XX 08-MAR-2001; 2001WO-GB001008.

XX 08-MAR-2000; 2000GB-00005573.

XX 15-JAN-2001; 2001GB-00001021.

XX (ZEAL-) ZEALAND PHARM AS.

XX (KIDD/) KIDDLE S.

XX Maitland N, Falck J, Bartek J, Lukas J, Lukas C, Syljuasen R;

XX WPI; 2001-589937/66.

PT Substance which is capable of inhibiting interaction of Cdc25A and cell cycle checkpoint kinase 1 or 2 for preparation of medicament for treatment of cancer or hyperproliferative disorder.

XX Claim 8; Page 4; 73pp; English.

CC The invention relates to the use of a substance (S) which is capable of inhibiting the interaction of CDC25A and cell cycle checkpoint kinase 1 (Chk1) or Chk2 for the preparation of a medicament for the treatment of cancer or a hyperproliferative disorder. The substances are derivatives or fragments of peptides based on regions of CDC25A which are phosphorylated by Chk1 or 2, i.e. regions surrounding serine residues at positions 123, 262, 292 and 504 of CDC25A. The substance is useful for the preparation of a medicament for the treatment of cancer or a hyperproliferative disorder such as psoriasis, arteriogenesis or inflammation and is useful in a method of medical treatment, for identifying binding partners of the substance or compounds having the property of binding to Chk1 or Chk2 and inhibiting the phosphorylation of CDC25A, and for raising antibodies capable of specifically binding to the CC CDC25A. Nucleic acids encoding the peptides are useful in gene therapy for treating cancer. The present sequence is a peptide derived from the CC region of CDC25A surrounding Ser123

XX Sequence 17 AA;

Query Match 35.9%; Score 28; DB 4; Length 17;  
 Best Local Similarity 50.0%; Pred. No. 9.2e+02;  
 Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 SIKRDHND 8  
 ::|||:  
 DB 3 ALKRSHSD 10

RESULT 62  
 ADR45757  
 ID ADR45757 standard; peptide; 18 AA.

XX ADR45757;

XX 18-NOV-2004 (first entry)

XX Peptide derived from antibody region binding to HIV-1 gp120.

XX gp120; human immunodeficiency virus type 1; HIV-1; sulphated tyrosine;  
 KW viral surface; immune cell; HIV-1 entry; AIDS; HIV infection;  
 KW CCR5 receptor.

XX Synthetic.

XX Key Location/Qualifiers

FT	Modified-site	2	/note= "this residue must be present, and is optionally sulphated"
FT	Modified-site	6	/note= "this residue must be present, and is optionally sulphated"
PR	WO2004072096-A2.		
PB	26-AUG-2004.		
XX			
XX	06-FEB-2004; 2004WO-US003467.		
PF			
XX	10-FEB-2003; 2003US-0445853P.		
PR	(BGHM ) BRIGHAM & WOMENS HOSPITAL.		
PA			
XX	Farzán MR, Dorfman TK;		
PI	WPI; 2004-616038/59.		
XX			
PT	New peptides that bind gp120 of HIV-1, useful for blocking the entry of HIV-1 into cells, for studying or treating AIDS, or for developing new approaches to control HIV infection.		
PT			
XX	Claim 1; SEQ ID NO 2; 27pp; English.		
PB			
CC	ADRA5756-ADRA5761 represent peptides which bind to gp120 of human immunodeficiency virus type 1 (HIV-1). The peptides are derived from the region of anti-HIV-1 antibodies which bind to gp120. This region has sulphated tyrosines, which must be present in the present peptides. The affinity of the peptides for gp120 on the HIV-1 viral surface may be increased by sulphating tyrosine residues. The peptides are useful for preventing the binding of gp120 to CCR5 receptors on the surface of immune cells, thus blocking the entry of HIV-1 into cells. They may be used for studying or treating AIDS and for developing new approaches to control HIV infection.		
CC			
XX	Sequence 18 AA;		
SQ			
Query Match	35.9%; Score 28; DB 8; Length 18;		
Best Local Similarity	66.7%; Pred. No. 9.8e+02;		
Matches	4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;		
Qy	5 DHNDYS 10  : : : 5 DYNDYA 10		
Db			
RESULT 63			
AEA89657			
ID	AEA89657 standard; peptide; 19 AA.		
XX			
AC	AEA89657;		
DT	25-AUG-2005 (first entry)		
XX			
DE	Tumor metastases treatment-related protein region #45.		
XX			
KM	metastasis; therapeutic; gene expression; cytostatic; tumor; breast tumor; sarcoma; nervous system tumor; prostate tumor; pancreas tumor; colon tumor; rectal tumor; medulloblastoma; b-cell lymphoma; c-cell lymphoma; multiple myeloma; lung tumor; cancer.		
KV			
OS	Unidentified.		
XX			
PN	WO2005056043-A2.		
PD			
XX	23-JUN-2005.		
PP			
XX	10-DEC-2004; 2004WO-IT000689.		
PK			
XX	11-DEC-2003; 2003IT-RM000572.		

XX	(ZOLL/) ZOLLO M.
PA	
XX	Zollo M,
PI	
XX	
DR	WPI, 2005-445065/45.
XX	
PT	Use of inhibitors of human-PRUNE cyclic nucleotide phosphodiesterase for
PR	preparation of medicament in the treatment of tumor metastases associated
XX	with overexpression of human-PRUNE.
XX	
PS	Example 1; Fig 1; 89pp; English.
XX	
CC	This invention relates to a novel method for preparing a medicament for
CC	the treatment of tumor metastases associated with overexpression of human
CC	-PRUNE. The method comprises using inhibitors of human-PRUNE cyclic
CC	nucleotide phosphodiesterase. The invention may be useful for the
CC	development of compounds with a cytostatic activity acting as human-PRUNE
CC	overexpression inhibitors. The invention is useful for preparation of
CC	medicaments in the treatment of tumor metastases, for example breast
CC	carcinoma, sarcoma, neuroblastoma, prostate tumor, pancreatic tumor,
CC	colonic tumor, rectal tumor, medulloblastoma, epithelioma, epatocarcinoma,
CC	cell T or cell B lymphomas, myeloma and melanoma and pulmonary tumor. As
CC	the h-PRUNE poses cyclic nucleotide phosphodiesterase activity with
CC	preferential activity for camp over cgm, the h-PRUNE overexpression can
CC	be effectively suppressed by certain pde inhibitors thus the pde
CC	inhibitor provides an effective alternative therapy for cancer treatment.
CC	The present sequence is that of a protein motif which was used during the
CC	development of the novel method of the invention.
XX	
SQ	Sequence 19 AA;
XX	
Query Match	35.9%; Score 28; DB 9; Length 19;
Beat Local Similarity	36.4%; Pred. No. 1e+03;
Matches	4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
OY	2 IKRDNDYSKN 12
	:::
DB	5 ILTDHNEFQS 15
XX	
RESULT 64	
ID	AAR15556
XX	AAR15556 standard; protein; 20 AA.
XX	
AC	AAR15556;
XX	
DT	02-MAR-1992 (first entry)
XX	
DR	Immunopeptide #7 derived from HPV16 E2 peptide.
XX	
KM	cervical cancer; cervical intraepithelial neoplasia; CIN; wart;
XX	squamous cell carcinoma; ELISA; HPV 16.
XX	
OS	Synthetic.
XX	
PN	MO9118294-A.
XX	
PD	28-NOV-1991.
XX	
PF	11-MAY-1990; 90SE-00001705.
XX	
PR	11-MAY-1990; 90SE-00001705.
XX	
PA	(MEDS-) MEDSCAND AB.
XX	
PI	Dillner J, Dillner L, Cheng HW;
XX	
DR	WPI, 1991-369390/50.
XX	
PT	Diagnosis of human papilloma virus infection and PV-carrying tumours -
XX	using synthetic peptide(s) to detect virus specific antigen-antibody
XX	complexes by immunoassay.

XX Disclosure; Page 38; 72pp; English.  
 PS  
 XX  
 CC This is one of a large number of peptides which have been synthesised on  
 CC the basis of the amino acid sequences for the E2, E4, E7, L1 or L2  
 CC proteins of HPV 1, 5, 6, 8, 11, 16, 18, 31 and 33. The selection of  
 CC peptide sequences was based on the assumption that an immunoreactive  
 CC region might be situated in the same relative region of a protein from  
 CC different HPV types. The peptides were used in diagnostic immunoassays to  
 CC detect HPV-infection. See AAR15523-R15601  
 CC  
 SQ Sequence 20 AA;  
 Query Match 35.9%; Score 28; DB 2; Length 20;  
 Best Local Similarity 60.0%; Pred. No. 1.1e+03;  
 Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 QY 3 KRDNDSKN 12  
 DB 7 KDDAEKYSKN 16  
 RESULT 65  
 AAR45558  
 ID AAR45558 standard; protein; 20 AA.  
 XX  
 AC AAR45558;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 13-JUL-1994 (first entry)  
 DE Cry j I pollen allergen peptide CJI-17.  
 XX  
 DE Japanese cedar; detection; allergy; treatment; diagnosis; T cell epitope;  
 KM sensitivity.  
 KM Cryptomeria japonica.  
 OS  
 XX WO9401560-A1.  
 XX  
 PD 20-JAN-1994.  
 XX  
 PF 15-JAN-1993; 93WO-US000139.  
 XX  
 PR 10-JUL-1992; 92WO-US005661.  
 PR 01-SEP-1992; 92US-00938990.  
 XX  
 PA (IMMU-) IMMUNOLOGIC PHARM CORP.  
 XX  
 PI Griffith ID, Pollock J, Bond JF, Garman RD, Kuo M;  
 XX  
 DR WPI, 1994-035066/04.  
 XX  
 PT Antigens derived from Japanese cedar pollen allergen Cry j I - contain at  
 PT least two T cell epitope(s), used to treat or diagnose allergy.  
 XX  
 PS Claim 1; Fig 13; 137pp; English.  
 XX  
 CC The sequence is that of an isolated peptide of the Japanese cedar pollen  
 CC allergen Cry j I (amino acids 161-180). The peptide, CJI-17, can be used  
 CC for the treatment and diagnosis of allergies associated with Japanese  
 CC cedar pollen. It has enhanced therapeutic properties but reduced side  
 CC effects compared to naturally occurring allergens. (Updated on 25-MAR-  
 CC 2003 to correct PN field.)  
 CC  
 SQ Sequence 20 AA;  
 Query Match 35.9%; Score 28; DB 2; Length 20;  
 Best Local Similarity 50.0%; Pred. No. 1.1e+03;  
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
 QY 5 DHNDYSKN 12  
 ||| : | :

DB 4 DHNSFSNS 11  
 RESULT 66  
 AAR82507  
 ID AAR82507 standard; protein; 20 AA.  
 XX  
 AC AAR82507;  
 XX  
 DT 27-AUG-2003 (revised)  
 DT 15-APR-1996 (first entry)  
 DE Cry j I Japanese Cedar pollen allergen peptide fragment (CJI-17).  
 XX  
 DE Cry j I; Japanese cedar pollen allergen; modified; drug production;  
 KM allergy; Cryptomeria japonica.  
 XX  
 OS Cryptomeria japonica.  
 XX  
 PN WO9527786-A1.  
 XX  
 PD 19-OCT-1995.  
 XX  
 PF 06-APR-1995; 95WO-US004249.  
 XX  
 PR 08-APR-1994; 94US-00226248.  
 PR 06-DEC-1994; 94US-00350225.  
 XX  
 PA (IMMU-) IMMUNOLOGIC PHARM CORP.  
 XX  
 PI Franzen HM, Powers SP, Kuo M, Evans S, Shaked Z, Chen X;  
 XX  
 DR WPI, 1995-366391/47.  
 XX  
 PT Modified Cryptomeria japonica (Cry j) I peptide(s) - useful for treating  
 PT allergy to Japanese cedar pollen allergen or immunologically cross  
 PT reactive allergens.  
 XX  
 PS Disclosure; Fig 2; 60pp; English.  
 XX  
 CC Novel peptides of cry j I have been modified as a part of a  
 CC preformulation scheme to develop an optimised drug product for  
 CC therapeutic treatment of humans suffering from allergy to Japanese cedar  
 CC pollen allergen or an allergen which is immunologically cross reactive  
 CC with Japanese cedar pollen allergen. Such modified peptides possess  
 CC certain characteristics which render them particularly suitable for drug  
 CC product formulation. Peptide fragments of Cry j I, modified and  
 CC unmodified, are given in AAR82491-R82525. This peptide fragment  
 CC corresponds to amino acids 161-180 of the allergen mature protein.  
 CC (Updated on 27-AUG-2003 to correct OS field.)  
 CC  
 SQ Sequence 20 AA;  
 Query Match 35.9%; Score 28; DB 2; Length 20;  
 Best Local Similarity 50.0%; Pred. No. 1.1e+03;  
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
 QY 5 DHNDYSKN 12  
 ||| : | :  
 DB 4 DHNSFSNS 11  
 RESULT 67  
 ADD93865  
 ID ADD93865 standard; peptide; 20 AA.  
 XX  
 AC ADD93865;  
 XX  
 DT 29-JAN-2004 (first entry)  
 XX  
 DE Japanese cedar pollen allergen Cry j I peptide, SEQ ID NO:17.  
 XX  
 KM Japanese cedar; pollen allergen; Cry j I; dog; Canis familiaris;

KM allergic dermatitis; veterinary; DNA vaccine; dermatological;  
 KM antiinflammatory; vaccine; gene therapy.  
 OS Cryptomeria japonica.  
 XX JP2003116556-A.  
 XX  
 PD 22-Apr-2003.  
 XX  
 XX 09-Oct-2001, 2001JP-00311433.  
 XX  
 XX 09-Oct-2001, 2001JP-00311433.  
 XX  
 XX 09-Oct-2001, 2001JP-00311433.  
 XX  
 PA (NIPZ ) NIPPON ZENYAKU KOGYO KK.  
 XX  
 DR WPI, 2003-771273/73.  
 XX  
 XX New cedar pollinosis antigen T-cell epitope in a dog useful for preparing  
 PT a DNA vaccine that can be used to prevent allergic dermatitis.  
 XX  
 XX Example 7, SEQ ID NO 17, 20pp; Japanese.  
 PS  
 CC The invention relates to T-cell epitopes of the Japanese cedar  
 CC (Cryptomeria japonica) pollen allergen Cry j 1 which stimulate an immune  
 CC response in dogs. The invention also encompasses DNA encoding the Cry j 1  
 CC T-cell epitopes, a vector comprising a Cry j 1 T-cell epitope-encoding  
 CC DNA, and DNA vaccine containing a vector of the invention for the  
 CC treatment of allergic dermatitis. The Cry j 1 T-cell epitopes and their  
 CC encoding nucleic acids are useful in the preparation of vaccines,  
 CC especially DNA vaccines, for the treatment of allergic dermatitis in  
 CC dogs. The DNA vaccine of the invention can be prepared inexpensively with  
 CC easier manufacturing and purification processes. The present sequence  
 CC represents a Cry j 1 peptide used in an example of the invention.  
 XX  
 XX Sequence 20 AA;  
 SQ  
 Query Match 35.9%; Score 28; DB 7; Length 20;  
 Best Local Similarity 50.0%; Pred. No. 1.1e+03;  
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
 QY 5 DHNDYSKN 12  
 ||| :| :  
 Db 4 DHNSFSNS 11  
 RESULT 68  
 AEB24275  
 ID AEB24275 standard; peptide; 20 AA.  
 XX  
 AC AEB24275;  
 XX  
 DT 22-SEP-2005 (first entry)  
 XX  
 DE Japanese cedar pollen allergen T-cell epitope, SEQ ID 203.  
 XX  
 KW pollen; allergen; transformation; antiallergic; pollinosis.  
 XX  
 OS Cryptomeria japonica.  
 OS  
 PN US2005152927-A1.  
 PN  
 PD 14-JUL-2005.  
 PD  
 XX 30-AUG-2004, 2004US-00931260.  
 XX  
 XX 12-JUL-1991, 91US-00729134.  
 PR 15-JUL-1991, 91US-00730452.  
 PR 01-SEP-1992, 92US-00938990.  
 PR 12-NOV-1992, 92US-00975179.  
 PR 15-JAN-1993, 93WO-US000139.  
 PR 08-APR-1994, 94US-00226248.  
 PR 29-JAN-1999, 99US-00240203.  
 XX

PA (IMMU-) IMMUNOLOGIC PHARM CORP.  
 XX  
 XX Griffith J, Pollock J, Bond JF, Garman RD, Kuo M, Powers SP;  
 PI Exley MA, Chen X, Shaked Z;  
 XX  
 DR WPI, 2005-496786/50.  
 XX  
 XX New Japanese cedar pollen allergen produced in a host cell, useful in  
 PT preparing a composition for diagnosing, treating or preventing Japanese  
 PT cedar pollinosis.  
 XX  
 PS Disclosure; SEQ ID NO 203; 189pp; English.  
 XX  
 CC The invention relates to a novel isolated Japanese cedar pollen allergen.  
 CC The allergen is produced in a host cell transformed with a nucleic acid,  
 CC comprising any of the fully defined sequences having 1337 or 1726 bp  
 CC (AEB24081 or AEB24213). The invention further comprises: an isolated  
 CC peptide of a Japanese cedar pollen allergen, comprising any of the fully  
 CC defined sequences having 374 or 514 amino acids (AEB24082 or AEB24214),  
 CC where the peptide has at least one epitope of the pollen allergen, and  
 CC where the epitope does not consist of amino acid residues 1-20 or 325-340  
 CC of the 374-amino acid sequence. The isolated Japanese cedar pollen  
 CC allergen has an antiallergic activity as it is useful in preparing a  
 CC composition for diagnosing, treating or preventing Japanese cedar  
 CC pollinosis. This sequence represents a Japanese cedar pollen allergen  
 CC epitope polypeptide of the invention.  
 XX  
 XX Sequence 20 AA;  
 SQ  
 Query Match 35.9%; Score 28; DB 9; Length 20;  
 Best Local Similarity 50.0%; Pred. No. 1.1e+03;  
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
 QY 5 DHNDYSKN 12  
 ||| :| :  
 Db 10 DHNSFSNS 17  
 RESULT 69  
 AEB24122  
 ID AEB24122 standard; peptide; 20 AA.  
 XX  
 AC AEB24122;  
 XX  
 DT 22-SEP-2005 (first entry)  
 XX  
 DE Japanese cedar pollen allergen T-cell epitope, SEQ ID 42.  
 XX  
 KW pollen; allergen; transformation; antiallergic; pollinosis.  
 XX  
 OS Cryptomeria japonica.  
 OS  
 PN US2005152927-A1.  
 PN  
 PD 14-JUL-2005.  
 PD  
 XX 30-AUG-2004, 2004US-00931260.  
 XX  
 XX 12-JUL-1991, 91US-00729134.  
 PR 15-JUL-1991, 91US-00730452.  
 PR 01-SEP-1992, 92US-00938990.  
 PR 12-NOV-1992, 92US-00975179.  
 PR 15-JAN-1993, 93WO-US000139.  
 PR 08-APR-1994, 94US-00226248.  
 PR 29-JAN-1999, 99US-00240203.  
 XX  
 PA (IMMU-) IMMUNOLOGIC PHARM CORP.  
 XX  
 XX Griffith J, Pollock J, Bond JF, Garman RD, Kuo M, Powers SP;  
 PI Exley MA, Chen X, Shaked Z;  
 XX  
 DR WPI, 2005-496786/50.  
 XX

PT New Japanese cedar pollen allergen produced in a host cell, useful in  
PT preparing a composition for diagnosing, treating or preventing Japanese  
PT cedar pollinosis.  
XX  
PS Example 6; SEQ ID NO 42; 189pp; English.  
CC The invention relates to a novel isolated Japanese cedar pollen allergen.  
CC The allergen is produced in a host cell transformed with a nucleic acid,  
CC comprising any of the fully defined sequences having 1337 or 1726 bp  
CC (AEB24081 or AEB24213). The invention further comprises: an isolated  
CC peptide of a Japanese cedar pollen allergen, comprising any of the fully  
CC defined sequences having 374 or 514 amino acids (AEB24082 or AEB24214),  
CC where the peptide has at least one epitope of the pollen allergen, and  
CC where the epitope does not consist of amino acid residues 1-20 or 325-340  
CC of the 374-amino acid sequence. The isolated Japanese cedar pollen  
CC allergen has an antiallergic activity as it is useful in preparing a  
CC composition for diagnosing, treating or preventing Japanese cedar  
CC pollinosis. This sequence represents a Japanese cedar pollen allergen  
CC epitope polypeptide of the invention.  
XX  
SQ Sequence 20 AA;  
Query Match 35.9%; Score 28; DB 9; Length 20;  
Best Local Similarity 50.0%; Pred. No. 1.1e+03;  
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
QY 5 DHNDYSKN 12  
DB 4 DHNSPSSNS 11  
RESULT 70  
ID ADR84038  
XX ADR84038 standard; peptide; 19 AA.  
XX ADR84038;  
XX  
DT 02-DEC-2004 (first entry)  
XX  
DE S. pyogenes hyperimmune system reactive antigen SPA3316.1.  
XX  
KM hyperimmune serum reactive antigen; vaccine; anticaline.  
XX  
OS Streptococcus pyogenes.  
XX  
PN MO2004078907-AA.  
XX  
PD 16-SEP-2004.  
XX  
PF 02-MAR-2004; 2004MO-EP002087.  
XX  
PR 04-MAR-2003; 2003EP-00450061.  
XX  
PA (INTE-) INTERCELL AG.  
XX  
PI Meinke A, Nagy E, Winkler B, Gelbmann D;  
XX  
DR WPI; 2004-653698/63.  
XX  
PT New isolated nucleic acid molecules encoding hyperimmune serum-reactive  
PT antigens from Streptococcus pyogenes, useful for diagnosing, preventing  
PT and treating S. pyogenes infections.  
XX  
XX  
PS Claim 14; Page 69; 145pp; English.  
CC This invention describes a novel nucleic acid molecule encoding a  
CC hyperimmune serum reactive antigen or its fragment from Streptococcus  
CC pyogenes. The nucleic acid molecule or hyperimmune serum-reactive antigen  
CC or its fragment are useful for the manufacture of a pharmaceutical  
CC preparation, especially a vaccine, against S. pyogenes infection. In  
CC addition, the hyperimmune serum reactive antigen or fragment is used for  
CC the isolation and/or purification and/or identification of an interaction  
CC partner of the hyperimmune serum reactive antigen or its fragment, for

CC the generation of a peptide (e.g. anticaline) binding to the antigen or  
CC fragment, or for the manufacture of a functional nucleic acid selected  
CC from aptamers and spligeners. The nucleic acid molecule may also be used  
CC for the manufacture of functional ribonucleic acids, such as ribozymes,  
CC antisense nucleic acids and siRNA. ADR83733-ADR84189 represent S.  
CC pyogenes hyperimmune serum reactive antigens, fragments and the encoding  
CC polynucleotide described in the invention.  
XX  
SQ Sequence 19 AA;  
Query Match 35.3%; Score 27.5; DB 8; Length 19;  
Best Local Similarity 54.5%; Pred. No. 1.3e+03;  
Matches 6; Conservative 2; Mismatches 2; Indels 1; Gaps 1;  
QY 3 KRDH-NDYSKN 12  
DB 4 RHDHVCYSRN 14  
RESULT 71  
ID AAE14547  
XX AAE14547 standard; peptide; 7 AA.  
XX AAE14547;  
XX  
DT 17-MAY-2002 (first entry)  
XX  
DE Human alpha-synuclein aggregation inhibitor #2.  
XX  
KM Alpha-synuclein; inhibitor; neurodegenerative disease; Lewy body;  
KM Parkinson's disease; Alzheimer's disease; diffuse Lewy body disease;  
KM multiple system atrophy; Hallervorden-Spatz disease; human.  
XX  
OS Homo sapiens.  
XX  
PN WO200204482-A1.  
XX  
PD 17-JAN-2002.  
XX  
PF 06-JUL-2001; 2001WO-US021379.  
XX  
PR 07-JUL-2000; 2000US-0217319P.  
XX  
PR 28-MAR-2001; 2001US-0279199P.  
XX  
PA (PANA-) PANACRA PHARM INC.  
XX  
PI Wolozin B, Ostrebova-Golts N, Lebowitz MS;  
XX  
DR WPI; 2002-179695/23.  
XX  
PT Determination of an agent capable of inhibiting aggregation of alpha  
PT synuclein useful for treating a neurodegenerative disease involves  
PT determining aggregation of alpha synuclein in the presence of exogenous  
PT iron or copper.  
XX  
PS Claim 40; Page 37; 52pp; English.  
XX  
XX  
CC The invention relates to screening of inhibitors of alpha-synuclein  
CC aggregation in the presence of exogenous iron or copper. The inhibitors  
CC are magnesium and alpha-synuclein binding peptides, which are useful for  
CC treating neurodegenerative disease that involves the formation of Lewy  
CC bodies e.g. Parkinson's disease (PD), Alzheimer's disease (AD), diffuse  
CC Lewy body disease, mixed AD-PD, multiple system atrophy and Hallervorden-  
CC Spatz disease. The present sequence is a peptide that binds to C-terminal  
CC portion of human alpha-synuclein and inhibits its aggregation  
XX  
SQ Sequence 7 AA;  
Query Match 34.6%; Score 27; DB 5; Length 7;  
Best Local Similarity 66.7%; Pred. No. 2e+06;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 9 YSKNPM 14

Db |::|:  
2 YAKKPI 7

RESULT 72  
ADSI4010  
ID ADSI4010 standard; peptide; 7 AA.  
XX  
AC ADSI4010,  
XX  
DT 02-DEC-2004 (first entry)  
XX  
DE Thrombin peptide inhibitor segment - SEQ ID 61.  
XX  
KM thrombin inhibitor; fibrinogen recognition exosite; anticoagulant.  
XX  
OS Synthetic.  
XX  
PN WO2004076484-A1.  
XX  
PD 10-SEP-2004.  
XX  
PF 27-FEB-2004; 2004WO-CA000301.  
XX  
PR 27-FEB-2003; 2003US-0449878P.  
XX  
PA (CANADA) NAT RES COUNCIL CANADA.  
XX  
PI N1 F, Su Z, Tolkatchev D, Natapova A, Koutychenko A;  
XX  
DR WPI; 2004-653369/63.  
XX  
PT New isolated or purified multivalent polypeptide inhibitors of thrombin  
PT containing only genetically encodable natural amino acids, useful as  
PT potent anticoagulants.  
XX  
PS Claim 5; SEQ ID NO 61; 158bp; English.  
XX  
CC The invention comprises peptide inhibitors of thrombin. The peptide  
CC inhibitors of the invention consist of the general formula: SBM-PPM-SBM;  
CC SBM is a sequence moiety comprising P-substrate residues of the thrombin  
CC inhibitor, PPM is a sequence moiety comprising P'-substrate residues of the  
CC thrombin inhibitor, and SBM is a peptide sequence moiety that binds to  
CC the fibrinogen recognition exosite of thrombin. The peptide inhibitors of  
CC the invention are useful for inhibiting thrombin or as anticoagulants.  
CC The present amino acid sequence represents a PPM segment of a thrombin  
CC inhibitor peptide of the invention.  
XX  
SQ Sequence 7 AA;  
XX

Query Match 34.6%; Score 27; DB 8; Length 7;  
Best Local Similarity 80.0%; Pred. No. 2e+06;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 RDND 8  
|::|:  
Db 2 QDND 6

RESULT 73  
AAM96968  
ID AAM96968 standard; peptide; 8 AA.  
XX  
AC AAM96968;  
XX  
DT 24-JAN-2002 (first entry)  
XX  
DE Human peptide #243 encoded by a SNP oligonucleotide.  
XX  
KM Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;  
KM neuroprotective; antimicrobial; gene therapy; vaccine; amylose; cancer;  
KM amyloid protein; angiotensin; apoptosis related protein; cadherin;  
KM cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;

KM complement related protein; cytochrome; kinesin; cytokine; interferon;  
KM interleukin; G-protein coupled receptor; thioesterase; inflammation;  
KM multifactorial disease; autoimmune disease; infection;  
KM nervous system disease.  
XX  
OS Homo sapiens.  
XX  
PN WO200147944-A2.  
XX  
PD 05-JUL-2001.  
XX  
PF 28-DEC-2000; 2000WO-US035498.  
XX  
PR 28-DEC-1999; 99US-0173419P.  
PR 27-DEC-2000; 2000US-00173419.  
XX  
PA (CURA-) CURAGEN CORP.  
XX  
PI Shinkets RA, Leach M;  
XX  
DR WPI; 2001-465210/50.  
XX  
XX Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,  
PT oncogenes and histones, useful for diagnosing and treating, e.g. cancer,  
PT autoimmune diseases and infections.  
XX  
PS Disclosure; Page 3721; 4143bp; English.  
XX  
CC The present invention relates to oligonucleotides (see AYL26793-AYL34659)  
CC encoding polymorphic variants of proteins related to amylases, amyloid  
CC proteins, angiotensin, apoptosis related proteins, cadherin, cyclin,  
CC polymerase, oncogenes, histones, kinases, colony stimulating factors,  
CC complement related proteins, cytochromes, kinesins, cytokines,  
CC interferons, interleukins, G-protein coupled receptors and thioesterases.  
CC The present sequence is a peptide encoded by one such oligonucleotide.  
CC The oligonucleotides and the peptides encoded by them may be used in the  
CC prevention, diagnosis and treatment of diseases associated with  
CC inappropriate expression of the proteins listed above. Disorders that may  
CC be prevented, diagnosed and/or treated include multifactorial diseases  
CC with a genetic component, such as autoimmune diseases (e.g. rheumatoid  
CC arthritis, multiple sclerosis, diabetes, systemic lupus erythematosus  
CC and Grave's disease), inflammation, cancer (e.g. cancers of the bladder,  
CC brain, breast, colon and kidney, leukaemia), diseases of the nervous  
CC system and an infection of pathogenic organisms  
XX  
SQ Sequence 8 AA;  
XX

Query Match 34.6%; Score 27; DB 4; Length 8;  
Best Local Similarity 83.3%; Pred. No. 2e+06;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 KRND 8  
|::|:  
Db 1 KRND 6

RESULT 74  
ADK08340  
ID ADK08340 standard; peptide; 9 AA.  
XX  
AC ADK08340;  
XX  
DT 06-MAY-2004 (first entry)  
XX  
DE Human papillomavirus peptide #395.  
XX  
KM pathogenic virus; alternative reading frame; antigenic determinant;  
KM viricide; vaccine; therapeutic agent; infection; HPV.  
XX  
OS Human papillomavirus.  
XX  
PN WO2004011650-A2.  
XX

PD 05-FEB-2004.  
XX  
PF 24-JUL-2003; 2003MO-BF008112.  
XX  
PR 24-JUL-2002; 2002AT-00001124.  
XX  
PR 11-JUL-2003; 2003EP-00450171.  
XX  
PA (INTE-) INTERCELL AG.  
XX  
PI Matner F, Schmidt W, Habel A;  
XX  
DR WPI, 2004-169243/16.  
XX  
PT Virus comprising an antigenic determinant, useful for treating or  
PT preventing an infection with the pathogenic virus.  
XX  
PS Claim 18; Page 177; 220pp; English.  
XX  
CC This invention relates to a novel polypeptide encoded by an alternative  
CC reading frame of a pathogenic virus, where the polypeptide starts with a  
CC methionine amino acid residue, which comprises an antigenic determinant  
CC and more than 7 amino acid residues. The invention may be useful for the  
CC production of compounds with a virucide activity or the development of a  
CC vaccine. The polypeptide or its fragments may be useful as a therapeutic  
CC agent. It is also useful for the manufacture of a medicament for treating  
CC or preventing an infection with the pathogenic virus. The present  
CC sequence is that of a human papillomavirus (HPV) epitope peptide of the  
CC invention.  
XX  
SQ Sequence 9 AA;  
XX  
Query Match 34.6%; Score 27; DB 8; Length 9;  
Best Local Similarity 62.5%; Pred. No. 2e+06; Indels 0; Gaps 0;  
Matches 5; Conservative 1; Mismatches 2;  
QY 5 DHNDYSKN 12  
Db 1 DHIDYWKH 8  
XX  
RESULT 75  
ABJ36831  
ID ABJ36831 standard; peptide; 11 AA.  
XX  
AC ABJ36831;  
XX  
DT 01-MAY-2003 (first entry)  
XX  
DE G protein coupled receptor related peptide SEQ ID NO 185.  
XX  
KW Nootropic; cardiant; antiarteriosclerotic; hypotensive; cyrostatic;  
KW antidiabetic; analgesic; antiallergic; antiaslomatic; antiinflammatory;  
KW osteopathic; neuroprotective; anxiolytic; anorectic; lead compound;  
KW G protein coupled receptor signaling inhibitor; GPCR; library;  
KW high throughput screening assay; stroke; myocardial infarction;  
KW restenosis; atherosclerosis; hypotension; cancer; infection; asthma;  
KW septic shock; pain; allergic disorder; inflammatory bowel disease;  
KW osteoporosis; obesity; psychotic; neurological disorder; anxiety;  
KW schizophrenia; Alzheimer's disease.  
XX  
OS Unidentified.  
XX  
PN WO200272778-A2.  
XX  
PD 19-SEP-2002.  
XX  
PF 14-MAR-2002; 2002MO-US007561.  
XX  
PR 14-MAR-2001; 2001US-0275472P.  
XX  
PR 11-MAY-2001; 2001US-00852910.  
XX  
PA (CUBB-) CUB BIOTECH.

XX  
PI Gilchrist A, Hamm HE;  
XX  
DR WPI, 2003-247841/24.  
XX  
PT Identifying G protein coupled receptor (GPCR) signalling inhibitors,  
PT useful in screening drugs for treating stroke, cancers or pain, by  
PT identifying compounds that block GPCR mediated signalling with high  
PT affinity and specificity.  
XX  
PS Claim 94; Page 65; 94pp; English.  
XX  
XX  
CC The invention relates to a novel method for identifying a G protein  
CC coupled receptor (GPCR) signalling inhibitor. The novel method comprises  
CC selecting or identifying a member of a library of peptides and/or  
CC candidate compounds, having binding to a GPCR of higher affinity than  
CC that of the native peptide. The peptide library is based on a native GPCR  
CC binding peptide. The method is useful for identifying inhibitors of a G  
CC protein coupled receptor (GPCR) signalling. The method is particularly  
CC useful for identifying drugs that antagonise the binding between a GPCR  
CC and its extracellular ligand(s). The method is especially useful in  
CC modern high throughput screening assays for identifying potent lead  
CC compounds. The compounds, peptides or inhibitors identified by the method  
CC are useful for preventing, ameliorating or treating diseases in which  
CC GPCR signaling is a causative factor or in which a specific class of G  
CC protein is relevant, e.g. stroke, myocardial infarction, restenosis,  
CC atherosclerosis, hypotension, cancer, infections, septic shock, pain,  
CC allergic disorders, asthma, inflammatory bowel disease, osteoporosis,  
CC obesity, or psychotic and neurological disorders (e.g. anxiety,  
CC schizophrenia or Alzheimer's disease). This sequence represents a peptide  
CC relating to the G protein coupled receptors of the invention  
XX  
SQ Sequence 11 AA;  
XX  
Query Match 34.6%; Score 27; DB 6; Length 11;  
Best Local Similarity 33.3%; Pred. No. 8.2e+02;  
Matches 3; Conservative 5; Mismatches 1; Indels 0; Gaps 0;  
QY 2 IKRDNDYS 10  
Db 1 LQNNHNEYN 9  
XX  
RESULT 76  
ADTS1259  
ID ADTS1259 standard; peptide; 11 AA.  
XX  
AC ADTS1259;  
XX  
DT 13-JAN-2005 (first entry)  
XX  
DE G protein coupled receptor signalling modifying peptide #160.  
XX  
KW cerebroprotective; vasotropic; cardiant; antiarteriosclerotic;  
KW hypotensive; cyrostatic; antibacterial; fungicide; virucide; analgesic;  
KW antiallergic; antiaslomatic; antiinflammatory; antiparkinsonian;  
KW neuroprotective; nootropic; gene therapy; G protein coupled receptor;  
KW GPC.  
XX  
OS Synthetic.  
XX  
PN WO2004092199-A2.  
XX  
PD 28-OCT-2004.  
XX  
PF 12-APR-2004; 2004MO-US011167.  
XX  
PR 11-APR-2003; 2003US-00411336.  
XX  
PA (CUBB-) CUB BIOTECH INC.  
XX  
PI Gilchrist A, Hamm HM;  
XX



DR WPI; 2004-766826/75.  
XX  
PT Identifying modulators of G protein coupled receptor (GPCR) signaling.  
PT useful for treating diseases associated with altered GPCR signaling (e.g.  
PT stroke), comprises screening a peptide library for high affinity binding  
PT to the GPCR.  
XX  
PS Disclosure; SEQ ID NO 185; 264pp; English.  
XX  
CC The invention relates to a method of identifying a G protein coupled  
CC receptor (GPCR) signaling modifying peptide by providing a peptide  
CC library based on a native GPCR binding peptide, screening the peptide  
CC library for high affinity binding to the GPCR, and selecting a member of  
CC the peptide library having binding to the GPCR of higher affinity than  
CC that of the native peptide. The composition and methods are useful for  
CC identifying modulators of GPCR signaling, for modulating the activity of  
CC GPCR or for drug designing. These may be used for diagnosing, preventing  
CC or treating diseases associated with altered GPCR signaling, such as  
CC stroke, myocardial infarction, atherosclerosis, hypertension, cancer,  
CC inflammation, Parkinson's disease and Alzheimer's disease. This sequence  
CC corresponds to a peptide of the invention.  
XX  
SQ Sequence 11 AA;  
XX  
Query Match 34.6%; Score 27; DB 8; Length 11;  
Best Local Similarity 33.3%; Pred. No. 8.2e+02;  
Matches 3; Conservative 5; Mismatches 1; Indels 0; Gaps 0;  
XX  
QY 2 IKRDHNDYS 10  
Db 1 LOMNHNEYN 9  
XX  
RESULT 77  
ID AAR83314 standard; peptide; 12 AA.  
XX  
AC AAR83314;  
XX  
DT 24-MAY-1996 (first entry)  
XX  
DE Kb-binding random peptide, B2.  
XX  
KM MHC; Kb; major histocompatibility complex; terminal; identification;  
KM investigation; random.  
XX  
OS Synthetic.  
XX  
PN WO9527901-A1.  
XX  
PD 19-OCT-1995.  
XX  
PF 10-APR-1995; 95WO-US004509.  
XX  
PR 11-APR-1994; 94US-00227101.  
XX  
PA (IXSY-) IXSYS INC.  
XX  
PI Gay DA;  
XX  
DR WPI; 1995-366462/47.  
XX  
PT Identifying peptide(s) which bind MHC molecules - using a library of  
PT random peptide(s) expressed as fusion proteins and obtaining terminal  
PT octamers or nonamers.  
XX  
PS Disclosure; Fig 5; 46pp; English.  
XX  
CC AAR83313-R83350 are random MHC binding peptides which are identified from  
CC a library of random peptides expressed as fusion proteins on the surface  
CC of a cell or virus. These peptides are isolated using the murine MHC  
CC molecule Kb. The identification method rapidly identifies MHC binding

CC motif, provides sequence information on neighbouring amino acids and  
CC relationships between amino acids within the peptides and reveals a  
CC preference for several amino acids at peptide positions previously  
CC thought to be indiscriminate  
XX  
SQ Sequence 12 AA;  
XX  
Query Match 34.6%; Score 27; DB 2; Length 12;  
Best Local Similarity 83.3%; Pred. No. 9.1e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
XX  
QY 8 DYSKNP 13  
Db 4 DYSWNP 9  
XX  
RESULT 78  
ID AAY88130 standard; peptide; 12 AA.  
XX  
AC AAY88130;  
XX  
DT 17-OCT-2000 (first entry)  
XX  
DE Fluorescein binding peptide fluorette #7.  
XX  
KM Fluorette; fluorophore dye; fluorescent; detection; diagnostic.  
XX  
OS Synthetic.  
XX  
PN WO200023463-A2.  
XX  
PD 27-APR-2000.  
XX  
PF 15-OCT-1999; 99WO-US024266.  
XX  
PR 16-OCT-1998; 98US-0104465P.  
XX  
PA (STRD ) UNIV LEELAND STANFORD JUNIOR.  
XX  
PI Nolan GP, Rozinov MN;  
XX  
DR WPI; 2000-339647/29.  
XX  
PT Novel fluorette peptides which bind with high specificity to fluorophore  
PT dyes, useful for detecting biological materials, molecules, target  
PT analytes, and intra- and inter-molecular interactions.  
XX  
PS Claim 11; Page 19; 64pp; English.  
XX  
CC This invention describes a novel peptide (I) termed a fluorette which  
CC comprises a sequence of at least 8 amino acids and which binds to a  
CC fluorophore dye. The fluorettes maybe used in detecting biological  
CC materials, molecules or target analytes, intracellular events, and intra-  
CC and inter-molecular interactions, as well as discovering effective  
CC inhibitors. They may also be used for in vitro assays using a large set  
CC of fluorophore dyes, e.g. in detection of viral and delivery systems,  
CC diagnostics and high throughput assays. The new peptides, due to their  
CC small size, are not intrusive to the systems being studied hence, permit  
CC detection and analysis of a target moiety or molecule while minimizing  
CC target modification. Unlike conventional techniques such as the light-  
CC emitting technique, the use of fluorettes minimize or avoid substantial  
CC genetic manipulations which may disrupt, interfere, or alter the process  
CC being measured. This sequence represents a peptide fluorette capable of  
CC binding to Fluorescein which is described in the method of the invention  
XX  
SQ Sequence 12 AA;  
XX  
Query Match 34.6%; Score 27; DB 3; Length 12;  
Best Local Similarity 100.0%; Pred. No. 9.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
QY 6 HNDY 9

```

Db          |||||
            2 HNDY 5

RESULT 79
ID  AAY88188 standard; peptide; 12 AA.
XX
AC  AAY88188;
XX
DT  17-OCT-2000 (first entry)
XX
DE  Fluorescein binding peptide fluorette from phage clone Flus315.
XX
KM  Fluorette; fluorophore dye; fluorescent; detection; diagnostic.
XX
OS  Synthetic.
XX
PN  WO200023463-A2.
XX
PD  27-APR-2000.
XX
PF  15-OCT-1999; 99WO-US024266.
XX
PR  16-OCT-1998; 98US-0104465P.
XX
PA  (STRD ) UNIV LELAND STANFORD JUNIOR.
XX
PI  Nolan GP, Rozhnov MN;
XX
DR  WPI; 2000-339647/29.
XX
PT  Novel fluorescent peptides which bind with high specificity to fluorophore
PT  dyes, useful for detecting biological materials, molecules, target
PT  analytes, and intra- and inter-molecular interactions.
XX
PS  Example 3; Page 41; 64pp; English.
XX
CC  This invention describes a novel peptide (I) termed a fluorette which
CC  comprises a sequence of at least 8 amino acids and which binds to a
CC  fluorophore dye. The fluorettes may be used in detecting biological
CC  materials, molecules or target analytes, intracellular events, and intra-
CC  and inter-molecular interactions, as well as discovering effective
CC  inhibitors. They may also be used for in vitro assays using a large set
CC  of fluorophore dyes, e.g. in detection of viral and delivery systems,
CC  diagnostics and high throughput assays. The new peptides, due to their
CC  small size, are not intrusive to the systems being studied hence, permit
CC  detection and analysis of a target moiety or molecule while maintaining
CC  target modification. Unlike conventional techniques such as the light-
CC  emitting technique, the use of fluorettes minimize or avoid substantial
CC  genetic manipulations which may disrupt, interfere, or alter the process
CC  being measured. This sequence represents a peptide fluorette capable of
CC  binding to Fluorescein which is described in the method of the invention
XX
SQ  Sequence 12 AA;

Query Match          34.6%; Score 27; DB 3; Length 12;
Best Local Similarity 100.0%; Pred. No. 9.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  6 HNDY 9
    |||||
Db  2 HNDY 5

RESULT 80
ID  AAM53909 standard; peptide; 14 AA.
XX
AC  AAM53909;
XX
DT  17-AUG-1998 (first entry)
XX

```

```

DE  Interleukin-1 receptor accessory molecule epitope P248-E261.
XX
KM  Interleukin-1 receptor accessory molecule; IL-1R AcM; human;
KM  signal transduction; agonist; antagonist; antibody; infection;
KM  septic shock; inflammation; rheumatoid arthritis; therapy; epitope;
XX  antigen.
XX
OS  Homo sapiens.
XX
PN  WO9808969-A1.
XX
PD  05-MAR-1998.
XX
PF  26-AUG-1996; 96WO-US013954.
XX
PR  26-AUG-1996; 96WO-US013954.
XX
PA  (HUMA-) HUMAN GENOME SCI INC.
XX
PI  Bednarik DP, Olsen HS, Rosen CA;
XX
DR  WPI; 1998-230267/20.
XX
PT  Nucleic acid encoding interleukin-1 receptor accessory protein - used for
PT  therapeutic modulation of IL-1 activity.
XX
PS  Claim 17; Page 83; 95pp; English.
XX
CC  This peptide corresponds to amino acids 248-261 of novel human
CC  Interleukin-1 receptor accessory molecule (IL-1R AcM) (see AAM53897), a
CC  new member of the immunoglobulin superfamily that forms a complex with
CC  type 1 IL-1-R. It comprises an epitope-bearing portion of IL-1R AcM. 18
CC  Antigenic peptides comprising epitope-bearing portions of human IL-1R
CC  are claimed (see AAM53898-915). These can be used to generate soluble IL-
CC  1R AcM-specific antibodies, and may be produced by chemical synthesis or
CC  by recombinant means using nucleic acid molecules (see AAV23659) of the
CC  invention. The antibodies are useful as immunoassay reagents for
CC  detecting IL-1R AcM, for affinity purification of IL-1R AcM and for
CC  identifying cells that express IL-1R AcM
XX
SQ  Sequence 14 AA;

Query Match          34.6%; Score 27; DB 2; Length 14;
Best Local Similarity 55.6%; Pred. No. 1.1e+03;
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY  5 DNDYSKNP 13
    |||||
Db  3 DHVYKEKP 11

RESULT 81
ID  ADN94288 standard; peptide; 15 AA.
XX
AC  ADN94288;
XX
DT  01-JUL-2004 (first entry)
XX
DE  Human 202P5A5v.1 protein epitope #4524.
XX
KM  202P5A5; human; cancer; tumour; epitope.
XX
OS  Homo sapiens.
XX
PN  WO2004016736-A2.
XX
PD  26-FEB-2004.
XX
PF  16-JUN-2003; 2003WO-US018906.
XX
PR  16-AUG-2002; 2002US-0404306P.
XX
    01-NOV-2002; 2002US-0423290P.
XX

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XX (AGEN-) AGENSYS INC.
PA Raitano AB, Faris M, Challita-Bid PM, Jakobovits A, Ge W,
XX WPI; 2004-203774/19.
XX
PT New compositions having the 202PSA5 gene and encoded protein, useful for
PT diagnosing, preventing, prognosticating or treating cancer of the
PT prostate, bladder, colon, lung, ovary, breast, stomach, cervix, lymphoma,
PT bone and/or skin.
XX
PS Claim 1; Fig 2A; 266pp; English.
XX
CC The invention relates to a composition comprising 202PSA5 proteins. The
CC composition and proteins are useful for detecting and treating cancer by
CC inhibiting the growth or viability of cancer cells. The present sequence
CC represents the amino acid sequence of a human 202PSA5v.1 protein epitope.
CC Note the epitope sequences are displayed in tables VIII-XLIX.
XX
SQ Sequence 15 AA;

Query Match      34.6%; Score 27; DB 8; Length 15;
Best Local Similarity 45.5%; Pred. No. 1.2e+03;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 SIKRDHNDYSK 11
   | : | | : | |
Db 3 SLNQDHLNSK 13

RESULT 82
ADN94725
ID ADN94725 standard; peptide; 15 AA.
XX
AC ADN94725;
XX
DT 01-JUL-2004 (first entry)
XX
DE Human 202PSA5v.1 protein epitope #4961.
XX
KM 202PSA5; human; cancer; tumour; epitope.
XX
OS Homo sapiens.
XX
PN WO2004016736-A2.
XX
PD 26-FEB-2004.
XX
PF 16-JUN-2003; 2003WO-US018906.
XX
PR 16-AUG-2002; 2002US-0404306P.
XX
PR 01-NOV-2002; 2002US-0423290P.
XX
PA (AGEN-) AGENSYS INC.
XX
PI Raitano AB, Faris M, Challita-Bid PM, Jakobovits A, Ge W;
XX WPI; 2004-203774/19.
XX
PT New compositions having the 202PSA5 gene and encoded protein, useful for
PT diagnosing, preventing, prognosticating or treating cancer of the
PT prostate, bladder, colon, lung, ovary, breast, stomach, cervix, lymphoma,
PT bone and/or skin.
XX
PS Claim 1; Fig 2A; 266pp; English.
XX
CC The invention relates to a composition comprising 202PSA5 proteins. The
CC composition and proteins are useful for detecting and treating cancer by
CC inhibiting the growth or viability of cancer cells. The present sequence
CC represents the amino acid sequence of a human 202PSA5v.1 protein epitope.
CC Note the epitope sequences are displayed in tables VIII-XLIX.
XX

```

```

SQ Sequence 15 AA;

Query Match      34.6%; Score 27; DB 8; Length 15;
Best Local Similarity 45.5%; Pred. No. 1.2e+03;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 SIKRDHNDYSK 11
   | : | | : | |
Db 3 SLNQDHLNSK 13

RESULT 83
ADN94151
ID ADN94151 standard; peptide; 15 AA.
XX
AC ADN94151;
XX
DT 01-JUL-2004 (first entry)
XX
DE Human 202PSA5v.1 protein epitope #4387.
XX
KM 202PSA5; human; cancer; tumour; epitope.
XX
OS Homo sapiens.
XX
PN WO2004016736-A2.
XX
PD 26-FEB-2004.
XX
PF 16-JUN-2003; 2003WO-US018906.
XX
PR 16-AUG-2002; 2002US-0404306P.
XX
PR 01-NOV-2002; 2002US-0423290P.
XX
PA (AGEN-) AGENSYS INC.
XX
PI Raitano AB, Faris M, Challita-Bid PM, Jakobovits A, Ge W;
XX WPI; 2004-203774/19.
XX
PT New compositions having the 202PSA5 gene and encoded protein, useful for
PT diagnosing, preventing, prognosticating or treating cancer of the
PT prostate, bladder, colon, lung, ovary, breast, stomach, cervix, lymphoma,
PT bone and/or skin.
XX
PS Claim 1; Fig 2A; 266pp; English.
XX
CC The invention relates to a composition comprising 202PSA5 proteins. The
CC composition and proteins are useful for detecting and treating cancer by
CC inhibiting the growth or viability of cancer cells. The present sequence
CC represents the amino acid sequence of a human 202PSA5v.1 protein epitope.
CC Note the epitope sequences are displayed in tables VIII-XLIX.
XX
SQ Sequence 15 AA;

Query Match      34.6%; Score 27; DB 8; Length 15;
Best Local Similarity 45.5%; Pred. No. 1.2e+03;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 SIKRDHNDYSK 11
   | : | | : | |
Db 3 SLNQDHLNSK 13

RESULT 84
ADN94437
ID ADN94437 standard; peptide; 15 AA.
XX
AC ADN94437;
XX
DT 01-JUL-2004 (first entry)
XX
DE Human 202PSA5v.1 protein epitope #4673.
XX

```

XX 202P5A5; human; cancer; tumour; epitope.  
XX Homo sapiens.  
OS WO2004016736-A2.  
XX  
XX 26-FEB-2004.  
XX  
XX 16-JUN-2003; 2003WO-US018906.  
XX  
XX 16-AUG-2002; 2002US-0404306P.  
XX  
XX 01-NOV-2002; 2002US-0423290P.  
XX  
XX (AGEN-) AGENSYS INC.  
XX  
XX Raitano AB, Paris M, Challita-Eid PM, Jakobovits A, Ge W,  
PI WPI; 2004-203774/19.  
XX  
XX New compositions having the 202P5A5 gene and encoded protein, useful for  
PT diagnosing, preventing, prognosticating or treating cancer of the  
PT prostate, bladder, colon, lung, ovary, breast, stomach, cervix, lymphoma,  
PT bone and/or skin.  
XX  
XX Claim 1; Fig 2A; 266pp; English.  
XX  
XX The invention relates to a composition comprising 202P5A5 proteins. The  
CC composition and proteins are useful for detecting and treating cancer by  
CC inhibiting the growth or viability of cancer cells. The present sequence  
CC represents the amino acid sequence of a human 202P5A5v.1 protein epitope.  
CC Note the epitope sequences are displayed in tables VII-XLIX.  
XX  
XX Sequence 15 AA;

Query Match 34.6%; Score 27; DB 8; Length 15;  
Best Local Similarity 45.5%; Pred. No. 1.2e+03;  
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 SIKRDNDYSK 11  
|:|:|:|:  
DB 3 SLNODHLNSK 13

RESULT 85  
ADO41934  
ID ADO41934 standard; peptide; 15 AA.  
XX  
AC ADO41934;  
XX  
DT 12-AUG-2004 (first entry)  
XX  
DE Escherichia coli heat labile enterotoxin mutant peptide SeqID 1.  
XX  
XX vaccination status; heat-labile enterotoxin mutant; rmlT;  
XX immunoprotective; vaccine; immunostimulant; diarrhoea;  
XX intestinal disorder.  
XX  
XX Escherichia coli.  
XX  
XX WO2004043286-A2.  
XX  
XX 27-MAY-2004.  
XX  
XX 10-NOV-2003; 2003WO-IB005103.  
XX  
XX 14-NOV-2002; 2002US-0426421P.  
XX  
XX (PF12 ) PFIZER PROD INC.  
XX  
XX Mcvey DS;  
XX  
XX WPI; 2004-420044/39.  
DR

XX Identifying an animal which has been vaccinated with an immunogen,  
PT comprises detecting the presence of antibodies or immune cells specific  
PT to recombinant substantially non-toxic E. coli heat-labile enterotoxin  
PT mutant in the animal.  
XX  
XX Claim 8; SEQ ID NO 1; 37pp; English.  
XX

CC This invention relates to a novel method for determining the vaccination  
CC status of an animal. Specifically, it refers to the detection of  
CC antibodies or immune cells that are specific to recombinant substantially  
CC non-toxic Escherichia coli (E. coli) heat-labile enterotoxin mutant  
CC (rmlT). The present invention describes a method for enhancing the  
CC immunoprotective effects of an immunogen in a vaccine composition, where  
CC the vaccine composition contains the immunogen (preferably from  
CC Mycoplasma hyopneumoniae), the substantially non-toxic rmlT and an oil-in  
CC -water emulsion adjuvant such as AMPHIGEN. Accordingly, this composition  
CC exhibits immunostimulant activity and provides a means to identify  
CC vaccinated animals such that they are protected against E. coli  
CC infections that cause diarrhoea and various intestinal disorders. This  
CC peptide sequence is an E. coli rmlT peptide of the invention.

Query Match 34.6%; Score 27; DB 8; Length 15;  
Best Local Similarity 66.7%; Pred. No. 1.2e+03;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 RDNDY 9  
|:|:|:  
DB 3 RGHNEY 8

RESULT 86  
ADT40418  
ID ADT40418 standard; peptide; 15 AA.  
XX  
AC ADT40418;  
XX  
DT 30-DEC-2004 (first entry)  
XX  
DE hSARS virus peptide, SEQ ID 1406.  
XX  
XX Virus; Severe Acute Respiratory Syndrome; SARS; vaccine.  
XX  
XX SARS coronavirus.  
XX  
XX WO2004085650-A1.  
XX  
XX 07-OCT-2004.  
XX  
XX 24-MAR-2004; 2004WO-CN000246.  
XX  
XX 24-MAR-2003; 2003US-0457031P.  
XX  
XX 26-MAR-2003; 2003US-0457730P.  
XX  
XX 02-APR-2003; 2003US-0459931P.  
XX  
XX 03-APR-2003; 2003US-0460357P.  
XX  
XX 08-APR-2003; 2003US-0461265P.  
XX  
XX 14-APR-2003; 2003US-0462805P.  
XX  
XX 23-APR-2003; 2003US-0464866P.  
XX  
XX 25-APR-2003; 2003US-0465738P.  
XX  
XX 14-MAY-2003; 2003US-0470935P.  
XX  
XX (UYHK-) UNITV HONG KONG.  
XX  
XX Chan K, Guan Y, Nicholas JM, Peiris JSM, Poon L, Yuen K;  
PI Lung FC;  
XX  
XX WPI; 2004-737326/72.  
XX  
XX New nucleic acid molecule encoding nucleocapsid- or spike-gene protein of  
PT a human Severe Acute Respiratory Syndrome (hSARS) virus, useful for  
PT diagnosing and treating SARS.

XX Example; SEQ ID NO 1406; 200pp; English.

PS The present invention relates to novel human Severe Acute Respiratory

CC Syndrome (hSARS) viral nucleic acid and protein sequences derived from a

CC hSARS virus having China Center for Type Culture Collection Deposit

CC Accession No. CCTCC-V200303. The present invention also relates to novel

CC nucleic acid molecules (I; ADT41483 or ADT41485) encoding a nucleocapsid-

CC (N) or spike (S)-gene protein of a hSARS virus. Also disclosed are

CC methods for detecting the presence of a N- or S-gene of the hSARS virus

CC or of the protein in a biological sample and identifying a subject

CC infected with the hSARS virus. The hSARS virus, nucleic acid and protein

CC sequences are useful as vaccines for diagnosing or treating SARS. They

CC are also useful in clinical and scientific research applications. The

CC hSARS virus genome (ADT39027) was obtained and the amino acid sequences

CC of all three reading frames were deduced from the complementary strand.

CC ADT40120 is the full-length protein encoded by the first reading frame of

CC the complementary strand and ADT40121-ADT40601 are the peptides from the

CC first reading frame protein. ADT40602 is the full-length protein encoded

CC by the second reading frame of the complementary strand and ADT40603-

CC ADT40976 are the peptides from the second reading frame protein. ADT40977

CC is the full-length protein encoded by the third reading frame of the

CC complementary strand and ADT40978-ADT41482 are the peptides from the

CC third reading frame protein.

XX

SO Sequence 15 AA;

QY 5 DHNDYSKN 12 34.6%; Score 27; DB 8; Length 15;

Best Local Similarity 62.5%; Pred. No. 1.2e+03;

Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

DB 7 DYNDNSHN 14

RESULT 87

AD879835

ID AD879835 standard; protein; 15 AA.

XX

AC AD879835;

XX

DT 30-DEC-2004 (first entry)

XX

DE SARS virus complementary DNA strand reading frame 1 protein #298.

XX

KM virucide; vaccine; detection; severe acute respiratory syndrome;

KW real-time quantitative polymerase chain reaction; SARS.

XX

OS SARS coronavirus.

XX

PN WO2004085455-A1.

XX

PD 07-OCT-2004.

XX

PF 24-MAR-2004; 2004WO-CN000247.

XX

PR 24-MAR-2003; 2003US-0457031P.

PR 26-MAR-2003; 2003US-0457730P.

PR 02-APR-2003; 2003US-045931P.

PR 03-APR-2003; 2003US-0460357P.

PR 08-APR-2003; 2003US-0461265P.

PR 14-APR-2003; 2003US-0462805P.

PR 23-APR-2003; 2003US-0464886P.

PR 05-MAY-2003; 2003US-0468139P.

PR 16-MAY-2003; 2003US-0471200P.

XX

PA (UYHK-) UNIV HONG KONG.

XX

PI Chan K, Guan Y, Nicholls JM, Peiris JSM, Poon L, Yuen K;

XX

DR WPI; 2004-737292/72.

XX

PT New isolated nucleic acid molecule useful for detecting, treating,

PT ameliorating, or preventing the virus causing severe acute respiratory

PT syndrome in humans using a real-time quantitative polymerase chain

PT reaction assay.

XX

PS Example; SEQ ID NO 1406; 183pp; English.

XX

CC The invention relates to an isolated nucleic acid molecule consisting

CC essentially of, and/or hybridizes under stringent conditions to a fully

CC defined nucleotide sequence of 16-25 base pairs (bp; SEQ ID NO: 2471-

CC 2476), or its complement. The methods and compositions of the present

CC invention are useful for the detection of the virus causing Severe Acute

CC Respiratory Syndrome (SARS) in humans using a real-time quantitative

CC polymerase chain reaction (PCR) assay. They can also be used in treating,

CC ameliorating, managing or preventing SARS. This sequence corresponds to a

CC partial SARS protein sequence from the complementary reading frame 1.

XX

SO Sequence 15 AA;

QY 5 DHNDYSKN 12 34.6%; Score 27; DB 8; Length 15;

Best Local Similarity 62.5%; Pred. No. 1.2e+03;

Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

DB 7 DYNDNSHN 14

RESULT 88

ADT37948

ID ADT37948 standard; peptide; 15 AA.

XX

AC ADT37948;

XX

DT 30-DEC-2004 (first entry)

XX

DE hSARS virus peptide, SEQ ID 1406.

XX

KM virucide; Severe Acute Respiratory Syndrome; SARS; vaccine.

XX

OS SARS coronavirus.

XX

PN WO2004085633-A1.

XX

PD 07-OCT-2004.

XX

PF 24-MAR-2004; 2004WO-CN000248.

XX

PR 24-MAR-2003; 2003US-0457031P.

PR 26-MAR-2003; 2003US-0457730P.

PR 02-APR-2003; 2003US-045931P.

PR 03-APR-2003; 2003US-0460357P.

PR 08-APR-2003; 2003US-0461265P.

PR 14-APR-2003; 2003US-0462805P.

PR 23-APR-2003; 2003US-0464886P.

XX

PA (UYHK-) UNIV HONG KONG.

XX

PI Chan K, Guan Y, Nicholls JM, Peiris JSM, Poon L, Yuen K;

XX

DR WPI; 2004-728736/71.

XX

PT New isolated human severe acute respiratory syndrome (hSARS) virus,

PT useful as vaccine for diagnosing or treating SARS or in clinical and

PT scientific research applications.

XX

PS Example; SEQ ID NO 1406; 176pp; English.

XX

CC The present invention relates to novel human Severe Acute Respiratory

CC Syndrome (hSARS) viral nucleic acid and protein sequences derived from a

CC hSARS virus having China Center for Type Culture Collection Deposit

CC Accession No. CCTCC-V200303. The hSARS virus, nucleic acid and protein

CC sequences are useful as vaccines for diagnosing or treating SARS. They  
CC are also useful in clinical and scientific research applications. The  
CC hSARS virus genome (ADT36557) was obtained and the amino acid sequences  
CC of all three reading frames were deduced from the complementary strand.  
CC ADT3650 is the full-length protein encoded by the first reading frame of  
CC the complementary strand and ADT3651-ADT3813 are the peptides from the  
CC first reading frame protein. ADT38132 is the full-length protein encoded  
CC by the second reading frame of the complementary strand and ADT38133-  
CC ADT38506 are the peptides from the second reading frame protein. ADT38507  
CC is the full-length protein encoded by the third reading frame of the  
CC complementary strand and ADT38508-ADT39012 are the peptides from the  
CC third reading frame protein.

XX Sequence 15 AA;

Query Match 34.6%; Score 27; DB 8; Length 15;  
Best Local Similarity 62.5%; Pred. No. 1.2e+03;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 DRNDYSKN 12  
|:|:|:|:  
Db 7 DYDNDSHN 14

RESULT 89  
ADC97706  
ID ADC97706 standard; peptide; 17 AA.  
XX  
AC ADC97706;  
XX  
DT 01-JUN-2004 (first entry)  
XX  
DE Mouse monoclonal antibody LL2 VH CDR2.

XX  
KM Mouse; monoclonal antibody; LL2; heavy chain variable region; VH;  
KW cytotoxic; complementarity determining region; CDR; B-lymphoma;  
KW leukaemia; humanised antibody.  
XX  
OS Mus sp.  
XX  
PN US2003103979-A1.  
XX  
PD 05-JUN-2003.  
XX  
PF 16-NOV-2001; 2001US-00988013.  
XX  
PR 16-NOV-2001; 2001US-00988013.

XX  
PA (LEUNG/) LEUNG S.  
XX (HANS/) HANSEN H.  
XX  
PI Leung S, Hansen H;  
XX  
DR WPI; 2003-801218/75.  
XX  
PT Novel LL2 monoclonal antibody useful for diagnosing and treating B-cell  
XX lymphoma or leukemia.  
XX  
PS Claim 10; Page 11; 30pp; English.

XX  
CC The invention relates to an isolated polynucleotide comprising a DNA  
CC sequence encoding the amino acid sequence of light chain (kappa) variable  
CC (VK) region or heavy chain variable (VH) region of LL2 monoclonal  
CC antibody (mab), and hLL2 VH domain or hLL2 VH domain. Also included are a  
CC protein encoded by the DNAs listed above, an isolated complementarity  
CC determining region-1 (CDR1, CDR2 or CDR3) polypeptide of the VK or VH  
CC region of the LL2 mab, a CL22 mab (comprising the light chain and heavy  
CC chains of the LL2 mab linked to the human kappa and human Igg 1 constant  
CC regions, respectively), an hLL2 mab (comprising a light chain and a heavy  
CC chain CDR of a mLL2 mab joined to a framework sequence of a human VK and  
CC human VH region, respectively, linked to human kappa and Igg 1 constant  
CC region domains, respectively, such that the hLL2 mab retains  
CC substantially the B-lymphoma cell and leukaemia cell targeting cell

CC internalisation characteristics of the parent mLL2 antibody) and a  
CC conjugate comprising a CLL2 or hLL2 antibody or its fragment covalently  
CC bound to a diagnostic or therapeutic reagent. The conjugate is useful for  
CC treating and diagnosing a B-cell lymphoma or leukaemia in a subject. The  
CC present sequence represents mouse LL2 VH CDR2.

XX Sequence 17 AA;

Query Match 34.6%; Score 27; DB 7; Length 17;  
Best Local Similarity 30.0%; Pred. No. 1.4e+03;  
Matches 3; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 3 KRNDYSKN 12  
|:|:|:|:  
Db 5 RNDYTFYNN 14

RESULT 90  
AEA89661  
ID AEA89661 standard; peptide; 19 AA.  
XX  
AC AEA89661;  
XX  
DT 25-AUG-2005 (first entry)  
XX  
DE Tumor metastases treatment-related protein region #49.

XX  
KM metastasis; therapeutic; gene expression; cytotoxic; tumor;  
KW breast tumor; sarcoma; nervous system tumor; prostate tumor;  
KW pancreas tumor; colon tumor; rectal tumor; medulloblastoma;  
KW b-cell lymphoma; t-cell lymphoma; multiple myeloma; lung tumor; cancer.  
XX  
OS Unidentified.

XX  
PN WO2005056043-A2.  
XX  
PD 23-JUN-2005.  
XX  
PF 10-DEC-2004; 2004WO-IT000689.  
XX  
PR 11-DEC-2003; 2003IT-RM000572.  
XX  
PA (ZOLLI/) ZOLLO M.  
XX  
PI Zollo M;  
XX  
DR WPI; 2005-445065/45.

XX  
PT Use of inhibitors of human-PRUNE cyclic nucleotide phosphodiesterase for  
XX preparation of medicament in the treatment of tumor metastases associated  
XX with overexpression of human-PRUNE.  
XX  
PS Example 1; Fig 1; 89pp; English.

XX  
CC This invention relates to a novel method for preparing a medicament for  
CC the treatment of tumor metastases associated with overexpression of human  
CC -PRUNE. The method comprise using inhibitors of human-PRUNE cyclic  
CC nucleotide phosphodiesterase. The invention may be useful for the  
CC development of compounds with a cytotoxic activity acting as human-PRUNE  
CC overexpression inhibitors. The invention is useful for preparation of  
CC medicaments in the treatment of tumor metastases, for example breast  
CC carcinoma, sarcoma, neuroblastoma, prostate tumor, pancreatic tumor,  
CC colonic tumor, rectal tumor, medulloblastoma, epiteloma, epatocarcinoma,  
CC cell T or cell B lymphomas, myeloma and melanoma and pulmonary tumor. As  
CC the h-PRUNE poses cyclic nucleotide phosphodiesterase activity with  
CC preferential activity for camp over cGMP, the h-PRUNE overexpression can  
CC be effectively suppressed by certain PDE inhibitors thus the PDE  
CC inhibitor provides an effective alternative therapy for cancer treatment.  
CC The present sequence is that of a protein motif which was used during the  
CC development of the novel method of the invention.

XX Sequence 19 AA;

Query Match 34.6%; Score 27; DB 9; Length 19;  
 Best Local Similarity 62.5%; Pred. No. 1.6e+03;  
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 5 DHNDYSK 12  
 |||  
 Db 8 DNDTPK 15

## RESULT 91

AAR45557  
 ID AAR45557 standard; protein; 20 AA.

AC AAR45557;

DT 25-MAR-2003 (revised)  
 DT 13-JUL-1994 (first entry)

DE Cry j I pollen allergen peptide CJI-16.

KM Japanese cedar; detection; allergy; treatment; diagnosis; T cell epitope;  
 KM sensitivity.

OS Cryptomeria japonica.

PN WO9401560-A1.

PD 20-JAN-1994.

PF 15-JAN-1993; 93WO-US000139.

PR 10-JUL-1992; 92WO-US005661.

PR 01-SEP-1992; 92US-00938990.

PA (IMMU-) IMMUNOLOGIC PHARM CORP.

PI Griffith IJ, Pollock J, Bond JF, Garman RD, Kuo M;  
 XX WPI; 1994-035066/04.

PT Antigens derived from Japanese cedar pollen allergen Cry j I - contain at  
 PT least two T cell epitope(s), used to treat or diagnose allergy.

PS Claim 1; Fig 13; 137pp; English.

CC The sequence is that of an isolated peptide of the Japanese cedar pollen  
 CC allergen Cry j I (amino acids 151-170). The peptide, CJI-16, can be used  
 CC for the treatment and diagnosis of allergies associated with Japanese  
 CC cedar pollen. It has enhanced therapeutic properties but reduced side  
 CC effects compared to naturally occurring allergens. (Updated on 25-MAR-  
 CC 2003 to correct PN field.)

XX  
 SQ Sequence 20 AA;

Query Match 34.6%; Score 27; DB 2; Length 20;  
 Best Local Similarity 66.7%; Pred. No. 1.7e+03;  
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 5 DHNDYS 10  
 |||  
 Db 14 DHNSFS 19

## RESULT 92

AAR82506  
 ID AAR82506 standard; protein; 20 AA.

AC AAR82506;

DT 27-AUG-2003 (revised)  
 DT 15-APR-1996 (first entry)

DE Cry j I Japanese Cedar pollen allergen peptide fragment (CJI-16).

XX Cry j I; Japanese cedar pollen allergen; modified; drug production;  
 KM allergy; Cryptomeria japonica.

OS Cryptomeria japonica.

PN WO9527786-A1.

PD 19-OCT-1995.

PF 06-APR-1995; 95WO-US004249.

PR 08-APR-1994; 94US-00226248.

PR 06-DEC-1994; 94US-00350225.

PA (IMMU-) IMMUNOLOGIC PHARM CORP.

PI Franzen HM, Powers SP, Kuo M, Evans S, Shaked Z, Chen X;  
 XX WPI; 1995-366391/47.

PT Modified Cryptomeria japonica (Cry j) I peptide(s) - useful for treating  
 PT allergy to Japanese cedar pollen allergen or immunologically cross  
 PT reactive allergens.

PS Disclosure; Fig 2; 60pp; English.

CC Novel peptides of cry j I have been modified as a part of a  
 CC preformulation scheme to develop an optimised drug product for  
 CC therapeutic treatment of humans suffering from allergy to Japanese cedar  
 CC pollen allergen or an allergen which is immunologically cross reactive  
 CC with Japanese cedar pollen allergen. Such modified peptides possess  
 CC certain characteristics which render them particularly suitable for drug  
 CC product formulation. Peptide fragments of Cry j I, modified and  
 CC unmodified, are given in AAR82491-R82525. This peptide fragment  
 CC corresponds to amino acids 151-170 of the allergen mature protein.  
 CC (Updated on 27-AUG-2003 to correct OS field.)

XX  
 SQ Sequence 20 AA;

Query Match 34.6%; Score 27; DB 2; Length 20;  
 Best Local Similarity 66.7%; Pred. No. 1.7e+03;  
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 5 DHNDYS 10  
 |||  
 Db 14 DHNSFS 19

## RESULT 93

AAB33555  
 ID AAB33555 standard; peptide; 20 AA.

AC AAB33555;

DT 12-SEP-2003 (revised)

DT 22-JAN-2001 (first entry)

DE 5/20 native Ara h 2 peptide #9.

KM Allergy; allergic reaction; allergen; anaphylactic antigen; peanut;  
 KM Ara h 1; Ara h 2; Ara h 3; epitope; binding; immunoglobulin E; IgE;  
 KM food antigen; sensitising; immune response; anti-allergic.

OS Arachis hypogaea.

PN WO200051647-A2.

PD 08-SEP-2000.

PF 03-MAR-2000; 2000WO-US005655.

PR 03-MAR-1999; 99US-0122960P.

```

DR 06-DEC-1999; 99US-00455294.
XX
XX (MOUN ) MOUNT SINAI SCHOOL MEDICINE.
XX
XX Sampson HA;
XX
XX WPI; 2000-611341/58.
XX
XX
XX Non-human animal sensitized to an antigen, useful as an animal model for
XX studying allergic reactions to allergens, such as those in food and in
XX the environment.
XX
XX Example 5; Page 62; 12app; English.
XX
XX The present invention describes an animal model which can be used for
XX studying allergic reactions to allergens. The animal is sensitized to a
XX selected antigen by administering the antigen itself or a nucleic acid
XX encoding the antigen, where preferably the antigen is an anaphylactic
XX antigen. The sensitized animal can then be used to screen for compounds
XX which may help to prevent, ameliorate, or cure allergic conditions in
XX humans. The animal model can be used for studying allergic reactions to
XX allergens, such as those in food (peanuts, fruit, berry, nut, bean, milk,
XX dairy products), or in the environment (weed pollen, grass pollen, tree
XX pollen, mite, animal, animal dander, fungal, and insect antigens).
XX AAB33478 to AAB33601 represent sequences which are used in examples from
XX the present invention to specifically examine the peanut allergy, and the
XX peanut anaphylactic antigens Ara h 1 to 3. (Updated on 12-SEP-2003 to
XX standardise OS field)
XX
XX Sequence 20 AA;
XX
XX
XX Query Match 34.6%; Score 27; DB 3; Length 20;
XX Best Local Similarity 36.4%; Pred. No. 1.7e+03;
XX Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0,
XX
XX 2 IKRDHNDYSKN 12
XX | : | | : | : :
XX 10 IQRDEDSYERD 20
XX
XX
XX RESULT 94
XX AAB23106
XX AAB23106 standard; peptide; 20 AA.
XX
XX AAB23106;
XX
XX AC
XX
XX DT 29-JAN-2001 (first entry)
XX
XX DE Peanut wild-type Ara h 2 20 residue peptide #9.
XX
XX KW Ara h 2 protein; peanut; epitope; antigen; allergy; anaphylaxis; asthma;
XX immunomodulation; unmethylated CpG oligonucleotide; anti-allergic.
XX
XX OS Arachis hypogaea.
XX
XX PN WO200054803-A2.
XX
XX PD 21-SEP-2000.
XX
XX PF 16-MAR-2000; 2000WO-US007213.
XX
XX PR 16-MAR-1999; 99US-0124595P.
XX 17-MAR-1999; 99US-0125071P.
XX
XX PA (PANA-) PANACEA PHARM LLC.
XX
XX Sotin HB, Caplan MO;
XX
XX WPI; 2000-628168/60.
XX
XX Immunostimulatory composition for treating or preventing an allergic
XX reaction leading to conditions such as asthma or anaphylaxis, comprises
XX oligonucleotides with unmethylated CpG sequences and antigens derived

```

from allergens.

Example 3, Page 67, 103pp; English.

The invention relates to an immunomodulatory composition comprising a Cpg oligonucleotide of the sequence 5' purine-purine-C-G-pyrimidine-pyrimidine 3', where C and G are unmethylated, and at least one antigen derived from an allergen that causes anaphylaxis. The composition is useful for treating allergy in an individual. The composition prevents or modulates an individual's immune response to an antigen which leads to asthma and/or anaphylaxis. Individuals susceptible to anaphylactic shock upon exposure to allergens from foods (e.g., peanut), venom or rubber may be treated using the composition. Sequences AAB23098-B23125 represent a series of 20-residue peptides from wild-type peanut Ara h 2 protein used in an exemplification of the invention

Sequence 20 AA;

Query Match	34.6%;	Score 27;	DB 3;	Length 20;
Best Local Similarity	36.4%;	Pred. No. 1.7e+03;		
Matches	4;	Conservative	4;	Mismatches 3;
			Indels	0;
			Gaps	0
QY	2	IKRDHNDYSKN	12	
		::  :: :: ::		
Db	10	IQRDEDSYERD	20	

RESULT 95

AAM19858

ID AAM19858 standard; protein; 20 AA.

XX AC AAM19858;

XX DT 12-OCT-2001 (first entry)

DB Peptide #6292 encoded by probe for measuring cervical gene expression.

XX KW Probe; human; microarray; gene expression; cervical epithelial cell;

XX KW cervical cancer.

XX OS Homo sapiens.

XX PN WO200157278-A2.

XX PD 09-AUG-2001.

XX PE 30-JAN-2001; 2001WO-US000670.

XX PR 04-FEB-2000; 2000US-0180312P.

XX PR 26-MAY-2000; 2000US-0207456P.

XX PR 30-JUN-2000; 2000US-00608408.

XX PR 03-AUG-2000; 2000US-00632365.

XX PR 21-SEP-2000; 2000US-0234687P.

XX PR 27-SEP-2000; 2000US-0236359P.

XX PR 04-OCT-2000; 2000GB-00024263.

XX PA (MOLE-) MOLECULAR DYNAMICS INC.

XX PI Penn SG, Hanzel DK, Chen W, Rank DR;

XX DR WPI; 2001-488901/53.

XX PT Human genome-derived single exon nucleic acid probes useful for analyzing

XX PT gene expression in human cervical epithelial cells.

XX PS Claim 27; SEQ ID NO 24684; 487P; English.

XX

The present invention relates to human single exon nucleic acid probes (SNP: see AAI10068-AI28459). The present sequence is a peptide encoded by one such probe. The SNPs are derived from human HeLa cells. The SNPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore



CC useful in grading and/or staging of diseases of the cervix, notably  
CC cervical cancer. Note: The sequence data for this patent did not form  
CC part of the printed specification, but was obtained in electronic format  
CC directly from WIPO at ftp.wipo.int/pub/published\_pcc\_sequences  
XX  
SQ Sequence 20 AA;

Query Match 34.6%; Score 27; DB 4; Length 20;

Best Local Similarity 40.0%; Pred. No. 1.7e+03;

Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 SIKRDNDYS 10  
:|:|:|:|:

Db 11 TPKKRNNDYT 20

## RESULT 96

AAV72517 standard; peptide; 20 AA.

ID AAV72517 standard; peptide; 20 AA.

XX AAV72517;

AC 02-MAY-2001 (first entry)

DE MBD-2-TQIF peptide derived from Escherichia coli F1mH protein.

XX F1mH, adhesin protein; type 1 pilus; mannose binding domain; MBD, COL;

KM collagen binding domain; prophylaxis; therapy; urinary tract infection;

KM UTI; immunogen; passive immunotherapy; vaccine; antibacterial;

XX MBD-2-TQIF.

OS Escherichia coli.

XX WO200105978-A1.

PD 25-JAN-2001.

PF 14-JUL-2000; 2000WO-US019402.

XX 15-JUL-1999; 99US-0144016P.

PA (MBDI-) MEDIMMUNE INC.

PI Hultgren SJ, Langermann S;

DR WPI; 2001-159539/16.

XX Polypeptides useful as vaccines for prevention and/or treatment of

PT diseases such as urinary tract infections, caused by Enterobacteriaceae,

XX comprises mannose-binding domains derived from adhesin molecules.

PS Example; Page 26; 53pp; English.

XX The present sequence is MBD-2 (mannose-binding domain-2)-TQIF peptide

CC derived from Escherichia coli F1mH protein. This sequence was tested for

CC its immunogenicity in mouse, rabbit and primates. F1mH is an adhesin

CC protein found in type 1 pili of bacteria of the family

CC Enterobacteriaceae, especially E. coli. The F1mH protein comprises

CC mannose-binding domains (MBDs) and collagen-binding domains (COL). The

CC present invention relates to engineered polypeptides comprising one or

CC more domains derived from F1mH protein. These polypeptides are used to

CC produce prophylactic vaccines which are useful for the prevention and/or

CC treatment of diseases, such as urinary tract infection (UTI) caused by a

CC bacterium of the family Enterobacteriaceae, especially E. coli in

CC animals, in particular humans. They are useful as immunogens to stimulate

CC the production of antibodies for use in passive immuno-therapy, as a

CC diagnostic reagent and as a reagent in other processes such as affinity

CC chromatography. The antibodies of the novel poly-peptides are also

CC useful for research purposes for studying protein-lectin or collagen

CC binding interactions

CC Sequence 20 AA;

Query Match 34.6%; Score 27; DB 4; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.7e+03;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 HNDY 9  
|||

Db 6 HNDY 9

## RESULT 97

ABB39771 standard; peptide; 20 AA.

ID ABB39771 standard; peptide; 20 AA.

XX ABB39771;

AC 04-FEB-2002 (first entry)

DE Peptide #7277 encoded by human foetal liver single exon probe.

XX Human; foetal liver; gene expression; single exon nucleic acid probe.

XX Homo sapiens.

OS WO200157277-A2.

PD 09-AUG-2001.

PF 30-JAN-2001; 2001WO-US000669.

XX 04-FEB-2000; 2000US-0180312P.

PR 26-MAY-2000; 2000US-0207456P.

PR 30-JUN-2000; 2000US-00608408.

PR 03-AUG-2000; 2000US-00632366.

PR 21-SEP-2000; 2000US-0234687P.

PR 27-SEP-2000; 2000US-0236359P.

PR 04-OCT-2000; 2000GB-00024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

PI Penn SG, Hanzel DK, Chen W, Rank DR;

DR WPI; 2001-463447/52.

XX Claim 27; SEQ ID NO 32406; 639pp + Sequence Listing; English.

CC The invention relates to a single exon nucleic acid probe for measuring

CC human gene expression in a sample derived from human foetal liver. The

CC single exon nucleic acid probes may be used for predicting, measuring and

CC displaying gene expression in samples derived from human foetal liver. The

CC present sequence is a peptide encoded by a single exon nucleic acid probe

CC of the invention. Note: The sequence data for this patent did not form

CC part of the printed specification, but was obtained in electronic format

CC directly from WIPO at ftp.wipo.int/pub/published\_pcc\_sequences

XX Sequence 20 AA;

Query Match 34.6%; Score 27; DB 4; Length 20;

Best Local Similarity 40.0%; Pred. No. 1.7e+03;

Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 SIKRDNDYS 10  
:|:|:|:|:

Db 11 TPKKRNNDYT 20

## RESULT 98

AAV33354 standard; protein; 20 AA.

ID AAV33354 standard; protein; 20 AA.

XX AAV33354;

```

XX 17-OCT-2001 (first entry)
DT Peptide #7391 encoded by probe for measuring placental gene expression.
DE Probe; microarray; human; placenta; antenatal diagnosis;
KM genetic disorder.
XX Homo sapiens.
OS
XX WO200157272-A2.
PN
XX 09-AUG-2001.
PD
XX 30-JAN-2001; 2001WO-US0000663.
PF
XX 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
PI WPI; 2001-48897/53.
XX
XX Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human placenta.
XX
XX Claim 27; SEQ ID NO 33623; 654bp; English.
XX
XX The present invention relates to single exon nucleic acid probes (SENP;
CC see A131315-A157546). The present sequence is a peptide encoded by one
CC such probe. The probes are useful for producing a microarray for
CC predicting, measuring and displaying gene expression in samples derived
CC from human placenta. The probes are useful for antenatal diagnosis of
CC human genetic disorders
XX
XX Sequence 20 AA;
SQ
Query Match 34.6%; Score 27; DB 4; Length 20;
Best Local Similarity 40.0%; Pred. No. 1.7e+03;
Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
QY 1 SIRRDNDYS 10
:|:|:|:
Db 11 TPKRRNDYT 20

```

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XX 06-DEC-1999; 99US-00455294.
PR 23-JUN-2000; 2000US-0213765P.
PR 27-SEP-2000; 2000US-0235797P.
XX
XX (PANA-) PANACEA PHARM LLC.
PA (UYAR-) UNIV ARKANSAS.
PA (MOUN ) MOUNT SINAI SCHOOL MEDICINE NEW YORK.
XX
XX Bannon GA, Burks WA, Caplan MJ, Sampson H, Sosin H,
PI WPI; 2001-381378/40.
XX
XX Antigenic fragments useful for reducing anaphylactic risk and reducing
PT the severity and/or number of allergic symptoms in individuals sensitive
PT to antigens, have reduced ability to bind Immunoglobulin E.
XX
XX Claim 40; Page 52; 100pp; English.
XX
XX The sequence represents the amino acid sequence of native anaphylactic
CC antigen Ara h 2 peptide #9. Ara h 2 is an anaphylactic antigen (A), which
CC was used to design antigenic peptides having a reduced ability to bind
CC IGE as compared with the intact (A), or having a sequence substantially
CC identical to a portion of sequence of an antigen that includes at least
CC one IGE binding site, where at least one IGE binding site of the peptide
CC is altered. The antigenic peptides are used in a composition which is
CC useful for reducing risk or severity of allergic reaction to an antigen.
CC This is done by identifying an individual at risk of allergic reaction to
CC an antigen by identifying prior display of allergic symptoms when exposed
CC to the antigen, or a familial relationship with an individual who
CC previously displayed allergic symptoms when exposed to the antigen.
CC Following this an antigen-specific IGE present on one or more mast cells
CC or basophils in the individual's serum is identified. The individual is
CC then contacted with a peptide corresponding to a portion of the antigen,
CC which is selected, formulated, and delivered so that binding of the
CC peptide to antigen-specific IGE is reduced as compared with IGE binding
CC of intact antigen. The composition is also useful for treating and
CC preventing allergic reactions
XX
XX Sequence 20 AA;
SQ
Query Match 34.6%; Score 27; DB 4; Length 20;
Best Local Similarity 36.4%; Pred. No. 1.7e+03;
Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
QY 2 IRDNDYSKN 12
:|:|:|:
Db 10 IQRDEDSYERD 20

```

```

RESULT 99
AAUD4768
ID AAU04768 standard; peptide; 20 AA.
XX
XX AAU04768;
AC
XX 23-OCT-2001 (first entry)
DT
XX Native anaphylactic antigen Ara h 2 peptide #9.
DE
XX Ara h 2; anaphylactic antigen; immunoglobulin E; IGE; immunogenic;
KM allergy; mast cell; basophil; mouse; epitope.
XX
XX Mus sp.
OS
XX WO200140264-A2.
PN
XX 07-JUN-2001.
PD
XX 06-DEC-2000; 2000WO-US033124.
PF

```

```

RESULT 100
ABB24400
ID ABB24400 standard; protein; 20 AA.
XX
XX ABB24400;
AC
XX 23-JAN-2002 (first entry)
DT
XX Protein #6399 encoded by probe for measuring heart cell gene expression.
DE
XX Human; gene expression; heart; microarray; vascular system;
KM cardiovascular disease; hypertension; cardiac arrhythmia;
KM congenital heart disease.
XX
XX Homo sapiens.
OS
XX WO200157274-A2.
PN
XX 09-AUG-2001.
PD
XX 30-JAN-2001; 2001WO-US000666.
PF
XX 04-FEB-2000; 2000US-0180312P.
PR

```

PR 26-MAY-2000; 2000US-0207456P.  
 PR 30-JUN-2000; 2000US-00608408.  
 PR 03-AUG-2000; 2000US-00632266.  
 PR 21-SEP-2000; 2000US-0234687P.  
 PR 27-SEP-2000; 2000US-0236359P.  
 PR 04-OCT-2000; 2000GB-00024263.  
 XX  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 XX  
 PI Penn SG, Hanzel DK, Chen W, Rank DR;  
 XX  
 DR WPI; 2001-488899/53.  
 XX  
 PT Single exon nucleic acid probes for analyzing gene expression in human  
 PT hearts.  
 XX  
 PS Claim 15; SEQ ID NO 26170; 530bp; English.  
 XX  
 CC The present invention relates to single exon nucleic acid probes for  
 CC measuring human gene expression in a sample derived from human heart (see  
 CC ABA21535-ABA41305). The present sequence is a protein encoded by one such  
 CC probe. The probes may be used for predicting, measuring and displaying  
 CC gene expression in samples derived from the human heart via microarrays.  
 CC By measuring gene expression, the probes are useful for predicting,  
 CC diagnosing, grading, staging, monitoring and prognosing diseases of the  
 CC human heart and vascular system e.g. cardiovascular disease,  
 CC hypertension, cardiac arrhythmias and congenital heart disease. Note: The  
 CC sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 20 AA;

Query Match 34.6%; Score 27; DB 4; Length 20;  
 Best Local Similarity 40.0%; Pred. No. 1.7e+03;  
 Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 SIKRDHNDYS 10  
 : : : : :  
 Db 11 TPKRRNNDYT 20

Search completed: January 20, 2006, 19:05:06  
 Job time : 57.9038 secs

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OM protein - protein search, using sw model

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Title: US-09-662-293-1  
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Maximum Match 100%  
Listing first 100 summaries

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6: /cgn2\_6/prodata/1/1aa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

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1	78	100.0	14	2	US-09-292-325-1
2	33	42.3	12	1	US-08-434-355-15
3	33	42.3	12	1	US-08-459-367-15
4	33	42.3	12	1	US-08-460-327-15
5	33	41.0	12	1	US-08-459-871-15
6	32	41.0	11	1	US-08-237-418-10
7	32	41.0	11	1	US-08-616-855-10
8	32	41.0	11	2	US-08-616-854-10
9	32	41.0	11	2	US-08-468-337-10
10	32	41.0	11	2	US-09-758-318-10
11	32	41.0	11	2	US-10-340-783-10
12	32	41.0	18	2	US-09-292-325-12
13	32	41.0	20	1	US-08-934-915-29
14	31	39.7	20	1	US-08-614-935-12
15	31	39.7	20	2	US-09-130-287-12
16	29	37.2	12	2	US-10-191-540-18
17	28	35.9	10	2	US-08-482-228-209
18	28	35.9	10	2	US-08-482-528-209
19	28	35.9	12	2	US-09-534-717-218
20	28	35.9	15	2	US-09-434-840-81
21	28	35.9	15	2	US-09-142-524D-47
22	28	35.9	20	1	US-08-934-915-34
23	28	35.9	20	2	US-08-467-023-42
24	28	35.9	20	2	US-08-467-023-203
25	27.5	35.3	16	2	US-09-456-199-11
26	27	34.6	7	2	US-09-901-187C-2
27	27	34.6	7	2	US-09-419-381-33

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29	27	34.6	13	2	US-08-980-326-10	Sequence 10, App1
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31	27	34.6	13	2	US-08-980-326-12	Sequence 12, App1
32	27	34.6	13	2	US-08-980-326-13	Sequence 13, App1
33	27	34.6	13	2	US-08-980-326-14	Sequence 14, App1
34	27	34.6	15	2	US-09-142-524D-46	Sequence 46, App1
35	27	34.6	19	2	US-09-938-901A-36	Sequence 36, App1
36	27	34.6	20	2	US-08-467-023-41	Sequence 41, App1
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38	26	33.3	12	1	US-09-611-829-6	Sequence 6, App1
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46	26	33.3	18	2	US-08-944-823A-50	Sequence 50, App1
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53	25	32.1	11	2	US-09-402-181B-145	Sequence 145, App
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55	25	32.1	12	2	US-10-185-815A-11	Sequence 11, App1
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61	25	32.1	13	2	US-09-981-194-14	Sequence 14, App1
62	25	32.1	13	2	US-09-981-194-15	Sequence 15, App1
63	25	32.1	14	2	US-09-765-111A-47	Sequence 47, App1
64	25	32.1	15	1	US-08-967-101-167	Sequence 167, App
65	25	32.1	15	1	US-08-592-541-167	Sequence 167, App
66	25	32.1	15	2	US-09-124-698-167	Sequence 167, App
67	25	32.1	15	2	US-09-127-480-167	Sequence 167, App
68	25	32.1	15	2	US-08-496-841C-164	Sequence 164, App
69	25	32.1	15	2	US-09-124-523-167	Sequence 167, App
70	25	32.1	15	2	US-09-636-796A-167	Sequence 167, App
71	25	32.1	16	1	US-08-480-190-188	Sequence 188, App
72	25	32.1	16	1	US-08-488-379-188	Sequence 188, App
73	25	32.1	16	2	US-08-837-226-7	Sequence 7, App1
74	25	32.1	16	2	US-09-025-169B-238	Sequence 238, App
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77	25	32.1	16	2	US-08-077-555A-188	Sequence 188, App
78	25	32.1	16	2	US-09-490-070A-238	Sequence 238, App
79	25	32.1	16	2	US-09-490-153-238	Sequence 238, App
80	25	32.1	16	2	US-09-490-324-238	Sequence 238, App
81	25	32.1	16	2	PCT-US93-07545-188	Sequence 188, App
82	25	32.1	17	4	US-09-177-249-281	Sequence 281, App
83	25	32.1	17	2	US-09-066-330-1	Sequence 1, App1
84	25	32.1	17	2	US-09-812-883-281	Sequence 281, App
85	25	32.1	18	2	US-08-406-142A-10	Sequence 10, App1
86	25	32.1	18	2	US-08-406-142B-10	Sequence 10, App1
87	25	32.1	20	1	US-08-934-915-139	Sequence 139, App
88	25	32.1	20	1	US-08-602-999A-126	Sequence 126, App
89	25	32.1	20	2	US-09-500-124-126	Sequence 126, App
90	25	32.1	20	2	US-09-605-703B-2436	Sequence 2436, App
91	24.5	31.4	8	1	US-08-102-209B-24	Sequence 24, App1
92	24.5	31.4	8	1	US-08-385-245-24	Sequence 24, App1
93	24.5	31.4	8	2	US-08-485-388-24	Sequence 24, App1
94	24.5	31.4	8	2	US-08-474-853-24	Sequence 24, App1
95	24.5	31.4	8	2	US-09-166-205B-24	Sequence 24, App1
96	24.5	31.4	8	4	PCT-US94-02629-24	Sequence 24, App1
97	24	30.8	7	1	US-08-724-354D-29	Sequence 29, App1
98	24	30.8	7	2	US-09-270-984A-29	Sequence 29, App1
99	24	30.8	7	2	US-08-574-899-15	Sequence 15, App1
100	24	30.8	9	2	US-09-336-447A-40	Sequence 40, App1

## ALIGNMENTS

RESULT 1  
US-09-292-225-1  
Sequence 1, Application US/09292225  
Patent No. 6455686  
GENERAL INFORMATION:  
APPLICANT: McCall, Catherine A.  
APPLICANT: Hunter, Shirley Wu  
APPLICANT: Weber, Eric R.  
TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS  
FILE REFERENCE: AL-2-C3  
CURRENT APPLICATION NUMBER: US/09/292,225  
CURRENT FILING DATE: 1999-04-15  
EARLIER APPLICATION NUMBER: 60/098,909  
EARLIER FILING DATE: 1998-09-02  
EARLIER APPLICATION NUMBER: 60/085,295  
EARLIER FILING DATE: 1998-05-13  
EARLIER APPLICATION NUMBER: 60/098,565  
EARLIER FILING DATE: 1998-04-17  
EARLIER APPLICATION NUMBER: 09/062,013  
NUMBER OF SEQ ID NOS: 49  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 1  
LENGTH: 14  
TYPE: PRT  
ORGANISM: Dermatophagoides farinae  
US-09-292-225-1

Query Match  
Best Local Similarity 100.0%; Score 78; DB 2; Length 14;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SIKRDNDYSKNPM 14  
DB 1 SIKRDNDYSKNPM 14

RESULT 2  
US-08-434-255-15  
Sequence 15, Application US/08434255  
Patent No. 5621089  
GENERAL INFORMATION:  
APPLICANT: Sloma, Alan P.  
APPLICANT: Outtrup, Helle  
APPLICANT: Dambmann, Claus  
APPLICANT: Aaeling, Dorrit  
TITLE OF INVENTION: ALKALINE PROTEASE  
NUMBER OF SEQUENCES: 27  
CORRESPONDENCE ADDRESS:  
ADDRESSER: No. 56210890 No. 5621089disk of No. 5621089th America, Inc.  
STREET: 405 Lexington Avenue, 64th Floor  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10174-6401  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/434,255  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Agis Dr., Cheryl H.  
REGISTRATION NUMBER: 34,086  
REGISTRATION NUMBER: 34,086

REFERENCE/DOCKET NUMBER: 3764,400-US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-867-0123  
TELEFAX: 212-878-9655  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-434-255-15

Query Match  
Best Local Similarity 42.3%; Score 33; DB 1; Length 12;  
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 DHNDYSKNPM 14  
DB 2 DFIDYDNNPM 11

RESULT 3  
US-08-459-967-15  
Sequence 15, Application US/08459967  
Patent No. 5622841  
GENERAL INFORMATION:  
APPLICANT: Sloma, Alan P.  
APPLICANT: Outtrup, Helle  
APPLICANT: Dambmann, Claus  
APPLICANT: Aaeling, Dorrit  
TITLE OF INVENTION: ALKALINE PROTEASE  
NUMBER OF SEQUENCES: 27  
CORRESPONDENCE ADDRESS:  
ADDRESSER: No. 56228410 No. 5622841disk of No. 5622841th America, Inc.  
STREET: 405 Lexington Avenue, 64th Floor  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10174-6401  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/459,967  
FILING DATE: 02-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/434,255  
FILING DATE: 03-MAY-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Agis Dr., Cheryl H.  
REGISTRATION NUMBER: 34,086  
REFERENCE/DOCKET NUMBER: 3764,400-US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-867-0123  
TELEFAX: 212-878-9655  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-459-967-15

Query Match  
Best Local Similarity 42.3%; Score 33; DB 1; Length 12;  
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 DHNDYSKNPM 14  
DB 2 DFIDYDNNPM 11

RESULT 4  
US-08-460-327-15  
Sequence 15, Application US/08460327  
Patent No. 5622850  
GENERAL INFORMATION:  
APPLICANT: Sigma, Alan P.  
APPLICANT: Outtrup, Helle  
APPLICANT: Dambmann, Claus  
TITLE OF INVENTION: ALKALINE PROTEASE  
NUMBER OF SEQUENCES: 27  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: No. 56228500 of No. 5622850th America, Inc.  
STREET: 405 Lexington Avenue, 64th Floor  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10174-6401  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/460,327  
FILING DATE: 02-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/434,255  
FILING DATE: 03-MAY-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Agtis Dr., Cheryl H.  
REGISTRATION NUMBER: 34,086  
REFERENCE/DOCKET NUMBER: 3764,400-US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-867-0123  
TELEFAX: 212-878-9655  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-460-327-15  
Query Match 42.3%; Score 33; DB 1; Length 12;  
Best Local Similarity 60.0%; Pred. No. 18;  
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 5 DHNDYSKNPM 14  
DB 2 DFDYDNNPM 11  
RESULT 5  
US-08-459-871-15  
Sequence 15, Application US/08459871  
Patent No. 5650326  
GENERAL INFORMATION:  
APPLICANT: Sigma, Alan P.  
APPLICANT: Outtrup, Helle  
APPLICANT: Dambmann, Claus  
TITLE OF INVENTION: ALKALINE PROTEASE  
NUMBER OF SEQUENCES: 27  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: No. 56503260 of No. 5650326th America, Inc.  
STREET: 405 Lexington Avenue, 64th Floor  
CITY: New York  
STATE: New York  
COUNTRY: USA

Zip: 10174-6401  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/459,871  
FILING DATE: 02-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/434,255  
FILING DATE: 03-MAY-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Agtis Dr., Cheryl H.  
REGISTRATION NUMBER: 34,086  
REFERENCE/DOCKET NUMBER: 3764,400-US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-867-0123  
TELEFAX: 212-878-9655  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-459-871-15  
Query Match 42.3%; Score 33; DB 1; Length 12;  
Best Local Similarity 60.0%; Pred. No. 18;  
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 5 DHNDYSKNPM 14  
DB 2 DFDYDNNPM 11  
RESULT 6  
US-08-237-418-10  
Sequence 10, Application US/08237418  
Patent No. 5601973  
GENERAL INFORMATION:  
APPLICANT: Mueller, Martin  
TITLE OF INVENTION: Seroreactive Regions on HPV 16 Proteins  
NUMBER OF SEQUENCES: 44  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Finnergan, Henderson, Farabow, Garrett &  
STREET: 1300 I Street, N.W., Suite 700  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005-3315  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/237,418  
FILING DATE: 07-JUL-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/913,613  
FILING DATE: 16-JUL-1992  
APPLICATION NUMBER: DB P 41 23 760.9  
FILING DATE: 18-JUL-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Binaudi, Carol P.  
REGISTRATION NUMBER: 33,220  
REFERENCE/DOCKET NUMBER: 02481-1199-00000

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-408-4000  
TELEFAX: 202-408-4400  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-237-418-10

Query Match 41.0%; Score 32; DB 1; Length 11;  
Best Local Similarity 66.7%; Pred. No. 25;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 RDNDYSKN 12  
DB 3 RDHDYWKH 11

RESULT 7  
US-08-616-855-10  
Sequence 10, Application US/08616855  
Patent No. 5770357

GENERAL INFORMATION:  
APPLICANT: Douvas, Angelina  
TITLE OF INVENTION: Method of Diagnosing Caprine  
TITLE OF INVENTION: Arthritis-Encephalitis Virus Infection  
NUMBER OF SEQUENCES: 21  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Campbell and Flores  
STREET: 4370 La Jolla Village Drive, Suite 700  
CITY: San Diego  
STATE: California  
COUNTRY: United States  
ZIP: 92122  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/616,855  
FILING DATE:  
CLASSIFICATION: 436  
ATTORNEY/AGENT INFORMATION:  
NAME: Campbell, Cathryn A.  
REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P-SI 1986  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 535-9001  
TELEFAX: (619) 535-8949  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-616-855-10

Query Match 41.0%; Score 32; DB 1; Length 11;  
Best Local Similarity 60.0%; Pred. No. 25;  
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 KRDNDYSKN 12  
DB 1 KRINKYKNKN 10

RESULT 8  
US-08-616-854-10  
Sequence 10, Application US/08616854

Patent No. 6033672  
GENERAL INFORMATION:  
APPLICANT: Douvas, Angelina  
TITLE OF INVENTION: Caprine Arthritis-Encephalitis Virus  
TITLE OF INVENTION: Provides Immunoprotection Against HIV-1 Infection  
NUMBER OF SEQUENCES: 21  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Campbell and Flores  
STREET: 4370 La Jolla Village Drive, Suite 700  
CITY: San Diego  
STATE: California  
COUNTRY: United States  
ZIP: 92122  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/616,854  
FILING DATE:  
CLASSIFICATION: 436  
ATTORNEY/AGENT INFORMATION:  
NAME: Campbell, Cathryn A.  
REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P-SI 1905  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 535-9001  
TELEFAX: (619) 535-8949  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-616-854-10

Query Match 41.0%; Score 32; DB 2; Length 11;  
Best Local Similarity 60.0%; Pred. No. 25;  
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 KRDNDYSKN 12  
DB 1 KRINKYKNKN 10

RESULT 9  
US-08-468-337-10  
Sequence 10, Application US/08468337  
Patent No. 6221577  
GENERAL INFORMATION:  
APPLICANT: Muller, Martin  
TITLE OF INVENTION: Seroreactive Regions on HPV 16 Proteins  
TITLE OF INVENTION: E1 and E2  
NUMBER OF SEQUENCES: 44  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
ADDRESS: Dunner  
STREET: 1300 I Street, N.W., Suite 700  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005-3315  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/468,337  
FILING DATE: 06-JUN-1995



CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE P 41 23 760.9  
FILING DATE: 18-JUL-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Einaudi, Carol P.  
REGISTRATION NUMBER: 33,220  
REFERENCE/DOCKET NUMBER: 05552-1199-02000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-408-4000  
TELEFAX: 202-408-4400  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-468-337-10

Query Match 41.0%; Score 32; DB 2; Length 11;  
Best Local Similarity 66.7%; Pred. No. 25;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 4 RDHNDYSKN 12  
Db 3 RDHIDYWKH 11

RESULT 10  
US-09-758-318-10  
Sequence 10, Application US/09758318  
Patent No. 6531127  
GENERAL INFORMATION:  
APPLICANT: Muller, Martin  
APPLICANT: Giesmann, Lutz  
TITLE OF INVENTION: Seroreactive Regions on HPV 16 Proteins  
TITLE OF INVENTION: E1 and E2  
NUMBER OF SEQUENCES: 44  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Flinnegan, Henderson, Farabow, Garrett &  
Dunner  
STREET: 1300 I Street, N.W., Suite 700  
City: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005-3315  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/758,318  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/468,337  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Einaudi, Carol P.  
REGISTRATION NUMBER: 33,220  
REFERENCE/DOCKET NUMBER: 05552-1199-02000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-408-4000  
TELEFAX: 202-408-4400  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-758-318-10

Query Match 41.0%; Score 32; DB 2; Length 11;  
Best Local Similarity 66.7%; Pred. No. 25;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 4 RDHNDYSKN 12  
Db 3 RDHIDYWKH 11

RESULT 11  
US-10-340-783-10  
Sequence 10, Application US/10340783  
Patent No. 6723317  
GENERAL INFORMATION:  
APPLICANT: Muller, Martin  
APPLICANT: Giesmann, Lutz  
TITLE OF INVENTION: Seroreactive Regions on HPV 16 Proteins  
TITLE OF INVENTION: E1 and E2  
NUMBER OF SEQUENCES: 44  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Flinnegan, Henderson, Farabow, Garrett &  
Dunner  
STREET: 1300 I Street, N.W., Suite 700  
City: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005-3315  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/340,783  
FILING DATE: 13-Jan-2003  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/758,318  
FILING DATE: <Unknown>  
APPLICATION NUMBER: 08/468,337  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Einaudi, Carol P.  
REGISTRATION NUMBER: 33,220  
REFERENCE/DOCKET NUMBER: 05552-1199-02000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-408-4000  
TELEFAX: 202-408-4400  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 10:  
US-10-340-783-10

Query Match 41.0%; Score 32; DB 2; Length 11;  
Best Local Similarity 66.7%; Pred. No. 25;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 4 RDHNDYSKN 12  
Db 3 RDHIDYWKH 11

RESULT 12  
US-09-292-225-12  
Sequence 12, Application US/09292225  
Patent No. 6455686  
GENERAL INFORMATION:  
APPLICANT: McCall, Catherine A.  
APPLICANT: Hunter, Shirley Wu

APPLICANT: Weber, Eric R.  
 TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS  
 FILE REFERENCE: AL-2-C3  
 CURRENT FILING DATE: 1999-04-15  
 EARLIER FILING DATE: 1998-09-02  
 EARLIER FILING DATE: 1998-09-02  
 EARLIER FILING DATE: 1998-05-13  
 EARLIER FILING DATE: 1998-04-17  
 EARLIER FILING DATE: 1998-04-17  
 NUMBER OF SEQ ID NOS: 49  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO: 12  
 LENGTH: 18  
 TYPE: PRT  
 ORGANISM: Dermatophagoides fariniae  
 US-09-292-225-12

Query Match 41.0%; Score 32; DB 2; Length 18;  
 Best Local Similarity 83.3%; Pred. No. 42;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 DYSKIP 13  
 DB 1 DYAKNP 6

RESULT 13  
 US-08-934-915-29  
 Sequence 29, Application US/08934915  
 Patent No. 5932412

GENERAL INFORMATION:  
 APPLICANT: DILLNER, JOAKIM  
 APPLICANT: DILLNER, LENA  
 APPLICANT: CHENG, HWEI-MING  
 TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN  
 TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,  
 TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,  
 TITLE OF INVENTION: USEFUL IN IMMUNOSSAY FOR  
 NUMBER OF SEQUENCES: 193  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: MASON & ASSOCIATES, P.A.  
 STREET: 1757 U.S. HWY. 19 NORTH, SUITE 500  
 CITY: CLEARWATER  
 STATE: FLORIDA  
 COUNTRY: U.S.A.  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: Windows 3.0  
 SOFTWARE: Microsoft Word 6.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/934,915  
 FILING DATE: 22-SEP-1997  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 07/949,836  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: LOUISE A. FOUTCH  
 REGISTRATION NUMBER: 37,133  
 REFERENCE/DOCKET NUMBER: 1946.6  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 813-538-3800  
 TELEFAX: 813-538-3820  
 TELEX:  
 INFORMATION FOR SEQ ID NO: 29:  
 SEQUENCE CHARACTERISTICS:

LENGTH: 20 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 US-08-934-915-29

Query Match 41.0%; Score 32; DB 1; Length 20;  
 Best Local Similarity 66.7%; Pred. No. 48;  
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 RDHNDYSKN 12  
 DB 12 RDHIDYWKH 20

RESULT 14  
 US-08-614-935-12  
 Sequence 12, Application US/08614935  
 Patent No. 5804201

GENERAL INFORMATION:  
 APPLICANT: King, Te P.  
 TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES OF VESPID  
 TITLE OF INVENTION: ANTIGEN 5  
 NUMBER OF SEQUENCES: 81  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: David A. Jackson, Esq.  
 STREET: 411 Hackensack Ave, Continental Plaza, 4th  
 STREET: Floor  
 CITY: Hackensack  
 STATE: New Jersey  
 COUNTRY: USA  
 ZIP: 07601  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/614,935  
 FILING DATE: 11-MAR-1996  
 CLASSIFICATION: 436  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Jackson Esq., David A.  
 REGISTRATION NUMBER: 26,742  
 REFERENCE/DOCKET NUMBER: 600-1-156  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 201-487-5800  
 TELEFAX: 201-343-1684  
 INFORMATION FOR SEQ ID NO: 12:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 20 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 FRAGMENT TYPE: Internal  
 US-08-614-935-12

Query Match 39.7%; Score 31; DB 1; Length 20;  
 Best Local Similarity 45.5%; Pred. No. 72;  
 Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 IKRDNDYSKN 12  
 DB 4 IKRDNDYFRON 14

RESULT 15  
 US-09-130-287-12  
 Sequence 12, Application US/09130287  
 Patent No. 6106844

```

; GENERAL INFORMATION:
; APPLICANT: King, Te P.
; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES OF VESPID
; TITLE OF INVENTION: ANTIGEN 5
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; STREET: Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/130,287
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/614,935
; FILING DATE: 11-MAR-1996
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-156 DIV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; US-09-130-287-12

Query Match      39.7%; Score 31; DB 2; Length 20;
Best Local Similarity 45.5%; Pred. No. 72;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY      2 IKRDNDYSKY 12
      | : ||| : |
      4 ILKRDNDPRON 14

RESULT 16
US-10-191-540-48
; Sequence 48; Application US/10191540
; Patent No. 6951745
; GENERAL INFORMATION:
; APPLICANT: Tsuyoshi No. 6951745, Tetsuya Yano, Shinya Kozaki and Tadamu Honma
; TITLE OF INVENTION: Polymyxin B-resistant-antibiotic-containing structure and manufacturing method
; TITLE OF INVENTION: chebec
; FILE REFERENCES: CE01534
; CURRENT APPLICATION NUMBER: US/10/191,540
; CURRENT FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: JP P2001-210052
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: JP P2002-172978
; PRIOR FILING DATE: 2002-06-13
; NUMBER OF SEQ ID NOS: 186
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 48
; LENGTH: 12
```

```

; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURES:
; OTHER INFORMATION: Carbon Black-binding peptide
; US-10-191-540-48

Query Match      37.2%; Score 29; DB 2; Length 12;
Best Local Similarity 62.5%; Pred. No. 92;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      6 HNDYSKNP 13
      | : ||| : |
      3 NNDWSKAP 10

RESULT 17
US-08-482-228-209
; Sequence 209; Application US/08482228
; Patent No. 5968753
; GENERAL INFORMATION:
; APPLICANT: Tseng-Law, Janet
; APPLICANT: Kobori, Joan A.
; APPLICANT: Al-Abdaly, Fahad A.
; APPLICANT: Helgeson, Roy L.
; APPLICANT: Deans, Robert J.
; TITLE OF INVENTION: POSITIVE AND NEGATIVE/CELL
; TITLE OF INVENTION: SELECTION MEDIATED BY PEPTIDE RELEASE
; NUMBER OF SEQUENCES: 215
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Janice Guttridge, Ph.D.
; STREET: P.O. Box 15210
; CITY: Irvine
; STATE: California
; COUNTRY: USA
; ZIP: 92713-5210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,228
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Guttridge, Janice
; REGISTRATION NUMBER: 35,170
; REFERENCE/DOCKET NUMBER: IT-4630CIP3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (714) 440-5353
; TELEFAX: (714) 553-1952
; INFORMATION FOR SEQ ID NO: 209:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-482-228-209

Query Match      35.9%; Score 28; DB 1; Length 10;
Best Local Similarity 50.0%; Pred. No. 11; Indels 0; Gaps 0;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      4 RDNDYSKY 11
      | : ||| : |
      1 KDNQSYQ 8

RESULT 18
US-08-482-528-209
; Sequence 209; Application US/08482528
; Patent No. 6017719
```

```
/ GENERAL INFORMATION:
/ APPLICANT: Tseng-Law, Janet
/ APPLICANT: Kobori, Joan A.
/ APPLICANT: Al-Abdaly, Fahad A.
/ APPLICANT: Guillermo, Roy
/ APPLICANT: Helgeson, Sam L.
/ APPLICANT: Deans, Robert J.
/ TITLE OF INVENTION: POSITIVE AND POSITIVE/NEGATIVE CELL
/ TITLE OF INVENTION: SELECTION MEDIATED BY PEPTIDE RELEASE
/ NUMBER OF SEQUENCES: 215
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Janice Guthrie, Ph.D.
/ STREET: P.O. Box 15210
/ CITY: Irvine
/ STATE: California
/ COUNTRY: USA
/ ZIP: 92713-5210
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/482,528
/ FILING DATE: 07-JUN-1995
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Guthrie, Janice
/ REGISTRATION NUMBER: 35,170
/ REFERENCE/DOCKET NUMBER: IT-4630CIP4
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (714) 440-5353
/ TELEFAX: (714) 553-1952
/ INFORMATION FOR SEQ ID NO: 209:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 10 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/
US-08-482-528-209

Query Match          35.9%; Score 28; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      4 RDNDYSK 11
       :|||:
       1 KQHYSYQ 8

RESULT 19
US-09-534-717-218
/ Sequence 218, Application US/09534717
/ Patent No. 6914128
/ GENERAL INFORMATION:
/ APPLICANT: Jochen, Salfeld et al.
/ TITLE OF INVENTION: Human Antibodies That Bind Human IL-12 And Methods For Producing
/ FILE REFERENCE: BBI-093CP
/ CURRENT APPLICATION NUMBER: US/09/534,717
/ EARLIER FILING DATE: 2000-03-24
/ EARLIER APPLICATION NUMBER: 60/126,603
/ EARLIER FILING DATE: March 25, 1999
/ NUMBER OF SEQ ID NOS: 675
/ SOFTWARE: Patentin Ver. 2.0
/ SEQ ID NO 218
/ LENGTH: 12
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/
US-09-534-717-218

Query Match          35.9%; Score 28; DB 2; Length 12;
Best Local Similarity 50.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      1 SIKRDNDYS 10
       :|||:
       2 SYDRGHNFS 11

RESULT 20
US-09-434-840-81
/ Sequence 81, Application US/09434840
/ Patent No. 6620985
/ GENERAL INFORMATION:
/ APPLICANT: Glazebrook, Jane
/ APPLICANT: Jirage, Dayadevi
/ APPLICANT: Tootle, Tina L
/ APPLICANT: Zhou, Nan
/ APPLICANT: Fays, Bart
/ TITLE OF INVENTION: PAD4 COMPOSITIONS AND METHODS THEREFOR
/ FILE REFERENCE: 043503.0009
/ CURRENT APPLICATION NUMBER: US/09/434,840
/ CURRENT FILING DATE: 1999-11-04
/ EARLIER APPLICATION NUMBER: 09/190,733
/ EARLIER FILING DATE: 1998-11-12
/ NUMBER OF SEQ ID NOS: 85
/ SOFTWARE: Patentin Ver. 2.0
/ SEQ ID NO 81
/ LENGTH: 15
/ TYPE: PRT
/ ORGANISM: Arabidopsis thaliana
/
US-09-434-840-81

Query Match          35.9%; Score 28; DB 2; Length 15;
Best Local Similarity 50.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      4 RDNDYSK 11
       :|||:
       8 RDHHSYEE 15

RESULT 21
US-09-142-524D-47
/ Sequence 47, Application US/09142524D
/ Patent No. 6719976
/ GENERAL INFORMATION:
/ APPLICANT: Sone, Toshio
/ APPLICANT: Kume, Akimori
/ APPLICANT: Dairiki, Kazuo
/ APPLICANT: Iwama, Akiko
/ APPLICANT: Kino, Kohsuke
/ TITLE OF INVENTION: Peptide-based Immunotherapeutic Agent for Treating Allergic Disease
/ FILE REFERENCE: SPO-103
/ CURRENT APPLICATION NUMBER: US/09/142,524D
/ CURRENT FILING DATE: 1998-09-09
/ PRIOR APPLICATION NUMBER: PCT/JP97/00740
/ PRIOR FILING DATE: 1997-03-10
/ NUMBER OF SEQ ID NOS: 174
/ SOFTWARE: Patentin version 3.1
/ SEQ ID NO 47
/ LENGTH: 15
/ TYPE: PRT
/ ORGANISM: Crytomera japonica
/ FEATURE:
/ NAME/KEY: MISC FEATURE
/ LOCATION: (1)..(15)
/ OTHER INFORMATION: Cryj1 peptide, Figure 1, Row 33
/
US-09-142-524D-47

Query Match          35.9%; Score 28; DB 2; Length 15;
Best Local Similarity 50.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      5 DHNDYSKN 12
       :|||:
       :
```

Db 4 DHNSFSNS 11

## RESULT 22

US-08-934-915-34

Sequence 34, Application US/08934915

Patent No. 5932412

## GENERAL INFORMATION:

APPLICANT: DILNER, JOAKIM

APPLICANT: DILNER, LENA

APPLICANT: CHENG, HWEI-MING

TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN

TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8

TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,

TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR

TITLE OF INVENTION: DIAGNOSTIC PURPOSES

NUMBER OF SEQUENCES: 193

## CORRESPONDENCE ADDRESSES:

ADDRESSEE: MASON &amp; ASSOCIATES, P. A.

STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500

CITY: CLEARWATER

STATE: FLORIDA

COUNTRY: U.S.A.

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: Windows 3.0

SOFTWARE: Microsoft Word 6.0

## CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/934,915

FILING DATE: 22-SEP-1997

## CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/949,836

## FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: LOUISE A. FOUTCH

REGISTRATION NUMBER: 37,133

REFERENCE/DOCKET NUMBER: 1946.6

TELECOMMUNICATION INFORMATION:

TELEPHONE: 813-538-3800

TELEFAX: 813-538-3820

## TELEX:

INFORMATION FOR SEQ ID NO: 34:

## SEQUENCE CHARACTERISTICS:

LENGTH: 20 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-934-915-34

Query Match 35.9%; Score 28; DB 1; Length 20;

Best Local Similarity 60.0%; Pred. No. 2.4e+02;

Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Db 3 KRHDNSKN 12

7 KDDAEKYSKN 16

Db 7 KDDAEKYSKN 16

## RESULT 23

US-08-467-023-42

Sequence 42, Application US/08467023

Patent No. 6090386

## GENERAL INFORMATION:

APPLICANT: Griffith, Irwin J.;

APPLICANT: Pollock, Joanne;

APPLICANT: Bond, Julian F.;

APPLICANT: Garman, Richard D.;

APPLICANT: Kuo, Mei-Chang;

APPLICANT: Yeung, Siu-mei H.;

APPLICANT: Brauer, Andrew;

APPLICANT: Exley, Mark A.;

APPLICANT: Powers, Steven P.

TITLE OF INVENTION: Allergenic Proteins And Peptides From

TITLE OF INVENTION: Japanese Cedar Pollen

NUMBER OF SEQUENCES: 261

## CORRESPONDENCE ADDRESS:

ADDRESSEE: Immunologic Pharmaceutical Corporation, Inc.

STREET: 610 Lincoln St

CITY: Waltham

STATE: MA

COUNTRY: USA

ZIP: 02154

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

## CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/467,023

FILING DATE: June 6, 1995

## CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/350,225

FILING DATE: December 6, 1994

## ATTORNEY/AGENT INFORMATION:

NAME: Jane E. Remillard

REGISTRATION NUMBER: 38,872

REFERENCE/DOCKET NUMBER: 025.6 USD2 (IMI-028CPD2)

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 227-7400

TELEFAX: (617) 227-5941

INFORMATION FOR SEQ ID NO: 42:

## SEQUENCE CHARACTERISTICS:

LENGTH: 20 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

FRAGMENT TYPE: internal

US-08-467-023-42

Query Match 35.9%; Score 28; DB 2; Length 20;

Best Local Similarity 50.0%; Pred. No. 2.4e+02;

Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Db 5 DHNDYSKN 12

4 DHNSFSNS 11

Db 4 DHNSFSNS 11

## RESULT 24

US-08-467-023-203

Sequence 203, Application US/08467023

Patent No. 6090386

## GENERAL INFORMATION:

APPLICANT: Griffith, Irwin J.;

APPLICANT: Pollock, Joanne;

APPLICANT: Bond, Julian F.;

APPLICANT: Garman, Richard D.;

APPLICANT: Kuo, Mei-Chang;

APPLICANT: Yeung, Siu-mei H.;

APPLICANT: Brauer, Andrew;

APPLICANT: Exley, Mark A.;

APPLICANT: Powers, Steven P.

TITLE OF INVENTION: Allergenic Proteins And Peptides From

NUMBER OF SEQUENCES: 261

## CORRESPONDENCE ADDRESS:

ADDRESSEE: Immunologic Pharmaceutical Corporation, Inc.

STREET: 610 Lincoln St

CITY: Waltham

STATE: MA

COUNTRY: USA

ZIP: 02154

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/467,023  
FILING DATE: June 6, 1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/350,225  
FILING DATE: December 6, 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Jane E. Remillard  
REGISTRATION NUMBER: 38,872  
REFERENCE/DOCKET NUMBER: 025.6 USD2 (IMI-028CPD2)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 227-7400  
TELEFAX: (617) 227-5941  
INFORMATION FOR SEQ ID NO: 203:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: internal  
US-08-467-023-203

Query Match 35.9%; Score 28; DB 2; Length 20;  
Best Local Similarity 50.0%; Pred. No. 2.4e+02;  
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 DHNDYSKN 12  
Db 10 DHNFSFNS 17

RESULT 25  
US-09-456-399-11  
Sequence 11, Application US/09456399  
Patent No. 6444801  
GENERAL INFORMATION:  
APPLICANT: Institute of CytoSignal Research, Inc.  
TITLE OF INVENTION: Transcriptional Inhibitor  
FILE REFERENCE: SI-802PCT-US  
CURRENT APPLICATION NUMBER: US/09/456,399  
CURRENT FILING DATE: 1999-12-08  
PRIOR APPLICATION NUMBER: JP 1996-305043  
PRIOR FILING DATE: 1996-11-15  
PRIOR APPLICATION NUMBER: PCT/JP97/04127  
PRIOR FILING DATE: 1997-11-12  
PRIOR APPLICATION NUMBER: US 09/308,160  
PRIOR FILING DATE: 1999-05-14  
NUMBER OF SEQ ID NOS: 15  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 11  
LENGTH: 16  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: an artificially  
OTHER INFORMATION: synthesized partial peptide sequence of SI-15  
US-09-456-399-11

Query Match 35.3%; Score 27.5; DB 2; Length 16;  
Best Local Similarity 50.0%; Pred. No. 2.3e+02;  
Matches 6; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

QY 2 IKRD-HNDYSKN 12  
Db 1 LORDPNNPYDN 12

RESULT 26

US-09-901-187C-2  
Sequence 2, Application US/09901187C  
Patent No. 6780971  
GENERAL INFORMATION:  
APPLICANT: WOLOZIN, BENJAMIN  
APPLICANT: OSTRETOVA-GOLTS, NATALIE  
APPLICANT: LEBOWITZ, MICHAEL  
TITLE OF INVENTION: METHODS FOR PREVENTING NEURAL TISSUE DAMAGE AND FOR THE  
TREATMENT OF ALPHA-SYNOCLEIN DISEASES  
FILE REFERENCE: 58729 (48933)  
CURRENT APPLICATION NUMBER: US/09/901,187C  
CURRENT FILING DATE: 2001-07-09  
PRIOR APPLICATION NUMBER: 60/279,199  
PRIOR FILING DATE: 2001-03-28  
PRIOR APPLICATION NUMBER: 60/217,319  
PRIOR FILING DATE: 2000-07-07  
NUMBER OF SEQ ID NOS: 14  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 2  
LENGTH: 7  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-901-187C-2

Query Match 34.6%; Score 27; DB 2; Length 7;  
Best Local Similarity 66.7%; Pred. No. 4.6e+05;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 9 YSKNPM 14  
Db 2 YAKNPI 7

RESULT 27  
US-09-419-381-33  
Sequence 33, Application US/09419381  
Patent No. 6747135  
GENERAL INFORMATION:  
APPLICANT: No. 6747135an, Garry P.  
APPLICANT: Rozhnov, Michael N.  
TITLE OF INVENTION: Fluorescent Dye Binding Peptides  
FILE REFERENCE: A65681-1/DJB/RMS/DSS  
CURRENT APPLICATION NUMBER: US/09/419,381  
CURRENT FILING DATE: 1999-10-15  
PRIOR APPLICATION NUMBER: 60/104,465  
PRIOR FILING DATE: 1998-10-16  
NUMBER OF SEQ ID NOS: 122  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 33  
LENGTH: 12  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: synthetic  
US-09-419-381-33

Query Match 34.6%; Score 27; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 HNDY 9  
Db 2 HNDY 5

RESULT 28  
US-08-980-326-9  
Sequence 9, Application US/08980326  
Patent No. 6703197  
GENERAL INFORMATION:  
APPLICANT: Gravel, Roy A.  
APPLICANT: Rozen, Rima  
APPLICANT: Leclerc, Daniel

```

; APPLICANT: Goyette, Philippe
; APPLICANT: Campeau, Eric
; TITLE OF INVENTION: HUMAN METHIONINE SYNTHASE: CLONING, AND
; TITLE OF INVENTION: METHODS FOR EVALUATING RISK OF NEURAL TUBE DEFECTS,
; TITLE OF INVENTION: CARDIOVASCULAR DISEASE AND CANCER
; FILE REFERENCE: 50004/002003
; CURRENT APPLICATION NUMBER: US/08/980,326
; CURRENT FILING DATE: 1997-11-26
; EARLIER APPLICATION NUMBER: 60/050,310
; EARLIER FILING DATE: 1997-06-20
; EARLIER APPLICATION NUMBER: 60/031,964
; EARLIER FILING DATE: 1996-11-27
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Escherichia coli
US-08-980-326-9

```

```

Query Match          34.6%; Score 27; DB 2; Length 13;
Best Local Similarity 41.7%; Pred. No. 2.3e+02;
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

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```

QY      1  SIKRDHNDYSKN 12
       :|:|:|:|:|
DB      2  TVKGDVHDIGKN 13

```

```

RESULT 29
US-08-980-326-10
; Sequence 10, Application US/08980326
; Patent No. 6703197
; GENERAL INFORMATION:
; APPLICANT: Gravel, Roy A.
; APPLICANT: Rozen, Rima
; APPLICANT: Leclerc, Daniel
; APPLICANT: Goyette, Philippe
; APPLICANT: Campeau, Eric
; TITLE OF INVENTION: HUMAN METHIONINE SYNTHASE: CLONING, AND
; TITLE OF INVENTION: METHODS FOR EVALUATING RISK OF NEURAL TUBE DEFECTS,
; FILE REFERENCE: 50004/002003
; CURRENT APPLICATION NUMBER: US/08/980,326
; CURRENT FILING DATE: 1997-11-26
; EARLIER APPLICATION NUMBER: 60/050,310
; EARLIER FILING DATE: 1997-06-20
; EARLIER APPLICATION NUMBER: 60/031,964
; EARLIER FILING DATE: 1996-11-27
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Cyanobacterium synechocystis
US-08-980-326-10

```

```

Query Match          34.6%; Score 27; DB 2; Length 13;
Best Local Similarity 41.7%; Pred. No. 2.3e+02;
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

```

```

QY      1  SIKRDHNDYSKN 12
       :|:|:|:|:|
DB      2  TVKGDVHDIGKN 13

```

```

RESULT 30
US-08-980-326-11
; Sequence 11, Application US/08980326
; Patent No. 6703197
; GENERAL INFORMATION:
; APPLICANT: Gravel, Roy A.
; APPLICANT: Rozen, Rima

```

```

; APPLICANT: Leclerc, Daniel
; APPLICANT: Goyette, Philippe
; APPLICANT: Campeau, Eric
; TITLE OF INVENTION: HUMAN METHIONINE SYNTHASE: CLONING, AND
; TITLE OF INVENTION: METHODS FOR EVALUATING RISK OF NEURAL TUBE DEFECTS,
; TITLE OF INVENTION: CARDIOVASCULAR DISEASE AND CANCER
; FILE REFERENCE: 50004/002003
; CURRENT APPLICATION NUMBER: US/08/980,326
; CURRENT FILING DATE: 1997-11-26
; EARLIER APPLICATION NUMBER: 60/050,310
; EARLIER FILING DATE: 1997-06-20
; EARLIER APPLICATION NUMBER: 60/031,964
; EARLIER FILING DATE: 1996-11-27
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 11
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Mycobacterium leprae
US-08-980-326-11

```

```

Query Match          34.6%; Score 27; DB 2; Length 13;
Best Local Similarity 41.7%; Pred. No. 2.3e+02;
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

```

```

QY      1  SIKRDHNDYSKN 12
       :|:|:|:|:|
DB      2  TVKGDVHDIGKN 13

```

```

RESULT 31
US-08-980-326-12
; Sequence 12, Application US/08980326
; Patent No. 6703197
; GENERAL INFORMATION:
; APPLICANT: Gravel, Roy A.
; APPLICANT: Rozen, Rima
; APPLICANT: Leclerc, Daniel
; APPLICANT: Goyette, Philippe
; APPLICANT: Campeau, Eric
; TITLE OF INVENTION: HUMAN METHIONINE SYNTHASE: CLONING, AND
; TITLE OF INVENTION: METHODS FOR EVALUATING RISK OF NEURAL TUBE DEFECTS,
; FILE REFERENCE: 50004/002003
; CURRENT APPLICATION NUMBER: US/08/980,326
; CURRENT FILING DATE: 1997-11-26
; EARLIER APPLICATION NUMBER: 60/050,310
; EARLIER FILING DATE: 1997-06-20
; EARLIER APPLICATION NUMBER: 60/031,964
; EARLIER FILING DATE: 1996-11-27
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Hemophilus influenzae
US-08-980-326-12

```

```

Query Match          34.6%; Score 27; DB 2; Length 13;
Best Local Similarity 41.7%; Pred. No. 2.3e+02;
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

```

```

QY      1  SIKRDHNDYSKN 12
       :|:|:|:|:|
DB      2  TVKGDVHDIGKN 13

```

```

RESULT 32
US-08-980-326-13
; Sequence 13, Application US/08980326
; Patent No. 6703197
; GENERAL INFORMATION:
; APPLICANT: Gravel, Roy A.

```

```
/ APPLICANT: Rozen, Rima
/ APPLICANT: Leclerc, Daniel
/ APPLICANT: Goyette, Philippe
/ APPLICANT: Campeau, Eric
/ TITLE OF INVENTION: HUMAN METHIONINE SYNTHASE: CLONING, AND
/ TITLE OF INVENTION: METHODS FOR EVALUATING RISK OF NEURAL TUBE DEFECTS,
/ FILE REFERENCE: 50004/002003
/ CURRENT APPLICATION NUMBER: US/08/980,326
/ CURRENT FILING DATE: 1997-11-26
/ EARLIER APPLICATION NUMBER: 60/050,310
/ EARLIER FILING DATE: 1997-06-20
/ EARLIER APPLICATION NUMBER: 60/031,964
/ EARLIER FILING DATE: 1996-11-27
/ NUMBER OF SEQ ID NOS: 75
/ SOFTWARE: PasteSeq for Windows Version 3.0
/ SEQ ID NO 13
/ LENGTH: 13
/ TYPE: PRT
/ ORGANISM: Caenorhabditis elegans
US-08-980-326-13
```

```
Query Match          34.6%; Score 27; DB 2; Length 13;
Best Local Similarity 41.7%; Pred. No. 2.3e+02;
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
```

```
QY      1 SIKRDHNDYSKN 12
         |||:|:|:|
Db      2 TVKGDVHDIGKN 13
```

```
RESULT 33
US-08-980-326-14
/ Sequence 14, Application US/08980326
/ Patent No. 6703197
/ GENERAL INFORMATION:
/ APPLICANT: Gravel, Roy A.
/ APPLICANT: Rozen, Rima
/ APPLICANT: Leclerc, Daniel
/ APPLICANT: Goyette, Philippe
/ APPLICANT: Campeau, Eric
/ TITLE OF INVENTION: HUMAN METHIONINE SYNTHASE: CLONING, AND
/ TITLE OF INVENTION: METHODS FOR EVALUATING RISK OF NEURAL TUBE DEFECTS,
/ FILE REFERENCE: 50004/002003
/ CURRENT APPLICATION NUMBER: US/08/980,326
/ CURRENT FILING DATE: 1997-11-26
/ EARLIER APPLICATION NUMBER: 60/050,310
/ EARLIER FILING DATE: 1997-06-20
/ EARLIER APPLICATION NUMBER: 60/031,964
/ EARLIER FILING DATE: 1996-11-27
/ NUMBER OF SEQ ID NOS: 75
/ SOFTWARE: PasteSeq for Windows Version 3.0
/ SEQ ID NO 14
/ LENGTH: 13
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-08-980-326-14
```

```
Query Match          34.6%; Score 27; DB 2; Length 13;
Best Local Similarity 41.7%; Pred. No. 2.3e+02;
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
```

```
QY      1 SIKRDHNDYSKN 12
         |||:|:|:|
Db      2 TVKGDVHDIGKN 13
```

```
RESULT 34
US-09-142-524D-46
/ Sequence 46, Application US/09142524D
/ Patent No. 671976
/ GENERAL INFORMATION:
```

```
/ APPLICANT: Sone, Toshio
/ APPLICANT: Kume, Akinori
/ APPLICANT: Daijiki, Kazuo
/ APPLICANT: Iwama, Akiyo
/ APPLICANT: Kuno, Kohsuke
/ TITLE OF INVENTION: Peptide-Based Immunotherapeutic Agent for Treating Allergic Dise-
/ FILE REFERENCE: SPO-103
/ CURRENT APPLICATION NUMBER: US/09/142,524D
/ CURRENT FILING DATE: 1998-09-09
/ PRIOR APPLICATION NUMBER: PCT/JP97/00740
/ PRIOR FILING DATE: 1997-03-10
/ NUMBER OF SEQ ID NOS: 174
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 46
/ LENGTH: 15
/ TYPE: PRT
/ ORGANISM: Cryptosporidia japonica
/ FEATURE:
/ NAME/KEY: MISC FEATURE
/ LOCATION: (1)..(15)
/ OTHER INFORMATION: Cryj1 peptide, Figure 1, Row 32
US-09-142-524D-46
```

```
Query Match          34.6%; Score 27; DB 2; Length 15;
Best Local Similarity 66.7%; Pred. No. 2.6e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      5 DHNDYS 10
         |||:|:|
Db      9 DHNSFS 14
```

```
RESULT 35
US-09-938-901A-36
/ Sequence 36, Application US/09938901A
/ Patent No. 6939949
/ GENERAL INFORMATION:
/ APPLICANT: Kuramitsu, Seiki
/ APPLICANT: Yokoyama, Shigeoyuki
/ TITLE OF INVENTION: No. 6939999e1 DNA Repair Enzymes, Nucleic Acids Encoding DNA Repa
/ FILE REFERENCE: 11283-013001/PH1261 US
/ CURRENT APPLICATION NUMBER: US/09/938,901A
/ CURRENT FILING DATE: 2001-08-24
/ PRIOR APPLICATION NUMBER: JP 47762/2001
/ PRIOR FILING DATE: 2001-02-23
/ NUMBER OF SEQ ID NOS: 65
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 36
/ LENGTH: 19
/ TYPE: PRT
/ ORGANISM: Saccharomyces cerevisiae
US-09-938-901A-36
```

```
Query Match          34.6%; Score 27; DB 2; Length 19;
Best Local Similarity 62.5%; Pred. No. 3.4e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      5 DHNDYSKN 12
         |||:|:|:|
Db      8 DNDTPPKN 15
```

```
RESULT 36
US-08-467-023-41
/ Sequence 41, Application US/08467023
/ Patent No. 6090386
/ GENERAL INFORMATION:
/ APPLICANT: Griffith, Irwin J.;
/ APPLICANT: Pollock, Joanne;
/ APPLICANT: Bond, Julian F.;
/ APPLICANT: Garman, Richard D.;
/ APPLICANT: Kuo, Mei-Chang;
```



APPLICANT: Yeung, Shu-mei H.;  
APPLICANT: Brauer, Andrew;  
APPLICANT: Exley, Mark A.;  
APPLICANT: Powers, Steven P.  
TITLE OF INVENTION: Allergenic Proteins And Peptides From  
TITLE OF INVENTION: Japanese Cedar Pollen  
NUMBER OF SEQUENCES: 261  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Immunologic Pharmaceutical Corporation, Inc.  
STREET: 610 Lincoln St  
CITY: Waltham  
STATE: MA  
COUNTRY: USA  
ZIP: 02154  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/467,023  
FILING DATE: June 6, 1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/350,225  
FILING DATE: December 6, 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Jane E. Remillard  
REGISTRATION NUMBER: 38,872  
REFERENCE/DOCKET NUMBER: 025.6 USD2 (IMI-028CPD2)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 227-7400  
TELEFAX: (617) 227-5941  
INFORMATION FOR SEQ ID NO: 41:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: internal  
US-08-467-023-41

Query Match 34.6%; Score 27; DB 2; Length 20;  
Best Local Similarity 66.7%; Pred. No. 3.6e+02;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 DHNDYS 10  
DB 14 DHNSPS 19

RESULT 37  
US-09-311-784A-441  
Sequence 441, Application US/09311784A  
Patent No. 6534482  
GENERAL INFORMATION:  
APPLICANT: Fikes, John D.  
APPLICANT: Hermanson, Gary G.  
APPLICANT: Sette, Alessandro  
APPLICANT: Ishioka, Glenn Y.  
APPLICANT: Livingston, Brian  
APPLICANT: Chesnut, Robert W.  
APPLICANT: EpiImmune Inc.  
TITLE OF INVENTION: Expression Vectors for Stimulating an  
TITLE OF INVENTION: Immune Response and Methods of Using the Same  
FILE REFERENCE: 39963-20022.01  
CURRENT APPLICATION NUMBER: US/09/311,784A  
CURRENT FILING DATE: 1999-05-13  
PRIOR APPLICATION NUMBER: US 60/085,751  
PRIOR FILING DATE: 1998-05-15  
NUMBER OF SEQ ID NOS: 463  
SOFTWARE: PatsEQ for Windows Version 3.0  
SEQ ID NO 441

LENGTH: 10  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: PE LSA1 59 (peptide 1167.47)  
US-09-311-784A-441

Query Match 33.3%; Score 26; DB 2; Length 10;  
Best Local Similarity 66.7%; Pred. No. 2.5e+02;  
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 HDNYSK 11  
DB 5 HNSYRK 10

RESULT 38  
US-09-611-829-6  
Sequence 6, Application US/09611829  
Patent No. 6713066  
GENERAL INFORMATION:  
APPLICANT: COLLINS, Peter L.  
APPLICANT: MURPHY, Brian R.  
APPLICANT: BERMINGHAM, Alison  
TITLE OF INVENTION: PRODUCTION OF ATTENUATED RESPIRATORY SYNCYTIAL VIRUS  
TITLE OF INVENTION: VACCINES INVOLVING MODIFICATION OF M ORF2  
FILE REFERENCE: 15280-4031005  
CURRENT APPLICATION NUMBER: US/09/611,829  
CURRENT FILING DATE: 2000-07-07  
PRIOR APPLICATION NUMBER: 60/143,097  
PRIOR FILING DATE: 1999-07-09  
NUMBER OF SEQ ID NOS: 8  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 6  
LENGTH: 11  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Amino acid  
OTHER INFORMATION: sequence corresponding to nucleotide sequence  
US-09-611-829-6

Query Match 33.3%; Score 26; DB 2; Length 11;  
Best Local Similarity 66.7%; Pred. No. 2.8e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 7 NDYSKN 12  
DB 2 NDPAKN 7

RESULT 39  
US-08-260-582-18  
Sequence 18, Application US/08260582  
Patent No. 5635182  
GENERAL INFORMATION:  
APPLICANT: McCoy, John M.  
APPLICANT: Lu, Zhijian  
TITLE OF INVENTION: METHOD OF DETECTING LIGAND  
TITLE OF INVENTION: INTERACTIONS  
NUMBER OF SEQUENCES: 76  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genetics Institute, Inc.  
STREET: 87 CambridgePark Drive  
CITY: Cambridge  
STATE: Massachusetts  
COUNTRY: U.S.  
ZIP: 02140  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

```
/ SOFTWARE: Patentin Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/260,582
/ FILING DATE: 16-JUN-1994
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Meinerdt, M. C.
/ REGISTRATION NUMBER: 31,544
/ REFERENCE/DOCKET NUMBER: GI 5236
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (617) 876-1170
/ TELEFAX: (617) 876-5851
/ INFORMATION FOR SEQ ID NO: 18:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 12 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ HYPOTHEICAL: NO
/ ANTI-SENSE: NO
US-08-260-582-18
```

```
Query Match 33.3% Score 26; DB 1; Length 12;
Best Local Similarity 57.1%; Pred. No. 3.1e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 4 RDHNDYS 10
DB 3 RDHDKFS 9
```

```
RESULT 40
PCT-US95-05471-18
/ Sequence 18, Application PC/TUS9505471
/ GENERAL INFORMATION:
/ APPLICANT:
/ TITLE OF INVENTION: METHOD OF DETECTING LIGAND INTERACTIONS
/ NUMBER OF SEQUENCES: 76
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.25 (SPO)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: PCT/US95/05471
/ INFORMATION FOR SEQ ID NO: 18:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 12 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ HYPOTHEICAL: NO
/ ANTI-SENSE: NO
PCT-US95-05471-18
```

```
Query Match 33.3% Score 26; DB 4; Length 12;
Best Local Similarity 57.1%; Pred. No. 3.1e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 4 RDHNDYS 10
DB 3 RDHDKFS 9
```

```
RESULT 41
US-09-391-104-15
/ Sequence 15, Application US/09391104
/ Patent No. 6399371
/ GENERAL INFORMATION:
/ APPLICANT: Abbott Laboratories
/ APPLICANT: Falduto, Michael T.
```

```
/ APPLICANT: Magnuson, Scott R.
/ APPLICANT: Morgan, Douglas W.
/ TITLE OF INVENTION: HUMAN MATRIX METALLOPROTEASE GENE.
/ TITLE OF INVENTION: PROTEINS ENCODED THEREFROM AND METHODS
/ TITLE OF INVENTION: OF USING SAME
/ FILE REFERENCE: 6073.US.P1
/ CURRENT APPLICATION NUMBER: US/09/391,104
/ CURRENT FILING DATE: 1999-09-07
/ PRIOR APPLICATION NUMBER: US 08/814,394
/ PRIOR FILING DATE: 1997-03-11
/ NUMBER OF SEQ ID NOS: 35
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 15
/ LENGTH: 15
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Synthetic peptides
US-09-391-104-15
```

```
Query Match 33.3% Score 26; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 5 DHND 8
DB 4 DHND 7
```

```
RESULT 42
US-09-671-089-53
/ Sequence 53, Application US/09671089
/ Patent No. 6780846
/ GENERAL INFORMATION:
/ APPLICANT: O'Mahony, Daniel J.
/ APPLICANT: Lambkin, Imelda J.
/ TITLE OF INVENTION: MEMBRANE TRANSLLOCATING PEPTIDE DRUG DELIVERY SYSTEM
/ FILE REFERENCE: E1067/20018
/ CURRENT APPLICATION NUMBER: US/09/671,089
/ CURRENT FILING DATE: 2000-09-27
/ PRIOR APPLICATION NUMBER: 60/156,246
/ PRIOR FILING DATE: 1999-09-27
/ NUMBER OF SEQ ID NOS: 59
/ SOFTWARE: Patentin version 3.1
/ SEQ ID NO 53
/ LENGTH: 16
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: D form retroinversion peptide
/ NAME/KEY: MOD RES
/ LOCATION: (1)..(1)
/ OTHER INFORMATION: danylated
/ FEATURE:
/ NAME/KEY: MISC FEATURE
/ LOCATION: (2)~(16)
/ OTHER INFORMATION: D form amino acid
US-09-671-089-53
```

```
Query Match 33.3% Score 26; DB 2; Length 16;
Best Local Similarity 27.3%; Pred. No. 4.3e+02;
Matches 3; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 2 IKRDHNDYSKN 12
DB 5 LRRNHSHSKAN 15
```

```
RESULT 43
US-08-616-844-50
/ Sequence 50, Application US/08616844
/ Patent No. 5849578
```

GENERAL INFORMATION:  
APPLICANT: FALB, DEAN A.  
TITLE OF INVENTION: COMPOSITION AND METHODS FOR THE  
TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE  
NUMBER OF SEQUENCES: 54  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PENNIE & EDMONDS  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/616,844  
FILING DATE: 15-MAR-1996  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/599,654  
FILING DATE: 09-FEB-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/485,573  
FILING DATE: 07-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/386,844  
FILING DATE: 10-FEB-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: CORUZZI, LAURA A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7853-053  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 50:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-616-844-50

Query Match 33.3%; Score 26; DB 1; Length 18;  
Best Local Similarity 66.7%; Pred. No. 4.8e+02;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 DYSKNP 13  
: |||  
DB 5 EYKNP 10

RESULT 44  
US-08-599-654-50  
Sequence 50, Application US/08599654  
Patent No. 5883925  
GENERAL INFORMATION:  
APPLICANT: FALB, DEAN A.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE  
TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE  
NUMBER OF SEQUENCES: 54  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PENNIE & EDMONDS  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/599,654  
FILING DATE: 09-FEB-1996  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/485,573  
FILING DATE: 07-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/386,844  
FILING DATE: 10-FEB-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: CORUZZI, LAURA A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7853-041  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 50:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-599-654-50

Query Match 33.3%; Score 26; DB 1; Length 18;  
Best Local Similarity 66.7%; Pred. No. 4.8e+02;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 DYSKNP 13  
: |||  
DB 5 EYKNP 10

RESULT 45  
US-08-944-868A-50  
Sequence 50, Application US/08944868A  
Patent No. 6018025  
GENERAL INFORMATION:  
APPLICANT: FALB, DEAN A.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE  
TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE  
NUMBER OF SEQUENCES: 54  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PENNIE & EDMONDS  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/944,868A  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/599,654  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/386,844  
FILING DATE: 10-FEB-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: CORUZZI, LAURA A.

REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7853-041  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 780-9090  
TELEFAX: (212) 869-8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 50:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-944-868A-50

Query Match 33.3%; Score 26; DB 2; Length 18;  
Best Local Similarity 66.7%; Pred. No. 4.8e+02;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 DYSKNP 13  
: ||||  
Db 5 EYKNP 10

RESULT 46  
US-08-944-423A-50  
Sequence 50, Application US/08944423A  
Patent No. 6020463  
GENERAL INFORMATION:  
APPLICANT: FALB, DEAN A  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE  
TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE  
NUMBER OF SEQUENCES: 54  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PENNIE & EDMONDS  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: WINDOWS 95  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/944,423A  
FILING DATE: 06-OCT-1997  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/599,654  
FILING DATE: 09-FEB-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/485,573  
FILING DATE: JUN-07-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/386,844  
FILING DATE: 10-FEB-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: CORUZZI, LAURA A  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7853-105  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 50:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide

US-08-944-423A-50

Query Match 33.3%; Score 26; DB 2; Length 18;  
Best Local Similarity 66.7%; Pred. No. 4.8e+02;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 DYSKNP 13  
: ||||  
Db 5 EYKNP 10

RESULT 47  
US-08-944-496-50  
Sequence 50, Application US/08944496  
Patent No. 6124433  
GENERAL INFORMATION:  
APPLICANT: FALB, DEAN A  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE  
TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE  
NUMBER OF SEQUENCES: 54  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PENNIE & EDMONDS LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/944,496  
FILING DATE: 06-OCT-1997  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/599,654  
FILING DATE: 09-FEB-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/485,573  
FILING DATE: 07-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/386,844  
FILING DATE: 10-FEB-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: CORUZZI, LAURA A  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7853-104  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 50:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-944-496-50

Query Match 33.3%; Score 26; DB 2; Length 18;  
Best Local Similarity 66.7%; Pred. No. 4.8e+02;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 DYSKNP 13  
: ||||  
Db 5 EYKNP 10

RESULT 48  
US-09-383-062-6

/ Sequence 6, Application US/09383062  
/ Patent No. 6670194  
/ GENERAL INFORMATION:  
/ APPLICANT: Aebereold, Rudolf H.  
/ APPLICANT: Gelb, Michael H  
/ APPLICANT: Gyg1, Steven  
/ APPLICANT: Scott, C R  
/ APPLICANT: Turecek, Prantisek  
/ APPLICANT: Garber, Scott A  
/ APPLICANT: Rist, Beate  
/ TITLE OF INVENTION: Rapid Quantitative Analysis of Proteins or Protein  
/ TITLE OF INVENTION: Function in Complex Mixture  
/ FILE REFERENCE: 64-98  
/ CURRENT APPLICATION NUMBER: US/09/383,062  
/ PRIOR FILING DATE: 1999-08-25  
/ PRIOR APPLICATION NUMBER: 60/097,788  
/ PRIOR FILING DATE: 1999-08-25  
/ NUMBER OF SEQ ID NOS: 64  
/ SOFTWARE: PatentIn Ver. 2.0  
/ SEQ ID NO 6  
/ LENGTH: 18  
/ TYPE: PRT  
/ ORGANISM: Artificial Sequence  
/ FEATURE:  
/ OTHER INFORMATION: Description of Artificial Sequence: Test peptide  
US-09-383-062-6

Query Match 33.3%; Score 26; DB 2; Length 18;  
Best Local Similarity 50.0%; Pred. No. 4.8e+02;  
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 3 KRDNDSKN 12  
| | | | |  
DB 1 KDDQNPSSN 10

RESULT 49  
US-09-839-884-6  
/ Sequence 6, Application US/09839884  
/ Patent No. 6852544  
/ GENERAL INFORMATION:  
/ APPLICANT: Aebereold, Rudolf H.  
/ APPLICANT: Gelb, Michael H  
/ APPLICANT: Gyg1, Steven  
/ APPLICANT: Scott, C R  
/ APPLICANT: Turecek, Prantisek  
/ APPLICANT: Garber, Scott A  
/ APPLICANT: Rist, Beate  
/ TITLE OF INVENTION: Rapid Quantitative Analysis of Proteins or Protein  
/ TITLE OF INVENTION: Function in Complex Mixture  
/ FILE REFERENCE: 64-98A  
/ CURRENT APPLICATION NUMBER: US/09/839,884  
/ PRIOR FILING DATE: 2001-04-20  
/ PRIOR APPLICATION NUMBER: 09/383,062  
/ PRIOR FILING DATE: 1999-08-25  
/ PRIOR APPLICATION NUMBER: 60/097,788  
/ PRIOR FILING DATE: 1998-08-25  
/ NUMBER OF SEQ ID NOS: 64  
/ SOFTWARE: PatentIn Ver. 2.0  
/ SEQ ID NO 6  
/ LENGTH: 18  
/ TYPE: PRT  
/ ORGANISM: Artificial Sequence  
/ FEATURE:  
/ OTHER INFORMATION: Description of Artificial Sequence: Test peptide  
US-09-839-884-6

Query Match 33.3%; Score 26; DB 2; Length 18;  
Best Local Similarity 50.0%; Pred. No. 4.8e+02;  
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 3 KRDNDSKN 12  
| | | | |

DB 1 KDDQNPSSN 10

RESULT 50  
US-07-931-931A-5  
/ Sequence 5, Application US/07931931A  
/ Patent No. 5521097  
/ GENERAL INFORMATION:  
/ APPLICANT: Uchida, Toyooki  
/ APPLICANT: Taugita, Akira  
/ APPLICANT: Takamoto, Keiji  
/ APPLICANT: Sarake, Kazuo  
/ TITLE OF INVENTION: Method of Determining Amino Acid  
/ TITLE OF INVENTION: Sequence of Protein or Peptide  
/ Patent No. 5521097  
/ NUMBER OF SEQUENCES: 6  
/ CORRESPONDENCE ADDRESS:  
/ ADDRESSER: Adams & Wilks  
/ STREET: 500 Fifth Avenue Suite 3200  
/ CITY: New York  
/ STATE: New York  
/ COUNTRY: United States of America  
/ ZIP: 10110  
/ COMPUTER READABLE FORM:  
/ MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb storage  
/ OPERATING SYSTEM: PC-DOS 3.30  
/ SOFTWARE: Wordperfect 5.1  
/ CURRENT APPLICATION DATA:  
/ APPLICATION NUMBER: US/07/931,931A  
/ FILING DATE: 19920818  
/ CLASSIFICATION: 435  
/ PRIOR APPLICATION DATA:  
/ APPLICATION NUMBER: JP 03-217437  
/ FILING DATE: 28 AUG 1991  
/ PRIOR APPLICATION DATA:  
/ APPLICATION NUMBER: JP 03-300818  
/ FILING DATE: 15 NOV 1991  
/ ATTORNEY/AGENT INFORMATION:  
/ NAME: Adams, Bruce L.  
/ REGISTRATION NUMBER: 25,386  
/ REFERENCE/DOCKET NUMBER: S004-2354  
/ TELECOMMUNICATION INFORMATION:  
/ TELEPHONE: (212) 575-2600  
/ TELEFAX: (212) 575-2604  
/ INFORMATION FOR SEQ ID NO: 5:  
/ LENGTH: 8  
/ TYPE: amino acid  
/ STRANDEDNESS:  
/ TOPOLOGY: linear chain  
US-07-931-931A-5

Query Match 32.1%; Score 25; DB 1; Length 8;  
Best Local Similarity 57.1%; Pred. No. 4.6e+05;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 KRDNNDY 9  
| | | | |  
DB 1 KKKHPDY 7

RESULT 51  
US-08-408-604A-152  
/ Sequence 152, Application US/08408604A  
/ Patent No. 5801149  
/ GENERAL INFORMATION:  
/ APPLICANT: Shoelson, Steven  
/ TITLE OF INVENTION: INHIBITION OF SIGNAL TRANSDUCTION MOLECULES  
/ NUMBER OF SEQUENCES: 211  
/ CORRESPONDENCE ADDRESS:  
/ ADDRESSER: LAHIVE & COCKFIELD  
/ STREET: 60 State Street, Suite 510

CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109-1875  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/408,604A  
FILING DATE: 21-MAR-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/134,558  
FILING DATE: 08-OCT-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/959,949  
FILING DATE: 09-OCT-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/722,359  
FILING DATE: 19-JUNE-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Myers, Louis  
REGISTRATION NUMBER: 35,965  
REFERENCE/DOCKET NUMBER: JDP-014CP3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)227-5941  
INFORMATION FOR SEQ ID NO: 152:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: internal  
US-08-408-604A-152

Query Match 32.1%; Score 25; DB 1; Length 11;  
Best Local Similarity 44.4%; Pred. No. 4.2e+02;  
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 5 DHNDYSKNP 13  
DB 1 DHQXYNDMP 9

RESULT 52  
US-08-974-549A-145  
Sequence 145, Application US/08974549A  
Patent No. 6166178  
GENERAL INFORMATION:  
APPLICANT: Cech, Thomas R.  
APPLICANT: Lingner, Joachim  
APPLICANT: Nakamura, Toru  
APPLICANT: Chapman, Karen B.  
APPLICANT: Morin, Gregg B.  
APPLICANT: Harley, Calvin B.  
APPLICANT: Andrews, William H.  
TITLE OF INVENTION: Human Telomerase Catalytic Subunit  
NUMBER OF SEQUENCES: 727  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/974,549A  
FILING DATE: 19-NOV-1997  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/724,643  
FILING DATE: 01-OCT-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/844,419  
FILING DATE: 18-APR-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/846,017  
FILING DATE: 25-APR-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/851,843  
FILING DATE: 06-MAY-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/854,050  
FILING DATE: 09-MAY-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/911,312  
FILING DATE: 14-AUG-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/912,951  
FILING DATE: 14-AUG-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/915,503  
FILING DATE: 14-AUG-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US97/17618  
FILING DATE: 01-OCT-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US97/17885  
FILING DATE: 01-OCT-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Apple, Randolph Ted  
REGISTRATION NUMBER: 36,429  
REFERENCE/DOCKET NUMBER: 015389-002610US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 145:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-974-549A-145

Query Match 32.1%; Score 25; DB 2; Length 11;  
Best Local Similarity 55.6%; Pred. No. 4.2e+02;  
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 IKRDNDYS 10  
DB 1 IKSGNDYS 9

RESULT 53  
US-09-402-181B-145  
Sequence 145, Application US/09402181B  
Patent No. 6610839  
GENERAL INFORMATION:  
APPLICANT: Cech, Thomas R.  
APPLICANT: Lingner, Joachim  
APPLICANT: Nakamura, Toru  
APPLICANT: Chapman, Karen B.  
APPLICANT: Morin, Gregg B.  
APPLICANT: Harley, Calvin B.  
APPLICANT: Andrews, William H.  
TITLE OF INVENTION: Human Telomerase Catalytic Subunit  
NUMBER OF SEQUENCES: 633

CORRESPONDENCE ADDRESS:  
ADDRESS: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/402,1818  
FILING DATE: 29-Sep-1997  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/724,643  
FILING DATE: 01-OCT-1996  
APPLICATION NUMBER: US 08/844,419  
FILING DATE: 18-APR-1997  
APPLICATION NUMBER: US 08/846,017  
FILING DATE: 25-APR-1997  
APPLICATION NUMBER: US 08/851,843  
FILING DATE: 06-MAY-1997  
APPLICATION NUMBER: US 08/854,050  
FILING DATE: 09-MAY-1997  
APPLICATION NUMBER: US 08/911,312  
FILING DATE: 14-AUG-1997  
APPLICATION NUMBER: US 08/912,951  
FILING DATE: 14-AUG-1997  
APPLICATION NUMBER: US 08/915,503  
FILING DATE: 14-AUG-1997  
APPLICATION NUMBER: WO PCT/US97/17885  
FILING DATE: 01-OCT-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Augenhue, Scott L.  
REGISTRATION NUMBER: 42,271  
REFERENCE/DOCKET NUMBER: 015389-002620US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 145:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 145:  
US-09-402-181B-145  
Query Match 32.1%; Score 25; DB 2; Length 11;  
Best Local Similarity 55.6%; Pred. No. 4.2e+02;  
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
QY 2 IKRDHNDYS 10  
DB 1 IKSGNEDYS 9  
RESULT 54  
US-09-721-456-145  
Sequence 145, Application US/09721456  
Patent No. 6617110  
GENERAL INFORMATION:  
APPLICANT: Cech, Thomas R.  
Lingner, Joachim  
Nakamura, Toru  
Chapman, Karen B.  
Morin, Gregg B.  
Harley, Calvin B.  
Andrews, William H.

TITLE OF INVENTION: Human Telomerase Catalytic Subunit  
NUMBER OF SEQUENCES: 727  
CORRESPONDENCE ADDRESS:  
ADDRESS: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/721,456  
FILING DATE: 22-No. 6617110-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/974,549A  
FILING DATE: 19-NOV-1997  
APPLICATION NUMBER: US 08/724,643  
FILING DATE: 01-OCT-1996  
APPLICATION NUMBER: US 08/844,419  
FILING DATE: 18-APR-1997  
APPLICATION NUMBER: US 08/846,017  
FILING DATE: 25-APR-1997  
APPLICATION NUMBER: US 08/851,843  
FILING DATE: 06-MAY-1997  
APPLICATION NUMBER: US 08/854,050  
FILING DATE: 09-MAY-1997  
APPLICATION NUMBER: US 08/911,312  
FILING DATE: 14-AUG-1997  
APPLICATION NUMBER: US 08/912,951  
FILING DATE: 14-AUG-1997  
APPLICATION NUMBER: US 08/915,503  
FILING DATE: 14-AUG-1997  
APPLICATION NUMBER: WO PCT/US97/17618  
FILING DATE: 01-OCT-1997  
APPLICATION NUMBER: WO PCT/US97/17885  
FILING DATE: 01-OCT-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Apple, Randolph Ted  
REGISTRATION NUMBER: 36,429  
REFERENCE/DOCKET NUMBER: 015389-002610US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 145:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 145:  
US-09-721-456-145  
Query Match 32.1%; Score 25; DB 2; Length 11;  
Best Local Similarity 55.6%; Pred. No. 4.2e+02;  
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
QY 2 IKRDHNDYS 10  
DB 1 IKSGNEDYS 9  
RESULT 55  
US-10-185-815A-11  
Sequence 11, Application US/10185815A  
Patent No. 6916789  
GENERAL INFORMATION:  
APPLICANT: Eian Corporation, plc

APPLICANT: O'Mahony, Daniel  
APPLICANT: Lambkin, Imelda  
APPLICANT: Higgins, Lisa  
TITLE OF INVENTION: Peyer's Patch And/Or M-Cell Targeting Ligands  
FILE REFERENCE: P26,480-A USA  
CURRENT APPLICATION NUMBER: US/10/185,815A  
CURRENT FILING DATE: 2002-06-28  
PRIOR APPLICATION NUMBER: 60/302,591  
PRIOR FILING DATE: 2001-07-02  
NUMBER OF SEQ ID NOS: 100  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 11  
LENGTH: 12  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: polypeptide ligand  
US-10-185-815A-11

Query Match 32.1%; Score 25; DB 2; Length 12;  
Best Local Similarity 66.7%; Pred. No. 4.6e+02; Indels 0; Gaps 0;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 9 YSRNPM 14  
:||||:  
Db 3 HSKNPV 8

RESULT 56  
US-08-837-226-3  
Sequence 3, Application US/08837226  
Patent No. 6043216  
GENERAL INFORMATION:  
APPLICANT: Toback, P. Gary  
APPLICANT: Lieske, John C.  
TITLE OF INVENTION: METHODS AND COMPOSITION FOR DETECTING  
TITLE OF INVENTION: AND TREATING KIDNEY DISEASES ASSOCIATED WITH ADHESION OF  
TITLE OF INVENTION: CRYSTALS TO KIDNEY CELLS  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSER: BRINKS, HOPER, GILSON & LIONE  
STREET: NBC Tower - Suite 3600, 455 N. Cityfront  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60611-5599  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/837,226  
FILING DATE: 08-APR-1997  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/389,005  
FILING DATE: 15-FEB-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Martin, Alice O.  
REGISTRATION NUMBER: 35,601  
REFERENCE/DOCKET NUMBER: 7814/24  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-321-4200  
TELEFAX: 312-321-4299  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 13 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide

US-08-837-226-3

Query Match 32.1%; Score 25; DB 2; Length 13;  
Best Local Similarity 66.7%; Pred. No. 5.1e+02; Indels 0; Gaps 0;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 6 HNDYSK 11  
:||||:  
Db 2 NNDYSQ 7

RESULT 57  
US-08-811-583-13  
Sequence 13, Application US/08811583  
Patent No. 6218142  
GENERAL INFORMATION:  
APPLICANT: Massenegger, Michael  
APPLICANT: Riedel, Leonhard  
APPLICANT: Schiebel, Winfried  
APPLICANT: Sanger, Heinz  
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING  
TITLE OF INVENTION: POLYPEPTIDES HAVING THE ENZYMATIC ACTIVITY OF AN  
TITLE OF INVENTION: RNA-DIRECTED RNA POLYMERASE (RDRP)  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSER: FISH & NEAVE  
STREET: 1251 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10020  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/811,583  
FILING DATE: 05-MAR-1997  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Haley, James F.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: MPG-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-596-9090  
TELEFAX: 212-596-9000  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 13 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-811-583-13

Query Match 32.1%; Score 25; DB 2; Length 13;  
Best Local Similarity 66.7%; Pred. No. 5.1e+02; Indels 0; Gaps 0;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 KRDNND 8  
:||||:  
Db 7 KRPNNE 12

RESULT 58  
US-09-484-114B-14  
Sequence 14, Application US/09484114B  
Patent No. 6329178  
GENERAL INFORMATION:  
APPLICANT: Patel, Premal H.  
APPLICANT: Loeb, Lawrence A.  
TITLE OF INVENTION: DNA POLYMERASE MUTANT HAVING ONE OR MORE



```

: TITLE OF INVENTION: MUTATIONS IN THE ACTIVE SITE
: FILE REFERENCE: 74890002US00
: CURRENT APPLICATION NUMBER: US/09/484,114B
: CURRENT FILING DATE: 2000-01-14
: NUMBER OF SEQ ID NOS: 40
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 14
: LENGTH: 13
: TYPE: PRT
: ORGANISM: Escherichia coli
US-09-484-114B-14

Query Match      32.1%; Score 25; DB 2; Length 13;
Best Local Similarity 57.1%; Pred. No. 5.1e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      8 DYSKNPM 14
      |||:|:
Db      6 DYSQNEL 12

RESULT 59
US-09-484-114B-15
: Sequence 15, Application US/09484114B
: Patent No. 6329178
: GENERAL INFORMATION:
: APPLICANT: Patel, Premal H.
: TITLE OF INVENTION: DNA POLYMERASE MUTANT HAVING ONE OR MORE
: TITLE OF INVENTION: MUTATIONS IN THE ACTIVE SITE
: FILE REFERENCE: 74890002US00
: CURRENT APPLICATION NUMBER: US/09/484,114B
: CURRENT FILING DATE: 2000-01-14
: NUMBER OF SEQ ID NOS: 40
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 15
: LENGTH: 13
: TYPE: PRT
: ORGANISM: Escherichia coli
US-09-484-114B-15

Query Match      32.1%; Score 25; DB 2; Length 13;
Best Local Similarity 57.1%; Pred. No. 5.1e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      8 DYSKNPM 14
      |||:|:
Db      6 DYSQNEL 12

RESULT 60
US-09-537-226-3
: Sequence 3, Application US/09537226
: Patent No. 6482934
: GENERAL INFORMATION:
: APPLICANT: TOBACK, P. GARY
: APPLICANT: LIESKE, JOHN C.
: TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING AND TREATING
: TITLE OF INVENTION: KIDNEY DISEASES ASSOCIATED WITH ADHESION OF CRYSTALS TO
: TITLE OF INVENTION: KIDNEY CELLS
: FILE REFERENCE: 21459/90606
: CURRENT APPLICATION NUMBER: US/09/537,226
: CURRENT FILING DATE: 2000-03-28
: PRIOR APPLICATION NUMBER: 08/389,005
: NUMBER OF SEQ ID NOS: 23
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 3
: LENGTH: 13
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: Synthetic
```

```

: OTHER INFORMATION: peptide
US-09-537-226-3

Query Match      32.1%; Score 25; DB 2; Length 13;
Best Local Similarity 66.7%; Pred. No. 5.1e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      6 HNDYSK 11
      :|||:
Db      2 NNDYSQ 7

RESULT 61
US-09-981-194-14
: Sequence 14, Application US/09981194
: Patent No. 6602695
: GENERAL INFORMATION:
: APPLICANT: Patel, Premal H.
: TITLE OF INVENTION: DNA POLYMERASE MUTANT HAVING ONE OR MORE
: TITLE OF INVENTION: MUTATIONS IN THE ACTIVE SITE
: FILE REFERENCE: 74890002US00
: CURRENT APPLICATION NUMBER: US/09/981,194
: CURRENT FILING DATE: 2001-10-16
: PRIOR APPLICATION NUMBER: US/09/484,114
: PRIOR FILING DATE: 2000-01-14
: NUMBER OF SEQ ID NOS: 40
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 14
: LENGTH: 13
: TYPE: PRT
: ORGANISM: Escherichia coli
US-09-981-194-14

Query Match      32.1%; Score 25; DB 2; Length 13;
Best Local Similarity 57.1%; Pred. No. 5.1e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      8 DYSKNPM 14
      |||:|:
Db      6 DYSQNEL 12

RESULT 62
US-09-981-194-15
: Sequence 15, Application US/09981194
: Patent No. 6602695
: GENERAL INFORMATION:
: APPLICANT: Patel, Premal H.
: APPLICANT: Loeb, Lawrence A.
: TITLE OF INVENTION: DNA POLYMERASE MUTANT HAVING ONE OR MORE
: TITLE OF INVENTION: MUTATIONS IN THE ACTIVE SITE
: FILE REFERENCE: 74890002US00
: CURRENT APPLICATION NUMBER: US/09/981,194
: CURRENT FILING DATE: 2001-10-16
: PRIOR APPLICATION NUMBER: US/09/484,114
: PRIOR FILING DATE: 2000-01-14
: NUMBER OF SEQ ID NOS: 40
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 15
: LENGTH: 13
: TYPE: PRT
: ORGANISM: Escherichia coli
US-09-981-194-15

Query Match      32.1%; Score 25; DB 2; Length 13;
Best Local Similarity 57.1%; Pred. No. 5.1e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      8 DYSKNPM 14
      |||:|:
Db      6 DYSQNEL 12
```

RESULT 63  
US-09-765-111A-47  
Sequence 47, Application US/09765111A  
Patent No. 6723506  
GENERAL INFORMATION:  
APPLICANT: Fletcher, Jonathan A.  
APPLICANT: Kroll, Todd G.  
TITLE OF INVENTION: PAX6-PREPARGAMMA NUCLEIC ACID MOLECULES  
FILE REFERENCE: B0801/7196/ERE/MAT  
CURRENT APPLICATION NUMBER: US/09/765,111A  
PRIOR FILING DATE: 2001-01-18  
PRIOR APPLICATION NUMBER: US 60/177,109  
PRIOR FILING DATE: 2000-01-20  
PRIOR APPLICATION NUMBER: US 60/225,079  
PRIOR FILING DATE: 2000-08-14  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 47  
LENGTH: 14  
TYPE: PRT  
ORGANISM: Homo Sapiens  
FEATURE:  
NAME/KEY: Unknown  
LOCATION: (8)...(8)  
OTHER INFORMATION: Xaa = any amino acid  
US-09-765-111A-47

Query Match 32.1%; Score 25; DB 2; Length 14;  
Best Local Similarity 33.3%; Pred. No. 5.5e+02;  
Matches 4; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 SIKRDNDYSKN 12  
:|:|:|:|:  
Db 3 NISQEXSEYSGN 14

RESULT 64  
US-08-967-101-167  
Sequence 167, Application US/08967101  
Patent No. 5840540  
GENERAL INFORMATION:  
APPLICANT: ST. GEORGE-HYSLOP, PETER H  
APPLICANT: ROWMENS, JOHANNA M  
APPLICANT: FRASER, PAUL E  
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED  
TITLE OF INVENTION: TO ALZHEIMER'S DISEASE  
NUMBER OF SEQUENCES: 183  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: TESTA, HURWITZ & THIBEAULT  
STREET: High Street Tower - 125 High Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: U.S.A.  
ZIP: 02110  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/967,101  
FILING DATE: 10-NOV-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/592,541  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Pitcher, Edmund R.  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 248-7000  
TELEFAX: (617) 248-7100

INFORMATION FOR SEQ ID NO: 167:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULAR TYPE: peptide  
US-08-967-101-167

Query Match 32.1%; Score 25; DB 1; Length 15;  
Best Local Similarity 50.0%; Pred. No. 5.9e+02;  
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 KRDND 8  
:|:|:|:|:  
Db 6 RQEHND 11

RESULT 65  
US-08-592-541-167  
Sequence 167, Application US/08592541  
Patent No. 5986054  
GENERAL INFORMATION:  
APPLICANT: ST. GEORGE-HYSLOP, PETER H  
APPLICANT: ROWMENS, JOHANNA M  
APPLICANT: FRASER, PAUL E  
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED  
TITLE OF INVENTION: TO ALZHEIMER'S DISEASE  
NUMBER OF SEQUENCES: 183  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: TESTA, HURWITZ & THIBEAULT  
STREET: High Street Tower - 125 High Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: U.S.A.  
ZIP: 02110  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/592,541  
FILING DATE:  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: Pitcher, Edmund R.  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 248-7000  
TELEFAX: (617) 248-7100  
INFORMATION FOR SEQ ID NO: 167:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULAR TYPE: peptide  
US-08-592-541-167

Query Match 32.1%; Score 25; DB 1; Length 15;  
Best Local Similarity 50.0%; Pred. No. 5.9e+02;  
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 KRDND 8  
:|:|:|:|:  
Db 6 RQEHND 11

RESULT 66  
US-09-124-698-167  
Sequence 167, Application US/09124698  
Patent No. 6117978  
GENERAL INFORMATION:

APPLICANT: ST. GEORGE-HYSLOP, PETER H  
APPLICANT: ROWMENS, JOHANNA M  
APPLICANT: FRASER, PAUL E  
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED  
TITLE OF INVENTION: TO ALZHEIMER'S DISEASE  
NUMBER OF SEQUENCES: 183  
CORRESPONDENCE ADDRESS:  
ADDRESSER: TESTA, HURWITZ & THIBEAULT  
STREET: High Street Tower - 125 High Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: U.S.A.  
ZIP: 02110  
COMPUTER READABLE FORM:  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/124,698  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/592,541  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Pletcher, Edmund R.  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 248-7000  
TELEFAX: (617) 248-7100  
INFORMATION FOR SEQ ID NO: 167:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-124-698-167

Query Match 32.1%; Score 25; DB 2; Length 15;  
Best Local Similarity 50.0%; Pred. No. 5.9e+02;  
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 KRDNH 8  
Db 6 ROEHD 11

RESULT 67  
US-09-127-480-167  
Sequence 167, Application US/09127480  
Patent No. 6194153  
GENERAL INFORMATION:  
APPLICANT: ST. GEORGE-HYSLOP, PETER H  
APPLICANT: ROWMENS, JOHANNA M  
APPLICANT: FRASER, PAUL E  
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED  
TITLE OF INVENTION: TO ALZHEIMER'S DISEASE  
NUMBER OF SEQUENCES: 183  
CORRESPONDENCE ADDRESS:  
ADDRESSER: TESTA, HURWITZ & THIBEAULT  
STREET: High Street Tower - 125 High Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: U.S.A.  
ZIP: 02110  
COMPUTER READABLE FORM:  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/127,480

FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/592,541  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Pletcher, Edmund R.  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 248-7000  
TELEFAX: (617) 248-7100  
INFORMATION FOR SEQ ID NO: 167:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-127-480-167

Query Match 32.1%; Score 25; DB 2; Length 15;  
Best Local Similarity 50.0%; Pred. No. 5.9e+02;  
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 KRDNH 8  
Db 6 ROEHD 11

RESULT 68  
US-08-496-841C-164  
Sequence 164, Application US/08496841C  
Patent No. 6210919  
GENERAL INFORMATION:  
APPLICANT: ST. GEORGE-HYSLOP, PETER H  
APPLICANT: ROWMENS, JOHANNA M  
APPLICANT: FRASER, PAUL E  
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED  
TITLE OF INVENTION: TO ALZHEIMER'S DISEASE  
NUMBER OF SEQUENCES: 175  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Darby & Darby, PC  
STREET: 805 Third Avenue  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10022  
COMPUTER READABLE FORM:  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/496,841C  
FILING DATE: 28-Jun-1995  
CLASSIFICATION: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Paul F. Fehner, Ph.D.  
REGISTRATION NUMBER: 35,135  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 527-7700  
TELEFAX: (212) 753-6237  
INFORMATION FOR SEQ ID NO: 164:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 164:  
US-08-496-841C-164

Query Match 32.1%; Score 25; DB 2; Length 15;  
Best Local Similarity 50.0%; Pred. No. 5.9e+02;

Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;  
QY 3 KRDNH 8  
Db 6 RQEHND 11

RESULT 69  
US-09-124-523-167  
Sequence 167, Application US/09124523  
Patent No. 6395960  
GENERAL INFORMATION:  
APPLICANT: ST. GEORGE-HYSLOP, PETER H  
APPLICANT: ROWMENS, JOHANNA M  
APPLICANT: FRASER, PAUL E  
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED  
TITLE OF INVENTION: TO ALZHEIMER'S DISEASE  
NUMBER OF SEQUENCES: 183  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: TESTA, HURWITZ & THIBEAULT  
STREET: High Street Tower - 125 High Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: U.S.A.  
ZIP: 02110  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/124,523  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/592,541  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Pletcher, Edmund R.  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 248-7000  
TELEFAX: (617) 248-7100  
INFORMATION FOR SEQ ID NO: 167:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-124-523-167

Query Match 32.1%; Score 25; DB 2; Length 15;  
Best Local Similarity 50.0%; Pred. No. 5.9e+02;  
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;  
QY 3 KRDNH 8  
Db 6 RQEHND 11

RESULT 70  
US-09-636-796A-167  
Sequence 167, Application US/09636796A  
Patent No. 6485911  
GENERAL INFORMATION:  
APPLICANT: ST. GEORGE-HYSLOP, PETER H  
APPLICANT: ROWMENS, JOHANNA M  
APPLICANT: FRASER, PAUL E  
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED  
TITLE OF INVENTION: TO ALZHEIMER'S DISEASE  
NUMBER OF SEQUENCES: 183  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: TESTA, HURWITZ & THIBEAULT

STREET: High Street Tower - 125 High Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: U.S.A.  
ZIP: 02110  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/636,796A  
FILING DATE: 11-Aug-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/592,541  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Pletcher, Edmund R.  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 248-7000  
TELEFAX: (617) 248-7100  
INFORMATION FOR SEQ ID NO: 167:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 167:  
US-09-636-796A-167

Query Match 32.1%; Score 25; DB 2; Length 15;  
Best Local Similarity 50.0%; Pred. No. 5.9e+02;  
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;  
QY 3 KRDNH 8  
Db 6 RQEHND 11

RESULT 71  
US-08-480-190-188  
Sequence 188, Application US/08480190  
Patent No. 5827516  
GENERAL INFORMATION:  
APPLICANT: Robert G. Urban  
APPLICANT: Roman M. Chicz  
APPLICANT: Dario A. A. Vignall  
APPLICANT: Mary L. Hedley  
APPLICANT: Lawrence J. Stern  
APPLICANT: Jack L. Strominger  
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES  
NUMBER OF SEQUENCES: 274  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: U.S.A.  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" diskette, 1.44 MB  
COMPUTER: IBM PS/2 Model 502 or 55SX  
OPERATING SYSTEM: MS-DOS (Version 5.0)  
SOFTWARE: Wordperfect (Version 5.1)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/480,190  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/077,255  
FILING DATE: June 15, 1993

APPLICATION NUMBER: 07/925,460  
FILING DATE: August 11, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Clark, Paul T.  
REGISTRATION NUMBER: 30,162  
REFERENCE/DOCKET NUMBER: 00246/168001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 542-5070  
TELEFAX: (617) 542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 188:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
US-08-480-190-188

Query Match 32.1%; Score 25; DB 1; Length 16;  
Best Local Similarity 66.7%; Pred. No. 6.4e+02;  
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 RDNDY 9  
| | | |  
| | | |  
Db 8 RGHNY 13

RESULT 72  
US-08-488-379-188  
Sequence 188, Application US/08488379  
Patent No. 5880103  
GENERAL INFORMATION:  
APPLICANT: Robert G. Urban  
APPLICANT: Roman M. Chicz  
APPLICANT: Darlo A. A. Vignal  
APPLICANT: Mary L. Hedley  
APPLICANT: Lawrence J. Stern  
APPLICANT: Jack L. Strominger  
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES  
NUMBER OF SEQUENCES: 274  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Fish & Richardson  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: U.S.A.  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
COMPUTER: IBM PS/2 Model 50Z or 55SX  
OPERATING SYSTEM: MS-DOS (Version 5.0)  
SOFTWARE: WordPerfect (Version 5.1)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/488,379  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/077,255  
FILING DATE: June 15, 1993  
APPLICATION NUMBER: 07/925,460  
FILING DATE: August 11, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Clark, Paul T.  
REGISTRATION NUMBER: 30,162  
REFERENCE/DOCKET NUMBER: 00246/168001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 542-5070  
TELEFAX: (617) 542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 188:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16  
TYPE: amino acid

STRANDEDNESS:  
TOPOLOGY: linear  
US-08-488-379-188

Query Match 32.1%; Score 25; DB 1; Length 16;  
Best Local Similarity 66.7%; Pred. No. 6.4e+02;  
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 RDNDY 9  
| | | |  
| | | |  
Db 8 RGHNY 13

RESULT 73  
US-08-837-226-7  
Sequence 7, Application US/08837226  
Patent No. 6043216  
GENERAL INFORMATION:  
APPLICANT: Toback, F. Gary  
APPLICANT: Lieske, John C.  
TITLE OF INVENTION: METHODS AND COMPOSITION FOR DETECTING  
AND TREATING KIDNEY DISEASES ASSOCIATED WITH ADHESION OF  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSER: BRINKS, HOFER, GILSON & LIONE  
STREET: NBC Tower - Suite 3600, 455 N. Clevfront  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60611-5599  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/837,226  
FILING DATE: 08-APR-1997  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/389,005  
FILING DATE: 15-FEB-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Martin, Alice O.  
REGISTRATION NUMBER: 35,601  
REFERENCE/DOCKET NUMBER: 7814/24  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-321-4200  
TELEFAX: 312-321-4299  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULAR TYPE: peptide  
US-08-837-226-7

Query Match 32.1%; Score 25; DB 2; Length 16;  
Best Local Similarity 66.7%; Pred. No. 6.4e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 6 HNDYSK 11  
| | | |  
| | | |  
Db 5 NNDYSQ 10

RESULT 74  
US-09-025-769B-238  
Sequence 238, Application US/09025769B  
Patent No. 630064

GENERAL INFORMATION:  
APPLICANT: Knappik, Achim  
APPLICANT: Pack, Peter  
APPLICANT: Ilag, Vlc  
APPLICANT: Ge, Laming  
APPLICANT: Moroney, Simon  
APPLICANT: Plueckhuhn, Andreas  
TITLE OF INVENTION: Protein/(Poly) peptide libraries  
NUMBER OF SEQUENCES: 373  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: James P. Haley, Jr., Esq. c/o Fish & Neave  
STREET: 1251 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10021  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30 (BPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/025,769B  
FILING DATE: 18-FEB-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 95 11 3021.0  
FILING DATE: 18-AUG-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: James P. Haley, Jr., Esq.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: MORPHO/5  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)596-9090  
TELEFAX: (212)596-9090  
INFORMATION FOR SEQ ID NO: 238:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: internal  
US-09-025-769B-238

Query Match 32.1%; Score 25; DB 2; Length 16;  
Best Local Similarity 54.5%; Pred. No. 6.4e+02;  
Matches 6; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

QY 4 RDNDYSKNPM 14  
DB 5 RDNFSY--DPM 13

RESULT 75  
US-09-537-226-21  
Sequence 21, Application US/09537226  
Patent No. 6482934  
GENERAL INFORMATION:  
APPLICANT: TOBACK, F. GARY  
APPLICANT: LIESKE, JOHN C.  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING AND TREATING  
TITLE OF INVENTION: KIDNEY DISEASES ASSOCIATED WITH ADHESION OF CRYSTALS TO  
FILE REFERENCE: 21459/90606  
CURRENT APPLICATION NUMBER: US/09/537,226  
CURRENT FILING DATE: 2000-03-28  
PRIOR APPLICATION NUMBER: 08/389,005  
PRIOR FILING DATE: 1995-02-15  
NUMBER OF SEQ ID NOS: 23  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 21  
LENGTH: 16  
TYPE: PRT

ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
OTHER INFORMATION: peptide  
US-09-537-226-21

Query Match 32.1%; Score 25; DB 2; Length 16;  
Best Local Similarity 66.7%; Pred. No. 6.4e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 6 HNDYSK 11  
DB 5 NNDYSQ 10

RESULT 76  
US-08-475-399A-188  
Sequence 188, Application US/08475399A  
Patent No. 6509033  
GENERAL INFORMATION:  
APPLICANT: Urban, Robert G.  
APPLICANT: Chicz, Roman M.  
APPLICANT: Vignali, Dario A.A.  
APPLICANT: Hedley, Mary L.  
APPLICANT: Stern, Lawrence J.  
APPLICANT: Strominger, Jack L.  
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES  
NUMBER OF SEQUENCES: 276  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson, P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: US  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/475,399A  
FILING DATE: 07-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/077,255  
FILING DATE: 15-JUN-1993  
APPLICATION NUMBER: 07/925,460  
FILING DATE: 11-AUG-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Fraser, Janis K.  
REGISTRATION NUMBER: 34,819  
REFERENCE/DOCKET NUMBER: 00246/168003  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/542-507  
TELEFAX: 617/542-890  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 188:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-475-399A-188

Query Match 32.1%; Score 25; DB 2; Length 16;  
Best Local Similarity 66.7%; Pred. No. 6.4e+02;  
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 RDNDY 9  
DB 8 RGNQY 13

RESULT 77

US-08-077-255A-188  
; Sequence 188, Application US/08077255A  
; Patent No. 6696061  
; GENERAL INFORMATION:  
; APPLICANT: Robert G. Urban  
; APPLICANT: Roman M. Chicz  
; APPLICANT: Mario A. A. Vignal  
; APPLICANT: Mary L. Hedley  
; APPLICANT: Lawrence J. Stern  
; APPLICANT: Jack L. Strominger  
; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES  
; NUMBER OF SEQUENCES: 274  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: U.S.A.  
; ZIP: 02110-2804  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; COMPUTER: IBM PS/2 Model 502 or 55SX  
; OPERATING SYSTEM: MS-DOS (Version 5.0)  
; SOFTWARE: WordPerfect (Version 5.1)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/077,255A  
; FILING DATE: June 15, 1993  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/925,460  
; FILING DATE: August 11, 1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Clark, Paul T.  
; REGISTRATION NUMBER: 30,162  
; REFERENCE/DOCKET NUMBER: 00246/168001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 542-5070  
; TELEFAX: (617) 542-8906  
; TELEX: 200154  
; INFORMATION FOR SEQ ID NO: 188:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 16  
; TYPE: amino acid  
; STRANDEDNESS: linear  
; TOPOLOGY: linear  
; US-08-077-255A-188  
Query Match 32.1%; Score 25; DB 2; Length 16;  
Best Local Similarity 66.7%; Pred. No. 6.4e+02;  
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 4 RDNDY 9  
Db 8 RGNQY 13  
RESULT 78  
US-09-490-070A-238  
; Sequence 238, Application US/09490070A  
; Patent No. 6696248  
; GENERAL INFORMATION:  
; APPLICANT: Knappik, Achim  
; APPLICANT: Pack, Peter  
; APPLICANT: Ilag, Vic  
; APPLICANT: Ge, Liming  
; APPLICANT: Moroney, Simon  
; APPLICANT: Plueckhuhn, Andreas  
; TITLE OF INVENTION: Protein/(Poly)peptide libraries  
; NUMBER OF SEQUENCES: 373  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman  
; White & McAuliffe  
; STREET: 1666 K Street, N.W., Suite 300

CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20006  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/490,070A  
FILING DATE: 24-Jan-2000  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 95 11 3021.0  
FILING DATE: 18-AUG-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Colin G. Sandercock, Esq.  
REGISTRATION NUMBER: 31,298  
REFERENCE/DOCKET NUMBER: 37629-0005  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 912-2000  
TELEFAX: (202) 912-2020  
INFORMATION FOR SEQ ID NO: 238:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: internal  
SEQUENCE DESCRIPTION: SEQ ID NO: 238:  
US-09-490-070A-238  
Query Match 32.1%; Score 25; DB 2; Length 16;  
Best Local Similarity 54.5%; Pred. No. 6.4e+02;  
Matches 6; Conservative 1; Mismatches 2; Indels 2; Gaps 1;  
QY 4 RDNDYSKNPM 14  
Db 5 RDNYSY-DPM 13  
RESULT 79  
US-09-490-153-238  
; Sequence 238, Application US/09490153  
; Patent No. 6706484  
; GENERAL INFORMATION:  
; APPLICANT: Knappik, Achim  
; APPLICANT: Pack, Peter  
; APPLICANT: Ilag, Vic  
; APPLICANT: Ge, Liming  
; APPLICANT: Moroney, Simon  
; APPLICANT: Plueckhuhn, Andreas  
; TITLE OF INVENTION: Protein/(Poly)peptide libraries  
; NUMBER OF SEQUENCES: 373  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
; STREET: 1251 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10021  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/490,153  
FILING DATE: 24-Jan-2000  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/025,769B  
FILING DATE: 18-FEB-1998

APPLICATION NUMBER: EP 95 11 3021.0  
FILING DATE: 18-AUG-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: James F. Haley, Jr., Esq.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: MORPHO/5  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)596-9000  
TELEFAX: (212)596-9090  
INFORMATION FOR SEQ ID NO: 238:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: internal  
SEQUENCE DESCRIPTION: SEQ ID NO: 238:  
US-09-490-153-238

Query Match 32.1%; Score 25; DB 2; Length 16;  
Best Local Similarity 54.5%; Pred. No. 6.4e+02;  
Matches 6; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

QY 4 RDNDYSKNPM 14  
DB 5 RDNFSY--DPM 13

RESULT 80  
US-09-490-324-238

Sequence 238, Application US/09490324  
Patent No. 6828422

GENERAL INFORMATION:

APPLICANT: Knappik, Achim

Pack, Peter

Ilag, Vic

Ge, Laming

Moroney, Simon

Plueckhuhn, Andreas

TITLE OF INVENTION: Protein(Poly)peptide libraries

NUMBER OF SEQUENCES: 373

CORRESPONDENCE ADDRESS:  
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave

STREET: 1251 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10021

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30 (BPO)

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/490,324

FILING DATE: 24-Jan-2000

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/025,769

FILING DATE: 18-FEB-1998

APPLICATION NUMBER: EP 95 11 3021.0

FILING DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:

NAME: James F. Haley, Jr., Esq.

REGISTRATION NUMBER: 27,794

REFERENCE/DOCKET NUMBER: MORPHO/5

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)596-9000

TELEFAX: (212)596-9090

INFORMATION FOR SEQ ID NO: 238:

SEQUENCE CHARACTERISTICS:  
LENGTH: 16 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: internal  
SEQUENCE DESCRIPTION: SEQ ID NO: 238:  
US-09-490-324-238

Query Match 32.1%; Score 25; DB 2; Length 16;  
Best Local Similarity 54.5%; Pred. No. 6.4e+02;  
Matches 6; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

QY 4 RDNDYSKNPM 14  
DB 5 RDNFSY--DPM 13

RESULT 81  
PCT-US93-07545-188

Sequence 188, Application PC/TUS9307545

GENERAL INFORMATION:

APPLICANT: Robert G. Urban

APPLICANT: Roman M. Chicz

APPLICANT: Darlo A. A. Vignall

APPLICANT: Mary L. Hedley

APPLICANT: Lawrence J. Stern

TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES

NUMBER OF SEQUENCES: 273

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson

STREET: 225 Franklin Street

CITY: Boston

STATE: Massachusetts

COUNTRY: U.S.A.

ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 MB

COMPUTER: IBM PS/2 Model 502 or 55SX

OPERATING SYSTEM: MS-DOS (Version 5.0)

SOFTWARE: Wordperfect (Version 5.1)

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/07545

FILING DATE: 19930811

CLASSIFICATION:

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/925,460

FILING DATE: August 11, 1992

ATTORNEY/AGENT INFORMATION:

NAME: Clark, Paul T.

REGISTRATION NUMBER: 30,162

REFERENCE/DOCKET NUMBER: 00246/168001

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 542-5070

TELEFAX: (617) 542-8906

TELEX: 200154

INFORMATION FOR SEQ ID NO: 188:

SEQUENCE CHARACTERISTICS:  
LENGTH: 16

TYPE: amino acid

STRANDEDNESS:  
TOPOLOGY: linear

PCT-US93-07545-188

Query Match

Best Local Similarity 32.1%; Score 25; DB 4; Length 16;  
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 RDNDY 9  
DB 8 RDNFY 13

RESULT 82



US-09-177-249-281  
; Sequence 281, Application US/09177249  
; Patent No. 6229064  
; GENERAL INFORMATION:  
; APPLICANT: Fiecher, Robert L.  
; APPLICANT: Ohad, Nir  
; APPLICANT: Kiyosue, Tomohiro  
; APPLICANT: Yadegari, Ramon  
; APPLICANT: Margossian, Linda  
; APPLICANT: Harada, John  
; APPLICANT: Goldberg, Robert B.  
; TITLE OF INVENTION: The Regents of the University of California  
; TITLE OF INVENTION: Nucleic Acids That Control Seed and Fruit  
; FILE REFERENCE: 023070-086120US  
; CURRENT APPLICATION NUMBER: US/09/177,249  
; PRIOR FILING DATE: 1998-10-22  
; PRIOR APPLICATION NUMBER: US 09/071,838  
; EARLIER FILING DATE: 1998-05-01  
; NUMBER OF SEQ ID NOS: 324  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 281  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Arabidopsis sp.  
US-09-177-249-281

Query Match 32.1%; Score 25; DB 2; Length 17;  
Best Local Similarity 71.4%; Pred. No. 6.8e+02;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 DYSKNPM 14  
DB 1 DTSANPM 7

RESULT 83  
US-09-066-330-1  
; Sequence 1, Application US/09066330A  
; Patent No. 6511666  
; GENERAL INFORMATION:  
; APPLICANT: Reynolds, Eric C.  
; APPLICANT: Bhogal, Peter S.  
; APPLICANT: Stakek, Nada  
; TITLE OF INVENTION: DIAGNOSTICS AND TREATMENTS OF PERIODONTAL DISEASE  
; FILE REFERENCE: Reynolds  
; CURRENT APPLICATION NUMBER: US/09/066,330A  
; CURRENT FILING DATE: 1998-09-15  
; EARLIER APPLICATION NUMBER: PN 6275  
; EARLIER FILING DATE: 1995-10-30  
; EARLIER APPLICATION NUMBER: PCT/AU96/00673  
; EARLIER FILING DATE: 1996-10-30  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Organism: Porphyromonas gingivalis  
US-09-066-330-1

Query Match 32.1%; Score 25; DB 2; Length 17;  
Best Local Similarity 40.0%; Pred. No. 6.8e+02;  
Matches 4; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 5 DHNDYSKNPM 14  
DB 5 DHGDLVNTPV 14

RESULT 84  
US-09-812-283-281  
; Sequence 281, Application US/09812283  
; Patent No. 6826477

; GENERAL INFORMATION:  
; APPLICANT: Fiecher, Robert L.  
; APPLICANT: Ohad, Nir  
; APPLICANT: Kiyosue, Tomohiro  
; APPLICANT: Yadegari, Ramon  
; APPLICANT: Margossian, Linda  
; APPLICANT: Harada, John  
; APPLICANT: Goldberg, Robert B.  
; TITLE OF INVENTION: The Regents of the University of California  
; TITLE OF INVENTION: Nucleic Acids That Control Seed and Fruit  
; FILE REFERENCE: 023070-086120US  
; CURRENT APPLICATION NUMBER: US/09/812,283  
; CURRENT FILING DATE: 2001-03-19  
; PRIOR APPLICATION NUMBER: 09/177,249  
; PRIOR FILING DATE: 1998-10-22  
; PRIOR APPLICATION NUMBER: US 09/071,838  
; PRIOR FILING DATE: 1998-05-01  
; NUMBER OF SEQ ID NOS: 324  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 281  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Arabidopsis sp.  
US-09-812-283-281

Query Match 32.1%; Score 25; DB 2; Length 17;  
Best Local Similarity 71.4%; Pred. No. 6.8e+02;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 DYSKNPM 14  
DB 1 DTSANPM 7

RESULT 85  
US-08-406-142A-10  
; Sequence 10, Application US/08406142A  
; Patent No. 6060451  
; GENERAL INFORMATION:  
; APPLICANT: Dimailo, John  
; APPLICANT: Ni, Feng  
; APPLICANT: Konishi, Yasuo  
; APPLICANT: Steinmetzer, Torsten  
; TITLE OF INVENTION: Thrombin Inhibitors Based on the Amino  
; TITLE OF INVENTION: Acid Sequence of Hirudin  
; Patent No. 6060451  
; NUMBER OF SEQUENCES: 33  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 3000 K St. N.W., Suite 500  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20007-5109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/406,142A  
; FILING DATE: 20-MAR-1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/302,245  
; FILING DATE: 08-SEP-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/960,425  
; FILING DATE: 10-FEB-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/CA91/00213  
; FILING DATE: 14-JUN-1991

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/538,322  
FILING DATE: 15-JUN-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: BENT, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 47998/109/BIPH  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-672-5300  
TELEFAX: 202-672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 1  
OTHER INFORMATION: /label= Acetyl-D-Cha  
OTHER INFORMATION: /note= "Acetyl group is attached to the N-terminal  
OTHER INFORMATION: of Cyclohexylalanine which is in the  
OTHER INFORMATION: D-configuration. D-Cha is attached to the first  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 2..3  
OTHER INFORMATION: /label= Linker  
OTHER INFORMATION: /note= "Portion of the linker is (CH2)2(CO)- and  
OTHER INFORMATION: is used to link the second residue Arginine to the  
OTHER INFORMATION: third residue Glutamine. "  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 17..18  
OTHER INFORMATION: /label= Cha  
OTHER INFORMATION: /note= "Cyclohexylalanine is included within the  
OTHER INFORMATION: peptide chain between the 17th residue Tyrosine and  
OTHER INFORMATION: the 18th residue Glutamine by peptide linkage. "  
US-08-406-142A-10  
Query Match 32.1%; Score 25; DB 2; Length 18;  
Best Local Similarity 33.3%; Pred. No. 7.3e+02;  
Matches 4; Conservative 3; Mismatches 5; Indels 0; Gaps 0;  
QY 3 KRDNHYSKNPM 14  
DB 2 RQSHNDGDPFPI 13  
RESULT 86  
US-08-406-142A-26  
Sequence 26, Application US/08406142A  
Patent No. 6060451  
GENERAL INFORMATION:  
APPLICANT: DiMaio, John  
APPLICANT: Ni, Feng  
APPLICANT: Konishi, Yasuo  
APPLICANT: Steinmetzer, Torsten  
TITLE OF INVENTION: Thrombin Inhibitors Based on the Amino  
TITLE OF INVENTION: Acid Sequence of Hirudin  
Patent No. 6060451  
NUMBER OF SEQUENCES: 33  
CORRESPONDENCE ADDRESSES:  
ADDRESSER: Foley & Lardner  
STREET: 3000 K St. N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/406,142A  
FILING DATE: 20-MAR-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/302,245  
FILING DATE: 08-SRP-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/960,425  
FILING DATE: 10-FEB-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/CA91/00213  
FILING DATE: 14-JUN-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/538,322  
FILING DATE: 15-JUN-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: BENT, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 47998/109/BIPH  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-672-5300  
TELEFAX: 202-672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 1  
OTHER INFORMATION: /label= Acetyl-D-config  
OTHER INFORMATION: /note= "An acetyl group is attached to the  
OTHER INFORMATION: N-terminal of the first residue Phenylalanine  
OTHER INFORMATION: which is in the D-configuration. "  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 3..4  
OTHER INFORMATION: /label= Linker  
OTHER INFORMATION: /note= "Portion of the linker is -(CH2)2CO- and is  
OTHER INFORMATION: used to link the third residue Arginine to the  
OTHER INFORMATION: fourth residue Glutamine. "  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 18..19  
OTHER INFORMATION: /label= Cha  
OTHER INFORMATION: /note= "Cyclohexylalanine is included within the  
OTHER INFORMATION: peptide chain between the 18th residue Tyrosine  
OTHER INFORMATION: and 19th residue Glutamine and is attached by  
US-08-406-142A-26  
Query Match 32.1%; Score 25; DB 2; Length 19;  
Best Local Similarity 33.3%; Pred. No. 7.7e+02;  
Matches 4; Conservative 3; Mismatches 5; Indels 0; Gaps 0;  
QY 3 KRDNHYSKNPM 14  
DB 3 RQSHNDGDPFPI 14  
RESULT 87  
US-08-934-915-139  
Sequence 139, Application US/08934915  
Patent No. 5932412  
GENERAL INFORMATION:  
APPLICANT: DILLNER, JOAKIM  
APPLICANT: DILLNER, LENA  
APPLICANT: CHENG, HWEE-MING  
TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN  
TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,

TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 55.  
TITLE OF INVENTION: USEFUL IN IMMUNODASSAY FOR  
TITLE OF INVENTION: DIAGNOSTIC PURPOSES  
NUMBER OF SEQUENCES: 193  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: MASON & ASSOCIATES, P.A.  
STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500  
CITY: CLEARWATER  
STATE: FLORIDA  
COUNTRY: U.S.A.  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: Windows 3.0  
SOFTWARE: Microsoft Word 6.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/934,915  
FILING DATE: 22-SEP-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/949,836  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: LOUISE A. FOUTCH  
REGISTRATION NUMBER: 37,133  
REFERENCE/DOCKET NUMBER: 1946.6  
TELEPHONE: 813-538-3800  
TELEFAX: 813-538-3820  
TELEX:  
INFORMATION FOR SEQ ID NO: 139:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-934-915-139

Query Match 32.1%; Score 25; DB 1; Length 20;  
Best Local Similarity 50.0%; Pred. No. 8.2e+02;  
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 3 KRDNHYSKN 12  
DB 7 KNAEKYSKN 16

RESULT 88  
US-08-602-999A-126  
Sequence 126, Application US/08602999A  
Patent No. 6184205  
GENERAL INFORMATION:  
APPLICANT: SPARKS, Andrew B.  
APPLICANT: KAY, Brian K.  
APPLICANT: THORN, Judith M.  
APPLICANT: QUILIAM, Lawrence A.  
APPLICANT: DER, Channing J.  
APPLICANT: FOWLES, Dana M.  
APPLICANT: RIDER, James B.  
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
TITLE OF INVENTION: ISOLATING AND USING SAME  
NUMBER OF SEQUENCES: 467  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/602,999A  
FILING DATE: 16-FEB-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Mierock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 1101-202  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 126:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-602-999A-126

Query Match 32.1%; Score 25; DB 2; Length 20;  
Best Local Similarity 57.1%; Pred. No. 8.2e+02;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 7 NDYSKNP 13  
DB 4 SDYSRPP 10

RESULT 89  
US-09-500-124-126  
Sequence 126, Application US/09500124  
Patent No. 6432920  
GENERAL INFORMATION:  
APPLICANT: SPARKS, Andrew B.  
APPLICANT: KAY, Brian K.  
APPLICANT: THORN, Judith M.  
APPLICANT: QUILIAM, Lawrence A.  
APPLICANT: DER, Channing J.  
APPLICANT: FOWLES, Dana M.  
APPLICANT: RIDER, James B.  
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
TITLE OF INVENTION: ISOLATING AND USING SAME  
NUMBER OF SEQUENCES: 467  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/500,124  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/602,999  
FILING DATE: 16-FEB-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Mierock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 1101-202  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 126:

SEQUENCE CHARACTERISTICS:  
 LENGTH: 20 amino acids  
 TYPE: amino acid  
 TOPOLOGY: unknown  
 MOLECULE TYPE: peptide  
 US-09-500-124-126

Query Match 32.1%; Score 25; DB 2; Length 20;  
 Best Local Similarity 57.1%; Pred. No. 8.2e+02;  
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 7 NDYSKNP 13  
 :|||:  
 Db 4 SDYSRPP 10

RESULT 90  
 US-09-605-703B-2436  
 Sequence 2436, Application US/09605703B  
 Patent No. 6962989  
 GENERAL INFORMATION:  
 APPLICANT: Pompejus, Markus  
 APPLICANT: Kroger, Burkhard  
 APPLICANT: Schroder, Hartwig  
 APPLICANT: Zelder, Oskar  
 APPLICANT: Habertauer, Gregor  
 TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING NOVEL  
 TITLE OF INVENTION: PROTEINS  
 FILE REFERENCE: BGI-129CP  
 CURRENT APPLICATION NUMBER: US/09/605,703B  
 CURRENT FILING DATE: 2000-06-27  
 PRIOR APPLICATION NUMBER: 60/142,764  
 PRIOR FILING DATE: 1999-07-08  
 PRIOR APPLICATION NUMBER: 60/152,318  
 PRIOR FILING DATE: 1999-09-03  
 NUMBER OF SEQ ID NOS: 2534  
 SEQ ID NO 2436  
 LENGTH: 20  
 TYPE: PRT  
 ORGANISM: Corynebacterium glutamicum  
 US-09-605-703B-2436

Query Match 32.1%; Score 25; DB 2; Length 20;  
 Best Local Similarity 44.4%; Pred. No. 8.2e+02;  
 Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 4 RDNNDYSKN 12  
 :|||:  
 Db 8 RDMDDYGED 16

RESULT 91  
 US-08-180-209B-24  
 Sequence 24, Application US/08180209B  
 Patent No. 5593877  
 GENERAL INFORMATION:  
 APPLICANT: King, Te-Piao  
 TITLE OF INVENTION: CLONING AND RECOMBINANT PRODUCTION OF  
 TITLE OF INVENTION: VESPID VENOM ENZYMES, SUCH AS PHOSPHOLIPASE AND  
 TITLE OF INVENTION: HYALURONIDASE, AND IMMUNOLOGICAL THERAPIES BASED  
 NUMBER OF SEQUENCES: 62  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Klauber & Jackson  
 STREET: 411 Hackensack Avenue  
 CITY: Hackensack  
 STATE: New Jersey  
 COUNTRY: USA  
 ZIP: 07601  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/180,209B  
 FILING DATE: 11-JAN-1994  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/031,400  
 FILING DATE: 11-MAR-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Jackson Esq., David A.  
 REGISTRATION NUMBER: 26,742  
 REFERENCE/DOCKET NUMBER: 600-1-074 CIP  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 201 487-5800  
 TELEFAX: 201 343-1684  
 TELEX: 133521  
 INFORMATION FOR SEQ ID NO: 24:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 8 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULAR TYPE: peptide  
 US-08-180-209B-24

Query Match 31.4%; Score 24.5; DB 1; Length 8;  
 Best Local Similarity 62.5%; Pred. No. 4.6e+05;  
 Matches 5; Conservative 2; Mismatches 0; Indels 1; Gaps 1;

QY 2 IRDNNDY 9  
 :|||:  
 Db 1 LKR-HNDF 7

RESULT 92  
 US-08-385-745-24  
 Sequence 24, Application US/08385745  
 Patent No. 561209  
 GENERAL INFORMATION:  
 APPLICANT: King, Te Piao  
 TITLE OF INVENTION: Cloning and Recombinant Production of  
 TITLE OF INVENTION: Vespid Venom Phospholipases, and Immunological Therapies  
 TITLE OF INVENTION: Based Thereon  
 NUMBER OF SEQUENCES: 27  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Pennie & Edmonds  
 STREET: 1155 Avenue of the Americas  
 CITY: New York  
 STATE: New York  
 COUNTRY: U.S.A.  
 ZIP: 10036-2711  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/385,745  
 FILING DATE:  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/08/031,400  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Mastrock, S. Leslie  
 REGISTRATION NUMBER: 18,872  
 REFERENCE/DOCKET NUMBER: 3288-020  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 212 790-9090  
 TELEFAX: 212 869-8664/9741  
 TELEX: 66141 PENNIE  
 INFORMATION FOR SEQ ID NO: 24:  
 SEQUENCE CHARACTERISTICS:

LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-385-745-24

Query Match 31.4%; Score 24.5; DB 1; Length 8;  
Best Local Similarity 62.5%; Pred. No. 4.6e+05;  
Matches 5; Conservative 2; Mismatches 0; Indels 1; Gaps 1;

QY 2 IKRDNDY 9  
: || ||| :  
Db 1 LKR-HNDF 7

RESULT 93  
US-08-485-388-24  
Sequence 24, Application US/08485388  
Patent No. 6270763

GENERAL INFORMATION:  
APPLICANT: King, Te Piao  
TITLE OF INVENTION: Cloning and Recombinant Production of  
TITLE OF INVENTION: Vespid Venom Phospholipases, and Immunological Therapies  
TITLE OF INVENTION: Based Thereon  
NUMBER OF SEQUENCES: 27

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Klauder & Jackson  
STREET: 411 Hackensack Avenue  
CITY: Hackensack  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07601

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/485,388  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/385,745  
FILING DATE: 08-FEB-1995  
CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/031,400  
FILING DATE: 11-MAR-1993  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Jackson Bq., David A.  
REGISTRATION NUMBER: 26,742  
REFERENCE/DOCKET NUMBER: 600-1-074 FWCA  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201 487-5800  
TELEFAX: 201 343-1684  
TELEX: 133521

INFORMATION FOR SEQ ID NO: 24:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-485-388-24

Query Match 31.4%; Score 24.5; DB 2; Length 8;  
Best Local Similarity 62.5%; Pred. No. 4.6e+05;  
Matches 5; Conservative 2; Mismatches 0; Indels 1; Gaps 1;

QY 2 IKRDNDY 9  
: || ||| :

Db 1 LKR-HNDF 7

RESULT 94  
US-08-474-853-24  
Sequence 24, Application US/08474853  
Patent No. 6287559

GENERAL INFORMATION:  
APPLICANT: King, Te Piao  
TITLE OF INVENTION: CLONING AND RECOMBINANT PRODUCTION OF  
TITLE OF INVENTION: VESPID VENOM ENZYMES, SUCH AS PHOSPHOLIPASE AND  
TITLE OF INVENTION: HYALURONIDASE, AND IMMUNOLOGICAL THERAPIES BASED THEREON  
NUMBER OF SEQUENCES: 62

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Klauder & Jackson  
STREET: 411 Hackensack Avenue  
CITY: Hackensack  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07601

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/474,853  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/180,209  
FILING DATE: 11-JAN-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/031,400  
FILING DATE: 11-MAR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Jackson Bq., David A.  
REGISTRATION NUMBER: 26,742  
REFERENCE/DOCKET NUMBER: 600-1-074 CIPB  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201 487-5800  
TELEFAX: 201 343-1684  
TELEX: 133521

INFORMATION FOR SEQ ID NO: 24:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-474-853-24

Query Match 31.4%; Score 24.5; DB 2; Length 8;  
Best Local Similarity 62.5%; Pred. No. 4.6e+05;  
Matches 5; Conservative 2; Mismatches 0; Indels 1; Gaps 1;

QY 2 IKRDNDY 9  
: || ||| :  
Db 1 LKR-HNDF 7

RESULT 95  
US-09-166-205B-24  
Sequence 24, Application US/09166205B  
Patent No. 6372471

GENERAL INFORMATION:  
APPLICANT: Te Piao King  
TITLE OF INVENTION: CLONING AND RECOMBINANT PRODUCTION OF VESPID VENOM ENZYMES,  
TITLE OF INVENTION: SUCH AS PHOSPHOLIPASE AND HYALURONIDASE, AND IMMUNOLOGICAL  
TITLE OF INVENTION: THERAPIES BASED THEREON  
FILE REFERENCE: 2313/0P138US  
CURRENT APPLICATION NUMBER: US/09/166,205B  
CURRENT FILING DATE: 1998-10-01

NUMBER OF SEQ ID NOS: 70  
SOFTWARE: FASTSEQ for Windows Version 3.0  
SEQ ID NO 24  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Dolichovespula maculata  
US-09-166-205B-24

Query Match 31.4%; Score 24.5; DB 2; Length 8;  
Best Local Similarity 62.5%; Pred. No. 4.6e+05;  
Matches 5; Conservative 2; Mismatches 0; Indels 1; Gaps 1;

QY 2 IKRDHNDY 9  
DB 1 LKR-HNDF 7

RESULT 96  
PCT-US94-02629-24  
Sequence 24, Application PC/TUS9402629  
GENERAL INFORMATION:  
APPLICANT: King, Te-Piao  
TITLE OF INVENTION: CLONING AND RECOMBINANT PRODUCTION OF  
TITLE OF INVENTION: VESPID VENOM ENZYMES, SUCH AS PHOSPHOLIPASE AND  
TITLE OF INVENTION: HYALURONIDASE, AND IMMUNOLOGICAL THERAPIES BASED THEREON  
NUMBER OF SEQUENCES: 62  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Klauber & Jackson  
STREET: 411 Hackensack Avenue  
CITY: Hackensack  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07601  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/02629  
FILING DATE: 10-MAR-1994  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/180,209  
FILING DATE: 11-JAN-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/031,400  
FILING DATE: 11-MAR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Jackson Esq., David A.  
REGISTRATION NUMBER: 26,742  
REFERENCE/DOCKET NUMBER: 600-1-074 PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201 487-5800  
TELEFAX: 201 343-1684  
TELEX: 133521  
INFORMATION FOR SEQ ID NO: 24:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULAR TYPE: peptide  
PCT-US94-02629-24

Query Match 31.4%; Score 24.5; DB 4; Length 8;  
Best Local Similarity 62.5%; Pred. No. 4.6e+05;  
Matches 5; Conservative 2; Mismatches 0; Indels 1; Gaps 1;

QY 2 IKRDHNDY 9  
DB 1 LKR-HNDF 7

RESULT 97  
US-08-724-354D-29  
Sequence 29, Application US/08724354D  
Patent No. 5994119  
GENERAL INFORMATION:  
APPLICANT: Dietz, Harry C.  
TITLE OF INVENTION: MAMMALIAN REGULATOR OF  
TITLE OF INVENTION: NONSENSE-MEDIATED RNA DEGRADATION  
NUMBER OF SEQUENCES: 29  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson, P.C.  
STREET: 4225 Executive Square, Suite 1400  
CITY: La Jolla  
STATE: CA  
COUNTRY: USA  
ZIP: 92037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/724,354D  
FILING DATE: 01-OCT-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/016,482  
FILING DATE: 29-APR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Hall, Lisa A.  
REGISTRATION NUMBER: 38,347  
REFERENCE/DOCKET NUMBER: 07265/090001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-678-5070  
TELEFAX: 619-678-5099  
INFORMATION FOR SEQ ID NO: 29:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULAR TYPE: peptide  
US-08-724-354D-29

Query Match 30.8%; Score 24; DB 1; Length 7;  
Best Local Similarity 80.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 NDYSK 11  
DB 3 NDYDK 7

RESULT 98  
US-09-270-984A-29  
Sequence 29, Application US/09270984A  
Patent No. 6048965  
GENERAL INFORMATION:  
APPLICANT: Dietz, Harry C.  
TITLE OF INVENTION: MAMMALIAN REGULATOR OF  
TITLE OF INVENTION: NONSENSE-MEDIATED RNA DEGRADATION  
NUMBER OF SEQUENCES: 29  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson, P.C.  
STREET: 4225 Executive Square, Suite 1400  
CITY: La Jolla  
STATE: CA  
COUNTRY: USA  
ZIP: 92037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: FASTSEQ for Windows Version 2.0

;; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/270,984A  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/724,354  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Haile, Lisa A.  
; REGISTRATION NUMBER: 38,347  
; REFERENCE/DOCKET NUMBER: 07265/090001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 619-678-5070  
; TELEFAX: 619-678-5099  
; INFORMATION FOR SEQ ID NO: 29:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-09-270-984A-29

Query Match 30.8%; Score 24; DB 2; Length 7;  
Best Local Similarity 80.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 NDYSK 11  
Db 3 NDYDK 7

RESULT 99  
US-08-974-899-15  
; Sequence 15, Application US/08974899  
; Patent No. 6037454  
; GENERAL INFORMATION:  
; APPLICANT: Presta, Leonard G.  
; TITLE OF INVENTION: Humanized Anti-CD11a Antibodies  
; NUMBER OF SEQUENCES: 24  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPacIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/974,899  
; FILING DATE:  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/031971  
; FILING DATE: 11/27/96  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lee, Wendy M.  
; REGISTRATION NUMBER: 40,378  
; REFERENCE/DOCKET NUMBER: P1014R1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-1994  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 15:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: linear  
US-08-974-899-15

Query Match 30.8%; Score 24; DB 2; Length 9;

Best Local Similarity 50.0%; Pred. No. 4.6e+05;  
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 RDNDY 9  
Db 1 QCHNEY 6

RESULT 100  
US-09-336-447A-40  
; Sequence 40, Application US/09336447A  
; Patent No. 6310190  
; GENERAL INFORMATION:  
; APPLICANT: HANSEN, ERIC J.  
; APPLICANT: ASBI, CHRISTOPH  
; APPLICANT: COPE, LESLIE D.  
; APPLICANT: MACIVER, ISOBEL  
; APPLICANT: FISKE, MICHAEL J.  
; APPLICANT: FREDENBURG, ROSS A.  
; TITLE OF INVENTION: USPA1 AND USPA2 ANTIGENS OF MORAXELLA CATARRHALIS  
; FILE REFERENCE: AMCY:024  
; CURRENT APPLICATION NUMBER: US/09/336,447A  
; CURRENT FILING DATE: 1999-06-21  
; NUMBER OF SEQ ID NOS: 98  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 40  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Moraxella catarrhalis  
US-09-336-447A-40

Query Match 30.8%; Score 24; DB 2; Length 9;  
Best Local Similarity 66.7%; Pred. No. 4.6e+05;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 DHNDYS 10  
Db 2 DKNEYS 7

Search completed: January 20, 2006, 19:14:10  
Job time : 16.6731 secs

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OM protein - protein search, using SW model

Run on: January 20, 2006, 19:11:21 ! Search time 50.4808 Seconds  
(without alignments)  
115.878 Million cell updates/sec

Title: US-09-662-293-1

Perfect score: 78  
Sequence: 1 SIRKDHNDYSKNPM 14

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417629326 residues

Total number of hits satisfying chosen parameters: 380452

Minimum DB seq length: 0

Maximum DB seq length: 20

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Published Applications AA Main:\*

1: /cgn2\_6/ptodaca/1/pubppaa/US07\_PUBCOMB.pep:\*

2: /cgn2\_6/ptodaca/1/pubppaa/US08\_PUBCOMB.pep:\*

3: /cgn2\_6/ptodaca/1/pubppaa/US09\_PUBCOMB.pep:\*

4: /cgn2\_6/ptodaca/1/pubppaa/US10A\_PUBCOMB.pep:\*

5: /cgn2\_6/ptodaca/1/pubppaa/US10B\_PUBCOMB.pep:\*

6: /cgn2\_6/ptodaca/1/pubppaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	* Query Match	Length	DB ID	Description
1	78	100.0	14	4 US-10-218-743-1	Sequence 1, Appl1
2	37	47.4	17	3 US-09-992-665-48	Sequence 48, Appl1
3	34	43.6	20	3 US-09-731-321-58	Sequence 58, Appl1
4	32	41.0	11	3 US-09-758-318-10	Sequence 10, Appl1
5	32	41.0	11	4 US-10-340-783-10	Sequence 10, Appl1
6	32	41.0	11	4 US-10-801-820-10	Sequence 10, Appl1
7	32	41.0	17	4 US-10-095-373A-22	Sequence 22, Appl1
8	32	41.0	18	4 US-10-218-743-12	Sequence 12, Appl1
9	30	38.5	20	3 US-09-731-221-59	Sequence 59, Appl1
10	30	38.5	20	4 US-10-079-167-98	Sequence 98, Appl1
11	30	38.5	20	4 US-10-345-000-20	Sequence 20, Appl1
12	29	37.2	9	4 US-10-365-761B-20	Sequence 20, Appl1
13	29	37.2	12	4 US-10-391-540-48	Sequence 48, Appl1
14	29	37.2	12	4 US-10-453-483-25	Sequence 25, Appl1
15	29	37.2	12	6 US-11-119-889-48	Sequence 22, Appl1
16	29	37.2	13	4 US-10-345-764-22	Sequence 22, Appl1
17	29	37.2	14	4 US-10-417-895A-43	Sequence 43, Appl1
18	29	37.2	16	4 US-10-417-895A-34	Sequence 34, Appl1
19	29	37.2	20	5 US-10-776-013-382	Sequence 382, Appl1
20	28.5	36.5	17	4 US-10-095-373A-12	Sequence 12, Appl1
21	28	35.9	8	5 US-10-996-316-195	Sequence 195, Appl1
22	28	35.9	10	4 US-10-794-899-21	Sequence 21, Appl1
23	28	35.9	11	3 US-09-852-910-247	Sequence 247, Appl1
24	28	35.9	11	4 US-10-411-336A-247	Sequence 247, Appl1
25	28	35.9	12	5 US-10-884-830-218	Sequence 218, Appl1
26	28	35.9	14	4 US-10-417-895A-45	Sequence 45, Appl1
27	28	35.9	15	4 US-10-354-240-47	Sequence 47, Appl1

28	28	35.9	17	3 US-09-949-196-2	Sequence 2, Appl1
29	28	35.9	18	4 US-10-772-089-2	Sequence 2, Appl1
30	28	35.9	20	5 US-10-931-260-42	Sequence 42, Appl1
31	28	35.9	20	5 US-10-931-260-203	Sequence 203, Appl1
32	27	34.6	7	3 US-09-901-187B-2	Sequence 2, Appl1
33	27	34.6	7	5 US-10-909-116-2	Sequence 2, Appl1
34	27	34.6	11	3 US-09-852-910-185	Sequence 185, Appl1
35	27	34.6	11	4 US-10-411-336A-185	Sequence 185, Appl1
36	27	34.6	12	4 US-10-692-151-33	Sequence 33, Appl1
37	27	34.6	13	4 US-10-607-712-9	Sequence 9, Appl1
38	27	34.6	13	4 US-10-607-712-10	Sequence 10, Appl1
39	27	34.6	13	4 US-10-607-712-11	Sequence 11, Appl1
40	27	34.6	13	4 US-10-607-712-12	Sequence 12, Appl1
41	27	34.6	13	4 US-10-607-712-13	Sequence 13, Appl1
42	27	34.6	13	4 US-10-607-712-14	Sequence 14, Appl1
43	27	34.6	15	4 US-10-354-240-46	Sequence 46, Appl1
44	27	34.6	15	4 US-10-714-679-1	Sequence 1, Appl1
45	27	34.6	15	5 US-10-808-187-1406	Sequence 1406, Appl1
46	27	34.6	15	5 US-10-807-807-1406	Sequence 1406, Appl1
47	27	34.6	16	5 US-10-946-647-65	Sequence 65, Appl1
48	27	34.6	16	5 US-10-946-647-368	Sequence 368, Appl1
49	27	34.6	16	5 US-10-946-647-517	Sequence 517, Appl1
50	27	34.6	16	5 US-10-946-647-635	Sequence 635, Appl1
51	27	34.6	20	3 US-09-731-221-57	Sequence 57, Appl1
52	27	34.6	20	3 US-09-864-761-39698	Sequence 39698, Appl1
53	27	34.6	20	5 US-10-931-260-41	Sequence 41, Appl1
54	26	33.3	8	4 US-10-089-549-12	Sequence 12, Appl1
55	26	33.3	9	4 US-10-245-871-459	Sequence 459, Appl1
56	26	33.3	9	4 US-10-253-286-459	Sequence 459, Appl1
57	26	33.3	10	4 US-09-894-018-263	Sequence 263, Appl1
58	26	33.3	10	4 US-10-360-836-33	Sequence 33, Appl1
59	26	33.3	10	4 US-10-371-525-441	Sequence 441, Appl1
60	26	33.3	10	4 US-10-371-069-441	Sequence 441, Appl1
61	26	33.3	10	4 US-10-371-645-441	Sequence 441, Appl1
62	26	33.3	10	4 US-10-371-260-441	Sequence 441, Appl1
63	26	33.3	10	5 US-10-474-960A-263	Sequence 263, Appl1
64	26	33.3	11	4 US-10-697-399-9	Sequence 9, Appl1
65	26	33.3	11	4 US-10-930-300-129	Sequence 129, Appl1
66	26	33.3	12	4 US-10-193-460A-16	Sequence 16, Appl1
67	26	33.3	12	4 US-10-652-407-44	Sequence 44, Appl1
68	26	33.3	12	5 US-10-958-765-35	Sequence 35, Appl1
69	26	33.3	13	3 US-09-992-665-15	Sequence 15, Appl1
70	26	33.3	15	3 US-09-391-104-15	Sequence 15, Appl1
71	26	33.3	15	4 US-10-124-986-33	Sequence 33, Appl1
72	26	33.3	15	4 US-10-116-275-44	Sequence 44, Appl1
73	26	33.3	15	4 US-10-475-104-129	Sequence 129, Appl1
74	26	33.3	16	4 US-10-126-845-53	Sequence 53, Appl1
75	26	33.3	16	4 US-10-764-235-53	Sequence 53, Appl1
76	26	33.3	16	5 US-10-955-656-53	Sequence 53, Appl1
77	26	33.3	17	5 US-10-660-370-87	Sequence 87, Appl1
78	26	33.3	18	3 US-09-839-984-6	Sequence 6, Appl1
79	26	33.3	18	3 US-09-371-900-50	Sequence 50, Appl1
80	26	33.3	18	3 US-09-924-417-16	Sequence 16, Appl1
81	26	33.3	18	3 US-09-839-984-6	Sequence 6, Appl1
82	26	33.3	18	4 US-10-225-567A-1380	Sequence 1380, Appl1
83	26	33.3	18	4 US-10-186-950-50	Sequence 50, Appl1
84	26	33.3	18	4 US-10-653-872-16	Sequence 16, Appl1
85	26	33.3	18	5 US-10-994-815-6	Sequence 6, Appl1
86	26	33.3	20	4 US-10-325-567A-2058	Sequence 2058, Appl1
87	26	33.3	20	4 US-10-378-173-190	Sequence 190, Appl1
88	26	33.3	20	4 US-10-466-085A-21	Sequence 21, Appl1
89	25.5	32.7	17	4 US-10-025-222A-36	Sequence 36, Appl1
90	25	32.1	9	3 US-09-834-765-658	Sequence 658, Appl1
91	25	32.1	9	3 US-09-338-864-180	Sequence 180, Appl1
92	25	32.1	9	3 US-09-791-477-180	Sequence 180, Appl1
93	25	32.1	9	3 US-09-785-019-180	Sequence 180, Appl1
94	25	32.1	9	4 US-10-125-635A-180	Sequence 180, Appl1
95	25	32.1	9	4 US-10-002-603-180	Sequence 180, Appl1
96	25	32.1	9	4 US-10-195-835-180	Sequence 180, Appl1
97	25	32.1	9	4 US-10-286-333-180	Sequence 180, Appl1
98	25	32.1	9	4 US-10-244-830-180	Sequence 180, Appl1
99	25	32.1	9	4 US-10-427-717-180	Sequence 180, Appl1
100	25	32.1	9	4 US-10-363-791-11	Sequence 11, Appl1

## ALIGNMENTS

RESULT 1  
US-10-218-743-1  
; Sequence 1, Application US/10218743  
; Publication No. US20030096779A1  
; GENERAL INFORMATION:  
; APPLICANT: McCall, Catherine A.  
; APPLICANT: Hunter, Shirley Wu  
; APPLICANT: Weber, Eric R.  
; TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS  
; TITLE OF INVENTION: AND USES THEREOF  
; FILE REFERENCE: AL-2-C3  
; CURRENT APPLICATION NUMBER: US/10/218,743  
; CURRENT FILING DATE: 2002-08-13  
; PRIOR APPLICATION NUMBER: US/09/292,225  
; PRIOR FILING DATE: 1999-04-15  
; PRIOR APPLICATION NUMBER: 60/098,909  
; PRIOR FILING DATE: 1998-09-02  
; PRIOR APPLICATION NUMBER: 60/085,295  
; PRIOR FILING DATE: 1998-05-13  
; PRIOR APPLICATION NUMBER: 60/098,565  
; PRIOR FILING DATE: 1998-04-17  
; PRIOR APPLICATION NUMBER: 09/062,013  
; PRIOR FILING DATE: 1998-04-17  
; NUMBER OF SEQ ID NOS: 49  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 14  
; TYPE: PR1  
; ORGANISM: Dermatophagoides farinase  
US-10-218-743-1

Query Match 100.0%; Score 78; DB 4; Length 14;  
Best Local Similarity 100.0%; Pred. No. 3.3e-06;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SIKRDNDYSKNP 14  
| | | | | | | | | | | | | | | |  
Db 1 SIKRDNDYSKNP 14  
| | | | | | | | | | | | | | | |  
RESULT 2  
US-09-992-665-48  
; Sequence 48, Application US/09992665  
; Publication No. US20030092009A1  
; GENERAL INFORMATION:  
; APPLICANT: Kala Palm  
; TITLE OF INVENTION: PROFILING TUMOR SPECIFIC MARKERS FOR THE  
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF NEOPLASTIC DISEASE  
; FILE REFERENCE: CEMINES.002A  
; CURRENT APPLICATION NUMBER: US/09/992,665  
; CURRENT FILING DATE: 2001-11-13  
; PRIOR APPLICATION NUMBER: 60/249,508  
; PRIOR FILING DATE: 2000-11-16  
; NUMBER OF SEQ ID NOS: 380  
; SOFTWARE: PaatSeq for Windows Version 4.0  
; SEQ ID NO 48  
; LENGTH: 17  
; TYPE: PR1  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Probe  
US-09-992-665-48

Query Match 47.4%; Score 37; DB 3; Length 17;  
Best Local Similarity 54.5%; Pred. No. 31;  
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
QY 3 KRDNNDYSKNP 13

Db 1 KRDHPDYKYP 11  
| : | | | | |  
| : | | | | |

RESULT 3  
US-09-731-221-58  
; Sequence 58, Application US/09731221  
; Patent No. US20020018778A1  
; GENERAL INFORMATION:  
; APPLICANT: Caplan, Michael  
; TITLE OF INVENTION: Passive Desensitization  
; FILE REFERENCE: 2002834-0103  
; CURRENT APPLICATION NUMBER: US/09/731,221  
; CURRENT FILING DATE: 2001-12-06  
; NUMBER OF SEQ ID NOS: 79  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 58  
; LENGTH: 20  
; TYPE: PR1  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:Arachis  
US-09-731-221-58

Query Match 43.6%; Score 34; DB 3; Length 20;  
Best Local Similarity 41.7%; Pred. No. 1.2e+02;  
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 2 IKRDNDYSKNP 13  
| : | | : | : |  
Db 5 IORDSDYERDP 16

RESULT 4  
US-09-758-318-10  
; Sequence 10, Application US/09758318  
; Patent No. US20010034021A1  
; GENERAL INFORMATION:  
; APPLICANT: Muller, Martin  
; APPLICANT: Gissmann, Lutz  
; TITLE OF INVENTION: Seroreactive Regions on HPV 16 Proteins  
; TITLE OF INVENTION: E1 and E2  
; NUMBER OF SEQUENCES: 44  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
; ADDRESSEE: Dunner  
; STREET: 1300 I Street, N.W., Suite 700  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20005-3315  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/758,318  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/468,337  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Rinaudi, Carol P.  
; REGISTRATION NUMBER: 33,220  
; REFERENCE/DOCKET NUMBER: 05552-1199-02000  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-408-4000  
; TELEFAX: 202-408-4400  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:

LENGTH: 11 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-758-318-10

Query Match 41.0%; Score 32; DB 3; Length 11;  
Best Local Similarity 66.7%; Pred. No. 1.3e+02;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 RDHNDYSKN 12  
||| |||  
Db 3 RDHIDYWKH 11

RESULT 5  
US-10-340-783-10  
Sequence 10, Application US/10340783  
Publication No. US20030147915A1  
GENERAL INFORMATION:  
APPLICANT: Muller, Martin  
Giesmann, Lutz  
TITLE OF INVENTION: Seroreactive Regions on HPV 16 Proteins  
R1 and R2  
NUMBER OF SEQUENCES: 44  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Flinnegan, Henderson, Farabow, Garrett &  
Dunner  
STREET: 1300 I Street, N.W., Suite 700  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005-3315  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/340,783  
FILING DATE: 13-Jan-2003  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/758,318  
FILING DATE: <Unknown>  
APPLICATION NUMBER: 08/468,337  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Elnaudt, Carol P.  
REGISTRATION NUMBER: 33,220  
REFERENCE/DOCKET NUMBER: 05552-1199-02000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-408-4000  
TELEFAX: 202-408-4400  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 10:  
US-10-340-783-10

Query Match 41.0%; Score 32; DB 4; Length 11;  
Best Local Similarity 66.7%; Pred. No. 1.3e+02;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 RDHNDYSKN 12  
||| |||  
Db 3 RDHIDYWKH 11

RESULT 6

US-10-801-820-10  
Sequence 10, Application US/10801820  
Publication No. US20040152074A1  
GENERAL INFORMATION:  
APPLICANT: Muller, Martin  
Giesmann, Lutz  
TITLE OF INVENTION: Seroreactive Regions on HPV 16 Proteins  
R1 and R2  
NUMBER OF SEQUENCES: 44  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Flinnegan, Henderson, Farabow, Garrett &  
Dunner  
STREET: 1300 I Street, N.W., Suite 700  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005-3315  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/801,820  
FILING DATE: 17-Mar-2004  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/758,318  
FILING DATE: 12-Jan-2001  
APPLICATION NUMBER: 08/468,337  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Elnaudt, Carol P.  
REGISTRATION NUMBER: 33,220  
REFERENCE/DOCKET NUMBER: 05552-1199-02000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-408-4000  
TELEFAX: 202-408-4400  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 10:  
US-10-801-820-10

Query Match 41.0%; Score 32; DB 4; Length 11;  
Best Local Similarity 66.7%; Pred. No. 1.3e+02;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 RDHNDYSKN 12  
||| |||  
Db 3 RDHIDYWKH 11

RESULT 7  
US-10-095-373A-22  
Sequence 22, Application US/10095373A  
Publication No. US20030199022A1  
GENERAL INFORMATION:  
APPLICANT: Shapiro, David J.  
TITLE OF INVENTION: A Tamoxifen AND 4-HYDROXY TAMOXIFEN-ACTIVATED SYSTEM FOR REGULATING  
PRODUCTION OF PROTEINS IN EUKARYOTIC CELLS  
FILING DATE: 10/30/2000  
CURRENT APPLICATION NUMBER: US/10/095,373A  
FILING DATE: 2002-06-21  
NUMBER OF SEQ ID NOS: 83  
SOFTWARE: Patentin version 3.1  
SEQUENCE ID NO 22  
LENGTH: 17  
TYPE: PRT

ORGANISM: Artificial sequence  
FEATURE:  
OTHER INFORMATION: Mutant DBD of ER  
US-10-095-373A-22

Query Match 41.0%; Score 32; DB 4; Length 17;  
Best Local Similarity 71.4%; Pred. No. 2.1e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 KRHDNDY 9  
|:|:|:|  
DB 11 KQGHNDY 17

RESULT 8  
US-10-218-743-12  
Sequence 12, Application US/10218743  
Publication No. US20030096779A1  
GENERAL INFORMATION:  
APPLICANT: McCall, Catherine A.  
APPLICANT: Hunter, Shirley Wu  
APPLICANT: Weber, Eric R.  
TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS  
FILE REFERENCE: AL-2-C3  
CURRENT APPLICATION NUMBER: US/10/218,743  
CURRENT FILING DATE: 2002-08-13  
PRIOR APPLICATION NUMBER: US/09/292,225  
PRIOR FILING DATE: 1999-04-15  
PRIOR APPLICATION NUMBER: 60/098,909  
PRIOR FILING DATE: 1998-09-02  
PRIOR APPLICATION NUMBER: 60/085,295  
PRIOR FILING DATE: 1998-05-13  
PRIOR APPLICATION NUMBER: 60/098,565  
PRIOR FILING DATE: 1998-04-17  
PRIOR APPLICATION NUMBER: 09/062,013  
PRIOR FILING DATE: 1998-04-17  
NUMBER OF SEQ ID NOS: 49  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 12  
LENGTH: 18  
TYPE: PRT  
ORGANISM: Dermatophagoides fariniae  
US-10-218-743-12

Query Match 41.0%; Score 32; DB 4; Length 18;  
Best Local Similarity 83.3%; Pred. No. 2.2e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 DYSKNP 13  
|:|:|:|  
DB 1 DYAKNP 6

RESULT 9  
US-09-731-221-59  
Sequence 59, Application US/09731221  
Patent No. US20020018778A1  
GENERAL INFORMATION:  
APPLICANT: Caplan, Michael  
TITLE OF INVENTION: Passive Desensitization  
FILE REFERENCE: 2002834-0103  
CURRENT APPLICATION NUMBER: US/09/731,221  
CURRENT FILING DATE: 2001-12-06  
NUMBER OF SEQ ID NOS: 79  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 59  
LENGTH: 20  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Arachis  
Hypogaea

US-09-731-221-59

Query Match 38.5%; Score 30; DB 3; Length 20;  
Best Local Similarity 36.4%; Pred. No. 5.4e+02;  
Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 3 KRHDNDYSKNP 13  
|:|:|:|:|:|  
DB 1 QRDSDSYERDP 11

RESULT 10  
US-10-079-167-98  
Sequence 98, Application US/10079167  
Publication No. US20030138454A1  
GENERAL INFORMATION:  
APPLICANT: Hall, Adrian V.S.  
APPLICANT: McShane, Helen  
APPLICANT: Gilbert, Sarah C.  
APPLICANT: Reece, William  
APPLICANT: Schneider, Joerg  
TITLE OF INVENTION: Vaccination Method  
FILE REFERENCE: 2907.1000-001  
CURRENT APPLICATION NUMBER: US/10/079,167  
CURRENT FILING DATE: 2002-02-19  
PRIOR APPLICATION NUMBER: US 09/454,204  
PRIOR FILING DATE: 1999-12-09  
PRIOR APPLICATION NUMBER: PCT/GB98/01681  
PRIOR FILING DATE: 1998-06-09  
PRIOR APPLICATION NUMBER: GB 97 11957.2  
PRIOR FILING DATE: 1997-06-09  
PRIOR APPLICATION NUMBER: PCT/GB01/04116  
PRIOR FILING DATE: 2001-09-13  
PRIOR APPLICATION NUMBER: GB 00 23203.3  
PRIOR FILING DATE: 2001-09-21  
NUMBER OF SEQ ID NOS: 99  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 98  
LENGTH: 20  
TYPE: PRT  
ORGANISM: Unknown  
FEATURE:  
OTHER INFORMATION: Peptide No. US20030138454A1 10 in the TTI-10 pool  
US-10-079-167-98

Query Match 38.5%; Score 30; DB 4; Length 20;  
Best Local Similarity 63.6%; Pred. No. 5.4e+02;  
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 IKRDNDYSKN 12  
|:|:|:|:|:|  
DB 10 IIRLHSDASKN 20

RESULT 11  
US-10-345-000-20  
Sequence 20, Application US/10345000  
Publication No. US20040018177A1  
GENERAL INFORMATION:  
APPLICANT: OXON PHARMACEUTICALS LIMITED  
TITLE OF INVENTION: VACCINATION METHOD  
FILE REFERENCE: 550-409  
CURRENT APPLICATION NUMBER: US/10/345,000  
CURRENT FILING DATE: 2003-02-20  
NUMBER OF SEQ ID NOS: 21  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 20  
LENGTH: 20  
TYPE: PRT  
ORGANISM: Plasmodium falciparum  
US-10-345-000-20

Query Match 38.5%; Score 30; DB 4; Length 20;

Best Local Similarity 63.6%; Pred. No. 5.4e+02;  
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 IKDNDYSKN 12  
|:|:|:|  
Db 10 IIRLHSDASKN 20

## RESULT 12

US-10-365-761B-20  
; Sequence 20; Application US/10365761B  
; Publication No. US20040023300A1  
; GENERAL INFORMATION:  
; APPLICANT: Grabe, Niels  
; TITLE OF INVENTION: METHOD FOR THE DETECTION OF A FUNCTIONAL  
; FILE REFERENCE: ABOHM7.001AUS  
; CURRENT APPLICATION NUMBER: US/10/365,761B  
; PRIOR FILING DATE: 2003-04-12  
; PRIOR APPLICATION NUMBER: EP 02003469.0  
; NUMBER OF SEQ ID NOS: 82  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 20  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; OTHER INFORMATION: synthesized phosphorylacton site  
US-10-365-761B-20

Query Match 37.2%; Score 29; DB 4; Length 12;  
Best Local Similarity 50.0%; Pred. No. 1.7e+06;  
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 5 DHNDYSKN 12  
|:|:|:|  
Db 1 DNMRYNNN 8

RESULT 13  
US-10-191-540-48  
; Sequence 48; Application US/10191540  
; Publication No. US20030224494A1  
; GENERAL INFORMATION:  
; APPLICANT: Tsuyoshi Nomoto, Tetsuya Yano, Shinya Kozaki and Tautomu Honma  
; TITLE OF INVENTION: Polyhydroxyalkanoate-containing structure and manufacturing method  
; FILE REFERENCE: CRO16534  
; CURRENT APPLICATION NUMBER: US/10/191,540  
; PRIOR FILING DATE: 2002-07-10  
; PRIOR APPLICATION NUMBER: JP P2001-210052  
; PRIOR FILING DATE: 2001-07-10  
; PRIOR APPLICATION NUMBER: JP P2002-112978  
; PRIOR FILING DATE: 2002-06-13  
; NUMBER OF SEQ ID NOS: 186  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 48  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; OTHER INFORMATION: Carbon Black-binding peptide  
US-10-191-540-48

Query Match 37.2%; Score 29; DB 4; Length 12;  
Best Local Similarity 62.5%; Pred. No. 4.6e+02;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 6 HNDYSKNP 13  
|:|:|:|  
Db 3 NNDWSKAP 10

RESULT 14  
US-10-453-483-25  
; Sequence 25; Application US/10453483  
; Publication No. US20040005638A1  
; GENERAL INFORMATION:  
; APPLICANT: Tautomu Honma  
; APPLICANT: Tetsuya Yano  
; APPLICANT: Tsuyoshi Nomoto  
; APPLICANT: Shinya Kozaki  
; TITLE OF INVENTION: Immunoassay, reagent for immunoassay, and production method of t  
; FILE REFERENCE: CRO17318  
; CURRENT APPLICATION NUMBER: US/10/453,483  
; PRIOR FILING DATE: 2002-09-05  
; PRIOR APPLICATION NUMBER: JP P2002-173027  
; PRIOR FILING DATE: 2002-06-13  
; PRIOR APPLICATION NUMBER: JP P2003-127099  
; PRIOR FILING DATE: 2003-05-02  
; NUMBER OF SEQ ID NOS: 129  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 25  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Artificial  
; OTHER INFORMATION: binding peptide  
US-10-453-483-25

Query Match 37.2%; Score 29; DB 4; Length 12;  
Best Local Similarity 62.5%; Pred. No. 4.6e+02;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 6 HNDYSKNP 13  
|:|:|:|  
Db 3 NNDWSKAP 10

RESULT 15  
US-11-119-889-48  
; Sequence 48; Application US/11119889  
; Publication No. US20050208635A1  
; GENERAL INFORMATION:  
; APPLICANT: Tsuyoshi Nomoto, Tetsuya Yano, Shinya Kozaki and Tautomu Honma  
; TITLE OF INVENTION: Polyhydroxyalkanoate-containing structure and manufacturing method  
; FILE REFERENCE: CRO16534  
; CURRENT APPLICATION NUMBER: US/11/119,889  
; PRIOR FILING DATE: 2005-05-03  
; PRIOR APPLICATION NUMBER: US/10/191,540  
; PRIOR FILING DATE: 2002-07-10  
; PRIOR APPLICATION NUMBER: JP P2001-210052  
; PRIOR FILING DATE: 2001-07-10  
; PRIOR APPLICATION NUMBER: JP P2002-112978  
; PRIOR FILING DATE: 2002-06-13  
; NUMBER OF SEQ ID NOS: 186  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 48  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; OTHER INFORMATION: Carbon Black-binding peptide  
US-11-119-889-48

Query Match 37.2%; Score 29; DB 6; Length 12;  
Best Local Similarity 62.5%; Pred. No. 4.6e+02;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 6 HNDYSKNP 13  
|:|:|:|  
Db 3 NNDWSKAP 10

```
RESULT 16
US-10-345-764-22
; Sequence 22, Application US/10345764
; Publication No. US20030138912A1
; GENERAL INFORMATION:
; APPLICANT: Busfield, S.
; APPLICANT: Gearling, D.
; TITLE OF INVENTION: EGF-LIKE NUCLEIC ACIDS AND POLYPEPTIDES
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 7853-198
; CURRENT APPLICATION NUMBER: US/10/345,764
; CURRENT FILING DATE: 2003-01-16
; PRIOR APPLICATION NUMBER: US/09/443,959
; PRIOR FILING DATE: 1999-11-19
; PRIOR APPLICATION NUMBER: 09/196,269
; PRIOR FILING DATE: 1998-11-19
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 22
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide used to generate polyclonal antibody
US-10-345-764-22
```

```
Query Match      37.2%; Score 29; DB 4; Length 13;
Best Local Similarity 62.5%; Pred. No. 5e+02;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      5 DHNDYSKN 12
      |||||
Db      5 DHNDYSKIN 12
```

```
RESULT 17
US-10-417-895A-43
; Sequence 43, Application US/10417895A
; Publication No. US20040033569A1
; GENERAL INFORMATION:
; APPLICANT: Crea, Roberto
; APPLICANT: Cappuccilli, Guido
; TITLE OF INVENTION: "DOPING" IN WALK-THROUGH MUTAGENESIS
; FILE REFERENCE: 1551.2002-001
; CURRENT APPLICATION NUMBER: US/10/417,895A
; CURRENT FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: 60/373,686
; PRIOR FILING DATE: 2002-04-17
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 43
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: variant peptide for second complementarity
; OTHER INFORMATION: determining region of Fv region of an
; OTHER INFORMATION: Immunoglobulin
US-10-417-895A-43
```

```
Query Match      37.2%; Score 29; DB 4; Length 14;
Best Local Similarity 50.0%; Pred. No. 5.5e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      5 DHNDYSKN 12
      |||||
Db      7 DHNDHGHQ 14
```

```
RESULT 18
US-10-417-895A-34
; Sequence 34, Application US/10417895A
```

```
; Publication No. US20040033569A1
; GENERAL INFORMATION:
; APPLICANT: Crea, Roberto
; APPLICANT: Cappuccilli, Guido
; TITLE OF INVENTION: "DOPING" IN WALK-THROUGH MUTAGENESIS
; FILE REFERENCE: 1551.2002-001
; CURRENT APPLICATION NUMBER: US/10/417,895A
; CURRENT FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: 60/373,686
; PRIOR FILING DATE: 2002-04-17
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: variant peptide for second complementarity
; OTHER INFORMATION: determining region of Fv region of an
; OTHER INFORMATION: Immunoglobulin
US-10-417-895A-34
```

```
Query Match      37.2%; Score 29; DB 4; Length 16;
Best Local Similarity 57.1%; Pred. No. 6.3e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      7 NDYSKNP 13
      |||||
Db      6 NDYARPT 12
```

```
RESULT 19
US-10-776-013-382
; Sequence 382, Application US/10776013
; Publication No. US20040226056A1
; GENERAL INFORMATION:
; APPLICANT: MYRIAD GENETICS, INC.
; APPLICANT: Roch, Jean-Marc
; APPLICANT: Bartel, Paul
; APPLICANT: Heichman, Karen
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING NEUROLOGICAL DISORDERS AND
; FILE REFERENCE: 1600.24
; CURRENT APPLICATION NUMBER: US/10/776,013
; CURRENT FILING DATE: 2004-02-09
; PRIOR APPLICATION NUMBER: 09/948904
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 09/466139
; PRIOR FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: 60/113534
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: 60/124120
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/141243
; PRIOR FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: 09/975072
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240790
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 10/194967
; PRIOR FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 60/304775
; PRIOR FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 695
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 382
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-776-013-382
```

```
Query Match      37.2%; Score 29; DB 5; Length 20;
Best Local Similarity 50.0%; Pred. No. 8e+02;
```

Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
Qy 6 HDYSKXP 13  
Db 3 HDNYRNP 10

## RESULT 20

US-10-095-373A-12  
; Sequence 12, Application US/10095373A  
; Publication No. US20030199022A1  
; GENERAL INFORMATION:  
; APPLICANT: Shaprio, David J.  
; TITLE OF INVENTION: A TAMOXIFEN AND 4-HYDROXY TAMOXIFEN-ACTIVATED SYSTEM FOR REGULATION OF INTRACELLULAR SIGNALING  
; FILE REFERENCE: 10322.25  
; CURRENT APPLICATION NUMBER: US/10/095,373A  
; CURRENT FILING DATE: 2002-06-21  
; NUMBER OF SEQ ID NOS: 83  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 12  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Mutant DBD of ER  
US-10-095-373A-12

Query Match 36.5%; Score 28.5; DB 4; Length 17;  
Best Local Similarity 77.8%; Pred. No. 8.1e+02;  
Matches 7; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy 1 SIKRDNDY 9  
Db 10 SIAR-HNDY 17

## RESULT 21

US-10-996-316-195  
; Sequence 195, Application US/10996316  
; Publication No. US20050129690A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexion Pharmaceuticals, Inc.  
; APPLICANT: Bowdish, Katherine S.  
; APPLICANT: McWhirter, John  
; APPLICANT: Kretz-Rommel, Anke  
; TITLE OF INVENTION: POLYPEPTIDES AND ANTIBODIES DERIVED FROM CHRONIC LYMPHOCYTIC LEUKEMIA CELLS AND USES THEREOF  
; FILE REFERENCE: 60 CIP IV (1087-43 CIP IV)  
; CURRENT APPLICATION NUMBER: US/10/996,316  
; CURRENT FILING DATE: 2004-11-23  
; PRIOR APPLICATION NUMBER: US 10/894,672  
; PRIOR FILING DATE: 2004-07-20  
; PRIOR APPLICATION NUMBER: US 10/736,188  
; PRIOR FILING DATE: 2003-12-15  
; PRIOR APPLICATION NUMBER: US 10/379,151  
; PRIOR FILING DATE: 2003-03-04  
; PRIOR APPLICATION NUMBER: PCT/US01/47931  
; PRIOR FILING DATE: 2001-12-10  
; PRIOR APPLICATION NUMBER: US 60/254,113  
; PRIOR FILING DATE: 2000-12-08  
; NUMBER OF SEQ ID NOS: 211  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 195  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: murine  
US-10-996-316-195

Query Match 35.9%; Score 28; DB 5; Length 8;  
Best Local Similarity 71.4%; Pred. No. 1.7e+06;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 KRDNDY 9  
Db 2 KRDYFDY 8

## RESULT 22

US-10-794-899-21  
; Sequence 21, Application US/10794899  
; Publication No. US20040146516A1  
; GENERAL INFORMATION:  
; APPLICANT: Utah Ventures  
; TITLE OF INVENTION: Lumen-Exposed Molecules and Methods Targeted Delivery  
; FILE REFERENCE: 27110-715  
; CURRENT APPLICATION NUMBER: US/10/794,899  
; CURRENT FILING DATE: 2004-03-05  
; NUMBER OF SEQ ID NOS: 121  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 21  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Trypsin Peptide  
US-10-794-899-21

Query Match 35.9%; Score 28; DB 4; Length 10;  
Best Local Similarity 57.1%; Pred. No. 5.6e+02;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 4 RDRNDYS 10  
Db 3 QDRDPS 9

## RESULT 23

US-09-852-910-247  
; Sequence 247, Application US/09852910  
; Publication No. US20030096297A1  
; GENERAL INFORMATION:  
; APPLICANT: Hamm, Heidi  
; APPLICANT: Gilchrist, Annette  
; TITLE OF INVENTION: Method for Identifying Inhibitors of G Protein Coupled Receptor  
; FILE REFERENCE: 2661-101  
; CURRENT APPLICATION NUMBER: US/09/852,910  
; CURRENT FILING DATE: 2001-09-18  
; PRIOR APPLICATION NUMBER: US 60/275,472  
; PRIOR FILING DATE: 2001-03-14  
; NUMBER OF SEQ ID NOS: 271  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 247  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)-(11)  
; OTHER INFORMATION: G11 library peptide  
US-09-852-910-247

Query Match 35.9%; Score 28; DB 3; Length 11;  
Best Local Similarity 50.0%; Pred. No. 6.2e+02;  
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 2 IKRDNDY 9  
Db 1 LDRDVEY 8

## RESULT 24

US-10-411-336A-247  
; Sequence 247, Application US/10411336A  
; Publication No. US20040018558A1  
; GENERAL INFORMATION:  
; APPLICANT: Gilchrist, ANNETTE

```
/ APPLICANT: HAMM, HEIDI
/ TITLE OF INVENTION: METHOD FOR IDENTIFYING MODULATORS OF G PROTEIN COUPLED RECEPTOR
/ TITLE OF INVENTION: SIGNALING
/ FILE REFERENCE: 2661-102
/ CURRENT APPLICATION NUMBER: US/10/411,336A
/ CURRENT FILING DATE: 2003-04-11
/ PRIOR APPLICATION NUMBER: US 09/852910
/ PRIOR FILING DATE: 2001-05-11
/ PRIOR APPLICATION NUMBER: US 60/275472
/ PRIOR FILING DATE: 2001-03-14
/ NUMBER OF SEQ ID NOS: 273
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 247
/ LENGTH: 11
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: G11 library peptide
US-10-411-336A-247
```

```
Query Match          35.9%; Score 28; DB 4; Length 11;
Best Local Similarity 50.0%; Pred. No. 6.2e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      2 IKRDHNDY 9
DB      1 LQRDHYEY 8
```

```
RESULT 25
US-10-884-830-218
/ Sequence 218, Application US/10884830
/ Publication No. US20050004354A1
/ GENERAL INFORMATION:
/ APPLICANT: Jochem, Salfeld et al.
/ TITLE OF INVENTION: Human Antibodies That Bind Human IL-12 And Methods For Producing
/ FILE REFERENCE: BBI-093CP
/ CURRENT APPLICATION NUMBER: US/10/884,830
/ CURRENT FILING DATE: 2004-07-01
/ PRIOR APPLICATION NUMBER: US/09/534,717
/ PRIOR FILING DATE: 2000-03-24
/ PRIOR APPLICATION NUMBER: 60/126,603
/ PRIOR FILING DATE: March 25, 1999
/ NUMBER OF SEQ ID NOS: 675
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 218
/ LENGTH: 12
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-884-830-218
```

```
Query Match          35.9%; Score 28; DB 5; Length 12;
Best Local Similarity 50.0%; Pred. No. 6.8e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      1 SIKRDHNDYS 10
DB      2 SYDRGNHNS 11
```

```
RESULT 26
US-10-417-895A-45
/ Sequence 45, Application US/10417895A
/ Publication No. US20040033569A1
/ GENERAL INFORMATION:
/ APPLICANT: Crea, Roberto
/ APPLICANT: Cappuccini, Guido
/ TITLE OF INVENTION: "DOPING" IN WALK-THROUGH MUTAGENESIS
/ FILE REFERENCE: 1551.2002-001
/ CURRENT APPLICATION NUMBER: US/10/417,895A
/ CURRENT FILING DATE: 2003-04-16
/ PRIOR APPLICATION NUMBER: 60/373,686
/ PRIOR FILING DATE: 2002-04-17
```

```
/ NUMBER OF SEQ ID NOS: 86
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 45
/ LENGTH: 14
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: variant peptide for second complementarity
/ OTHER INFORMATION: determining region of Fv region of an
/ OTHER INFORMATION: Immunoglobulin
US-10-417-895A-45
```

```
Query Match          35.9%; Score 28; DB 4; Length 14;
Best Local Similarity 57.1%; Pred. No. 8e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      5 DHNDYSK 11
DB      7 DHSDHDK 13
```

```
RESULT 27
US-10-354-240-47
/ Sequence 47, Application US/10354240
/ Publication No. US20030185847A1
/ GENERAL INFORMATION:
/ APPLICANT: Sone, Toshio
/ APPLICANT: Kume, Akimori
/ APPLICANT: Dairiki, Kazuo
/ APPLICANT: Iwama, Akiko
/ APPLICANT: Kino, Kohsuke
/ TITLE OF INVENTION: Peptide-Based Immunotherapeutic Agent for Treating Allergic Disease
/ FILE REFERENCE: SPO-103D1
/ CURRENT APPLICATION NUMBER: US/10/354,240
/ CURRENT FILING DATE: 2003-01-29
/ PRIOR APPLICATION NUMBER: PCT/JP97/00740
/ PRIOR FILING DATE: 1997-03-10
/ PRIOR APPLICATION NUMBER: US 09/142,524
/ PRIOR FILING DATE: 1998-09-09
/ NUMBER OF SEQ ID NOS: 174
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 47
/ LENGTH: 15
/ TYPE: PRT
/ ORGANISM: Cryptomeria japonica
/ NAME/KEY: MISC FEATURE
/ LOCATION: (1) .. (15)
/ OTHER INFORMATION: CryJ1 peptide, Figure 1, Row 33
US-10-354-240-47
```

```
Query Match          35.9%; Score 28; DB 4; Length 15;
Best Local Similarity 50.0%; Pred. No. 8.6e+02;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      5 DHNDYSKN 12
DB      4 DHNSFSNS 11
```

```
RESULT 28
US-09-949-196-2
/ Sequence 2, Application US/09949196
/ Patent No. US20020147145A1
/ GENERAL INFORMATION:
/ APPLICANT: Zealand Pharmaceuticals A/S
/ TITLE OF INVENTION: MATERIALS AND METHODS RELATING TO THE DEGRADATION OF Cdc25A IN Rf
/ FILE REFERENCE: 55868 (45487)
/ CURRENT APPLICATION NUMBER: US/09/949,196
/ CURRENT FILING DATE: 2001-07-09
/ NUMBER OF SEQ ID NOS: 45
/ SOFTWARE: PatentIn version 3.1
```



SEQ ID NO 2  
LENGTH: 17  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURES:  
OTHER INFORMATION: Description of Artificial Sequence: synthetic peptide sequence  
US-09-949-196-2

Query Match 35.9%; Score 28; DB 3; Length 17;  
Best Local Similarity 50.0%; Pred. No. 9.9e+02;  
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SIKRDND 8  
:|:|:|:  
Db 3 AKRSHSD 10

RESULT 29  
US-10-772-089-2  
Sequence 2, Application US/10772089  
Publication No. US20040192609A1  
GENERAL INFORMATION:  
APPLICANT: The Brigham & Women's Hospital, Inc.  
APPLICANT: Farzan, Michael R  
APPLICANT: Dorfman, Tatyana K  
TITLE OF INVENTION: Peptides Binding gp120 of HIV-1  
FILE REFERENCE: 7570/80211  
CURRENT APPLICATION NUMBER: US/10/772,089  
CURRENT FILING DATE: 2004-02-05  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 2  
LENGTH: 18  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-772-089-2

Query Match 35.9%; Score 28; DB 4; Length 18;  
Best Local Similarity 66.7%; Pred. No. 1.1e+03;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 5 DHNDYS 10  
:|:|:|:  
Db 5 DYNDYA 10

RESULT 30  
US-10-931-260-42  
Sequence 42, Application US/10931260  
Publication No. US20050152927A1  
GENERAL INFORMATION:  
APPLICANT: Griffith, Irwin J.;  
Pollock, Joanne;  
Bond, Julian P.;  
Garman, Richard D;  
Kuo, Mei-Chang;  
Powers, Stephen P.;  
Exley, Mark A.;  
Chen, Xian;  
Shaked, Ze'ev

TITLE OF INVENTION: Allergenic Proteins And Peptides From  
Japanese Cedar Pollen

NUMBER OF SEQUENCES: 283

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lathive & Cockfield, LLP  
STREET: 28 State St  
CITY: Boston

STATE: MA  
COUNTRY: USA

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/931,260  
FILING DATE: 30-Aug-2004  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/240,203  
FILING DATE: 29-Jan-1999  
APPLICATION NUMBER: 08/467,023  
FILING DATE: 1995-JUN-06  
APPLICATION NUMBER: 08/350,225  
FILING DATE: 1994-DEC-06  
APPLICATION NUMBER: 08/226,248  
FILING DATE: 1994-APR-08  
APPLICATION NUMBER: PCT/US93/00139  
FILING DATE: 1993-JAN-15  
APPLICATION NUMBER: 07/938,990  
FILING DATE: 1992-SEP-01  
APPLICATION NUMBER: 07/730,452  
FILING DATE: 1991-JUL-15  
APPLICATION NUMBER: 07/729,134  
FILING DATE: 1991-JUL-12  
APPLICATION NUMBER: 07/975,179  
FILING DATE: 1992-NOV-12  
APPLICATION NUMBER: PCT/US92/05661  
FILING DATE: 1992-JUL-10

ATTORNEY/AGENT INFORMATION:

NAME: Amy E. Mandragouras, Esq.

REGISTRATION NUMBER: 36,207

REFERENCE/DOCKET NUMBER: IMI-028CD2CCPA2

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 227-7400

TELEFAX: (617) 742-4214

INFORMATION FOR SEQ ID NO: 42:

SEQUENCE CHARACTERISTICS:

LENGTH: 20 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULAR TYPE: peptide

FRAGMENT TYPE: internal

SEQUENCE DESCRIPTION: SEQ ID NO: 42:

Query Match 35.9%; Score 28; DB 5; Length 20;  
Best Local Similarity 50.0%; Pred. No. 1.2e+03;  
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 5 DHNDYSKN 12  
:|:|:|:  
Db 4 DHNSFSNS 11

RESULT 31  
US-10-931-260-203  
Sequence 203, Application US/10931260  
Publication No. US20050152927A1  
GENERAL INFORMATION:  
APPLICANT: Griffith, Irwin J.;  
Pollock, Joanne;  
Bond, Julian P.;  
Garman, Richard D;  
Kuo, Mei-Chang;  
Powers, Stephen P.;  
Exley, Mark A.;  
Chen, Xian;  
Shaked, Ze'ev

TITLE OF INVENTION: Allergenic Proteins And Peptides From  
Japanese Cedar Pollen

NUMBER OF SEQUENCES: 283

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lathive & Cockfield, LLP  
STREET: 28 State St

```

; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/931,260
; FILING DATE: 30-Aug-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/240,203
; FILING DATE: 29-Jan-1999
; APPLICATION NUMBER: 08/467,023
; FILING DATE: 1995-JUN-06
; APPLICATION NUMBER: 08/350,225
; FILING DATE: 1994-DEC-06
; APPLICATION NUMBER: 08/226,248
; FILING DATE: 1994-APR-08
; APPLICATION NUMBER: PCT/US93/00139
; FILING DATE: 1993-JAN-15
; APPLICATION NUMBER: 07/938,990
; FILING DATE: 1992-SEP-01
; APPLICATION NUMBER: 07/730,452
; FILING DATE: 1991-JUL-15
; APPLICATION NUMBER: 07/729,134
; FILING DATE: 1991-JUL-12
; APPLICATION NUMBER: 07/975,179
; FILING DATE: 1992-NOV-12
; APPLICATION NUMBER: PCT/US92/05661
; FILING DATE: 1992-JUL-10
; ATTORNEY/AGENT INFORMATION:
; NAME: Amy E. Mandragouras, Esq.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: IMI-028CD2CCPA2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 742-4214
; INFORMATION FOR SEQ ID NO: 203:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 203:
US-10-931-260-203
Query Match 35.9%; Score 28; DB 5; Length 20;
Best Local Similarity 50.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 5 DHNDYSGN 12
DB 10 DHNSFSNS 17
RESULT 32
US-09-901-187B-2
; Sequence 2, Application US/09901187B
; Patent No. US2002015164A1
; GENERAL INFORMATION:
; APPLICANT: Panacea Pharmaceuticals, Inc.
; APPLICANT: Molozin, Benjamin
; APPLICANT: Ostretova-Golts, Natalie
; APPLICANT: Lebowitz, Michael S.
; TITLE OF INVENTION: Methods for Preventing Neural Tissue Damage and for the Treatment
; FILE REFERENCE: PAN01/00205
; CURRENT APPLICATION NUMBER: US/09/901,187B
```

```

; CURRENT FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US 60/217,319
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/279,199
; PRIOR FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patent version 3.1
; SEQ ID NO 2
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-901-187B-2
Query Match 34.6%; Score 27; DB 3; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.7e+06;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 9 YSKNPM 14
DB 2 YAKNPI 7
RESULT 33
US-10-909-116-2
; Sequence 2, Application US/10909116
; Publication No. US2005003231A1
; GENERAL INFORMATION:
; APPLICANT: Panacea Pharmaceuticals, Inc.
; APPLICANT: Molozin, Benjamin
; APPLICANT: Ostretova-Golts, Natalie
; APPLICANT: Lebowitz, Michael S.
; TITLE OF INVENTION: Methods for Preventing Neural Tissue Damage and for the Treatment
; FILE REFERENCE: PAN01/00205
; CURRENT APPLICATION NUMBER: US/10/909,116
; CURRENT FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: US/09/901,187
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US 60/217,319
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/279,199
; PRIOR FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patent version 3.1
; SEQ ID NO 2
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-909-116-2
Query Match 34.6%; Score 27; DB 5; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.7e+06;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 9 YSKNPM 14
DB 2 YAKNPI 7
RESULT 34
US-09-852-910-185
; Sequence 185, Application US/09852910
; Publication No. US20030096297A1
; GENERAL INFORMATION:
; APPLICANT: Hamm, Heidi
; APPLICANT: Gilchrist, Annette
; TITLE OF INVENTION: Method for Identifying Inhibitors of G Protein Coupled Receptor S
; FILE REFERENCE: 2661-101
; CURRENT APPLICATION NUMBER: US/09/852,910
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US 60/275,472
; PRIOR FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 271
```

```
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 185
/ LENGTH: 11
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (1)-(11)
/ OTHER INFORMATION: G alpha library peptide
US-09-852-910-185
```

```
Query Match          34.6%; Score 27; DB 3; Length 11;
Best Local Similarity 33.3%; Pred. No. 9.1e+02;
Matches 3; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
```

```
OY      2 IKRDHNDYS 10
       : : : : :
Db       1 LQNMHNENY 9
```

```
RESULT 35
US-10-411-336A-185
/ Sequence 185, Application US/10411336A
/ Publication No. US20040018558A1
/ GENERAL INFORMATION:
/ APPLICANT: GLICHRIST, ANNETTE
/ APPLICANT: HAMM, HEIDI
/ TITLE OF INVENTION: METHOD FOR IDENTIFYING MODULATORS OF G PROTEIN COUPLED RECEPTOR
/ FILE REFERENCE: 2661-102
/ CURRENT APPLICATION NUMBER: US/10/411,336A
/ PRIOR FILING DATE: 2003-04-11
/ PRIOR APPLICATION NUMBER: US 09/852910
/ PRIOR FILING DATE: 2001-05-11
/ PRIOR APPLICATION NUMBER: US 60/275472
/ PRIOR FILING DATE: 2001-03-14
/ NUMBER OF SEQ ID NOS: 273
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 185
/ LENGTH: 11
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: G alpha library peptide
US-10-411-336A-185
```

```
Query Match          34.6%; Score 27; DB 4; Length 11;
Best Local Similarity 33.3%; Pred. No. 9.1e+02;
Matches 3; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
```

```
OY      2 IKRDHNDYS 10
       : : : : :
Db       1 LQNMHNENY 9
```

```
RESULT 36
US-10-692-151-33
/ Sequence 33, Application US/10692151
/ Publication No. US20040176578A1
/ GENERAL INFORMATION:
/ APPLICANT: Nolan, Garry P.
/ APPLICANT: Rozinov, Michael N.
/ TITLE OF INVENTION: Fluorescent Dye Binding Peptides
/ FILE REFERENCE: A65681-2/RMS/RMK/SPL
/ CURRENT APPLICATION NUMBER: US/10/692,151
/ PRIOR FILING DATE: 2003-10-14
/ PRIOR APPLICATION NUMBER: 09/419,381
/ PRIOR FILING DATE: 1999-10-15
/ PRIOR APPLICATION NUMBER: 60/104,465
/ PRIOR FILING DATE: 1998-10-16
/ NUMBER OF SEQ ID NOS: 122
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 33
```

```
/ LENGTH: 12
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-10-692-151-33
```

```
Query Match          34.6%; Score 27; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      6 HNDY 9
       : : : : :
Db       2 TVKGDVHDIGKN 13
```

```
RESULT 37
US-10-607-712-9
/ Sequence 9, Application US/10607712
/ Publication No. US20040073018A1
/ GENERAL INFORMATION:
/ APPLICANT: Gravel, Roy A.
/ APPLICANT: Rozen, Rima
/ APPLICANT: LeClerc, Daniel
/ APPLICANT: Goyette, Philippe
/ APPLICANT: Campeau, Eric
/ TITLE OF INVENTION: HUMAN METHIONINE SYNTHASE: CLONING, AND
/ TITLE OF INVENTION: METHODS FOR EVALUATING RISK OF NEURAL TUBE DEFECTS,
/ FILE REFERENCE: 50004/002005
/ CURRENT APPLICATION NUMBER: US/10/607,712
/ PRIOR FILING DATE: 2003-06-27
/ PRIOR APPLICATION NUMBER: 08/980,326
/ PRIOR FILING DATE: 1997-11-26
/ PRIOR APPLICATION NUMBER: 60/031,964
/ PRIOR FILING DATE: 1996-11-27
/ PRIOR APPLICATION NUMBER: 60/050,310
/ PRIOR FILING DATE: 1997-06-20
/ NUMBER OF SEQ ID NOS: 76
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 9
/ LENGTH: 13
/ TYPE: PRT
/ ORGANISM: Escherichia coli
US-10-607-712-9
```

```
Query Match          34.6%; Score 27; DB 4; Length 13;
Best Local Similarity 41.7%; Pred. No. 1.1e+03;
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
```

```
OY      1 SIKRDHNDYSKN 12
       : : : : :
Db       2 TVKGDVHDIGKN 13
```

```
RESULT 38
US-10-607-712-10
/ Sequence 10, Application US/10607712
/ Publication No. US20040073018A1
/ GENERAL INFORMATION:
/ APPLICANT: Gravel, Roy A.
/ APPLICANT: Rozen, Rima
/ APPLICANT: LeClerc, Daniel
/ APPLICANT: Goyette, Philippe
/ APPLICANT: Campeau, Eric
/ TITLE OF INVENTION: HUMAN METHIONINE SYNTHASE: CLONING, AND
/ TITLE OF INVENTION: METHODS FOR EVALUATING RISK OF NEURAL TUBE DEFECTS,
/ FILE REFERENCE: 50004/002005
/ CURRENT APPLICATION NUMBER: US/10/607,712
/ PRIOR FILING DATE: 2003-06-27
/ PRIOR APPLICATION NUMBER: 08/980,326
/ PRIOR FILING DATE: 1997-11-26
```

```
/ PRIOR APPLICATION NUMBER: 60/031,964
/ PRIOR FILING DATE: 1996-11-27
/ PRIOR APPLICATION NUMBER: 60/050,310
/ PRIOR FILING DATE: 1997-06-20
/ NUMBER OF SEQ ID NOS: 76
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 10
/ LENGTH: 13
/ TYPE: PRT
/ ORGANISM: Cyanobacterium synechocystis
US-10-607-712-10
```

```
Query Match          34.6%; Score 27; DB 4; Length 13;
Best Local Similarity 41.7%; Pred. No. 1.le+03;
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
```

```
QY      1 SIKRDHNDYSKN 12
       :|:|:|:|
Db      2 TVKGDVHDIGKN 13
```

```
RESULT 39
US-10-607-712-11
/ Sequence 11, Application US/10607712
/ Publication No. US20040073018A1
/ GENERAL INFORMATION:
/ APPLICANT: Gravel, Roy A.
/ APPLICANT: Rozen, Rima
/ APPLICANT: Leclerc, Daniel
/ APPLICANT: Goyette, Philippe
/ APPLICANT: Campeau, Eric
/ TITLE OF INVENTION: HUMAN METHIONINE SYNTHASE: CLONING, AND
/ TITLE OF INVENTION: METHODS FOR EVALUATING RISK OF NEURAL TUBE DEFECTS,
/ TITLE OF INVENTION: CARDIOVASCULAR DISEASE, AND CANCER
/ FILE REFERENCE: 50004/002005
/ CURRENT APPLICATION NUMBER: US/10/607,712
/ PRIOR FILING DATE: 2003-06-27
/ PRIOR APPLICATION NUMBER: 08/980,326
/ PRIOR FILING DATE: 1997-11-26
/ PRIOR APPLICATION NUMBER: 60/031,964
/ PRIOR FILING DATE: 1996-11-27
/ PRIOR APPLICATION NUMBER: 60/050,310
/ NUMBER OF SEQ ID NOS: 76
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 11
/ LENGTH: 13
/ TYPE: PRT
/ ORGANISM: Mycobacterium leprae
US-10-607-712-11
```

```
Query Match          34.6%; Score 27; DB 4; Length 13;
Best Local Similarity 41.7%; Pred. No. 1.le+03;
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
```

```
QY      1 SIKRDHNDYSKN 12
       :|:|:|:|
Db      2 TVKGDVHDIGKN 13
```

```
RESULT 40
US-10-607-712-12
/ Sequence 12, Application US/10607712
/ Publication No. US20040073018A1
/ GENERAL INFORMATION:
/ APPLICANT: Gravel, Roy A.
/ APPLICANT: Rozen, Rima
/ APPLICANT: Leclerc, Daniel
/ APPLICANT: Goyette, Philippe
/ APPLICANT: Campeau, Eric
/ TITLE OF INVENTION: HUMAN METHIONINE SYNTHASE: CLONING, AND
/ TITLE OF INVENTION: METHODS FOR EVALUATING RISK OF NEURAL TUBE DEFECTS,
/ TITLE OF INVENTION: CARDIOVASCULAR DISEASE, AND CANCER
```

```
/ FILE REFERENCE: 50004/002005
/ CURRENT APPLICATION NUMBER: US/10/607,712
/ CURRENT FILING DATE: 2003-06-27
/ PRIOR APPLICATION NUMBER: 08/980,326
/ PRIOR FILING DATE: 1997-11-26
/ PRIOR APPLICATION NUMBER: 60/031,964
/ PRIOR FILING DATE: 1996-11-27
/ PRIOR APPLICATION NUMBER: 60/050,310
/ PRIOR FILING DATE: 1997-06-20
/ NUMBER OF SEQ ID NOS: 76
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 12
/ LENGTH: 13
/ TYPE: PRT
/ ORGANISM: Hemophilus influenzae
US-10-607-712-12
```

```
Query Match          34.6%; Score 27; DB 4; Length 13;
Best Local Similarity 41.7%; Pred. No. 1.le+03;
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
```

```
QY      1 SIKRDHNDYSKN 12
       :|:|:|:|
Db      2 TVKGDVHDIGKN 13
```

```
RESULT 41
US-10-607-712-13
/ Sequence 13, Application US/10607712
/ Publication No. US20040073018A1
/ GENERAL INFORMATION:
/ APPLICANT: Gravel, Roy A.
/ APPLICANT: Rozen, Rima
/ APPLICANT: Leclerc, Daniel
/ APPLICANT: Goyette, Philippe
/ APPLICANT: Campeau, Eric
/ TITLE OF INVENTION: HUMAN METHIONINE SYNTHASE: CLONING, AND
/ TITLE OF INVENTION: METHODS FOR EVALUATING RISK OF NEURAL TUBE DEFECTS,
/ TITLE OF INVENTION: CARDIOVASCULAR DISEASE, AND CANCER
/ FILE REFERENCE: 50004/002005
/ CURRENT APPLICATION NUMBER: US/10/607,712
/ PRIOR FILING DATE: 2003-06-27
/ PRIOR APPLICATION NUMBER: 08/980,326
/ PRIOR FILING DATE: 1997-11-26
/ PRIOR APPLICATION NUMBER: 60/031,964
/ PRIOR FILING DATE: 1996-11-27
/ PRIOR APPLICATION NUMBER: 60/050,310
/ NUMBER OF SEQ ID NOS: 76
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 13
/ LENGTH: 13
/ TYPE: PRT
/ ORGANISM: Caenorhabditis elegans
US-10-607-712-13
```

```
Query Match          34.6%; Score 27; DB 4; Length 13;
Best Local Similarity 41.7%; Pred. No. 1.le+03;
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
```

```
QY      1 SIKRDHNDYSKN 12
       :|:|:|:|
Db      2 TVKGDVHDIGKN 13
```

```
RESULT 42
US-10-607-712-14
/ Sequence 14, Application US/10607712
/ Publication No. US20040073018A1
/ GENERAL INFORMATION:
/ APPLICANT: Gravel, Roy A.
/ APPLICANT: Rozen, Rima
/ APPLICANT: Leclerc, Daniel
```

```

; APPLICANT: Goyette, Philippe
; APPLICANT: Campeau, Eric
; TITLE OF INVENTION: HUMAN METHIONINE SYNTHASE: CLONING, AND
; TITLE OF INVENTION: METHODS FOR EVALUATING RISK OF NEURAL TUBE DEFECTS,
; TITLE OF INVENTION: CARDIOVASCULAR DISEASE, AND CANCER
; FILE REFERENCE: 50004/002005
; CURRENT APPLICATION NUMBER: US/10/607,712
; PRIOR FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: 08/980,326
; PRIOR FILING DATE: 1997-11-26
; PRIOR APPLICATION NUMBER: 60/031,964
; PRIOR FILING DATE: 1996-11-27
; PRIOR APPLICATION NUMBER: 60/050,310
; PRIOR FILING DATE: 1997-06-20
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-607-712-14

Query Match          34.6%; Score 27; DB 4; Length 13;
Best Local Similarity 41.7%; Pred. No. 1.3e+03;
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 SIRDNDYSGN 12
DB 2 TVKGDVHDIQKN 13

RESULT 43
US-10-354-240-46
; Sequence 46, Application US/10354240
; Publication No. US20030185847A1
; GENERAL INFORMATION:
; APPLICANT: Some, Toshio
; APPLICANT: Kume, Akimori
; APPLICANT: Daitiki, Kazuo
; APPLICANT: Iwama, Akiko
; APPLICANT: Kino, Kohsuke
; TITLE OF INVENTION: Peptide-Based Immunotherapeutic Agent for Treating Allergic Disease
; FILE REFERENCE: SPO-10301
; CURRENT APPLICATION NUMBER: US/10/354,240
; PRIOR FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: PCT/JP97/00740
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: US 09/142,524
; PRIOR FILING DATE: 1998-09-09
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 46
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Cryptomeria japonica
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)-(15)
; OTHER INFORMATION: CRYJ1 peptide, Figure 1, Row 32
US-10-354-240-46

Query Match          34.6%; Score 27; DB 4; Length 15;
Best Local Similarity 66.7%; Pred. No. 1.3e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 DHDNDY 10
DB 9 DHDNSFS 14

RESULT 44
US-10-714-679-1
; Sequence 1, Application US/10714679
```

```

; Publication No. US20040170637A1
; GENERAL INFORMATION:
; APPLICANT: McVey, David Scott
; TITLE OF INVENTION: Use of rmlt as a Marker Antigen for Vaccines and as a Synergistic
; TITLE OF INVENTION: Adjuvant with Amphigen
; FILE REFERENCE: P15827 (PC25075)
; CURRENT APPLICATION NUMBER: US/10/714,679
; PRIOR FILING DATE: 2003-11-14
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Marker peptides from the rmlt sequence
US-10-714-679-1

Query Match          34.6%; Score 27; DB 4; Length 15;
Best Local Similarity 66.7%; Pred. No. 1.3e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 RDNDY 9
DB 3 RGNRY 8

RESULT 45
US-10-808-187-1406
; Sequence 1406, Application US/10808187
; Publication No. US2005009009A1
; GENERAL INFORMATION:
; APPLICANT: PEIRIS, JOSEPH S. M.
; APPLICANT: YUEN, KWOK YUNG
; APPLICANT: POON, LIT MAN
; APPLICANT: CHAN, XI
; APPLICANT: NICHOLS, JOHN
; TITLE OF INVENTION: A DIAGNOSTIC ASSAY FOR THE HUMAN VIRUS CAUSING SEVERE ACUTE
; FILE REFERENCE: V9661.0078
; CURRENT APPLICATION NUMBER: US/10/808,187
; PRIOR FILING DATE: 2004-03-24
; PRIOR APPLICATION NUMBER: 60/457,031
; PRIOR FILING DATE: 2003-03-24
; PRIOR APPLICATION NUMBER: 60/457,730
; PRIOR FILING DATE: 2003-03-26
; PRIOR APPLICATION NUMBER: 60/459,931
; PRIOR FILING DATE: 2003-04-02
; PRIOR APPLICATION NUMBER: 60/460,357
; PRIOR FILING DATE: 2003-04-03
; PRIOR APPLICATION NUMBER: 60/461,265
; PRIOR FILING DATE: 2003-04-08
; PRIOR APPLICATION NUMBER: 60/462,805
; PRIOR FILING DATE: 2003-04-14
; PRIOR APPLICATION NUMBER: 60/468,139
; PRIOR FILING DATE: 2003-05-05
; PRIOR APPLICATION NUMBER: 60/464,886
; PRIOR FILING DATE: 2003-04-23
; PRIOR APPLICATION NUMBER: 60/471,200
; PRIOR FILING DATE: 2003-05-16
; NUMBER OF SEQ ID NOS: 2476
; SOFTWARE: PatentIn ver. 3.2
; SEQ ID NO 1406
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Human severe acute respiratory system virus
US-10-808-187-1406

Query Match          34.6%; Score 27; DB 5; Length 15;
Best Local Similarity 62.5%; Pred. No. 1.3e+03;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

Qy 5 HNDYSKN 12  
|:|:|:|  
Db 7 DYNDNSHN 14

## RESULT 46

US-10-807-1406  
Sequence 1406, Application US/10807807  
Publication No. US20050181357A1  
GENERAL INFORMATION:  
APPLICANT: LEUNG, FREDERICK C.  
APPLICANT: PEIRIS, JOSEPH S. M.  
APPLICANT: YUEN, KWOK YUNG  
APPLICANT: POON, LIT MAN  
APPLICANT: GUAN, YI  
APPLICANT: CHAN, KWOK HUNG  
APPLICANT: NICHOLLS, JOHN M.  
TITLE OF INVENTION: A HIGH-THROUGHPUT DIAGNOSTIC ASSAY FOR THE HUMAN VIRUS  
FILE REFERENCE: V9661.0077  
CURRENT APPLICATION NUMBER: US/10/807,807  
CURRENT FILING DATE: 2004-03-24  
PRIOR APPLICATION NUMBER: 60/457,031  
PRIOR FILING DATE: 2003-03-24  
PRIOR APPLICATION NUMBER: 60/457,730  
PRIOR FILING DATE: 2003-03-26  
PRIOR APPLICATION NUMBER: 60/459,931  
PRIOR FILING DATE: 2003-04-02  
PRIOR APPLICATION NUMBER: 60/460,357  
PRIOR FILING DATE: 2003-04-03  
PRIOR APPLICATION NUMBER: 60/461,265  
PRIOR FILING DATE: 2003-04-08  
PRIOR APPLICATION NUMBER: 60/462,805  
PRIOR FILING DATE: 2003-04-14  
PRIOR APPLICATION NUMBER: 60/464,886  
PRIOR FILING DATE: 2003-04-23  
PRIOR APPLICATION NUMBER: 60/465,738  
PRIOR FILING DATE: 2003-04-25  
PRIOR APPLICATION NUMBER: 60/470,935  
PRIOR FILING DATE: 2003-05-14  
NUMBER OF SEQ ID NOS: 2487  
SOFTWARE: PatentIn ver. 3.2  
SEQ ID NO 1406  
LENGTH: 15  
TYPE: PRT  
ORGANISM: Human severe acute respiratory system virus  
US-10-807-807-1406

Query Match 34.6%; Score 27; DB 5; Length 15;  
Best Local Similarity 62.5%; Pred. No. 1.3e+03;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 5 HNDYSKN 12  
|:|:|:|  
Db 7 DYNDNSHN 14

## RESULT 47

US-10-946-647-65  
Sequence 65, Application US/10946647  
Publication No. US20050186217A1  
GENERAL INFORMATION:  
APPLICANT: EMERY, DARYL A.  
APPLICANT: STRAUB, DARREN E.  
APPLICANT: WONDERLING, LAURA  
TITLE OF INVENTION: COMPOSITIONS PRODUCED USING ENTERIC PATHOGENS AND METHODS OF USE  
FILE REFERENCE: 293.00340101  
CURRENT APPLICATION NUMBER: US/10/946,647  
CURRENT FILING DATE: 2004-09-20  
PRIOR APPLICATION NUMBER: 60/504,119  
PRIOR FILING DATE: 2003-09-19  
NUMBER OF SEQ ID NOS: 1448  
SOFTWARE: PatentIn version 3.3

SEQ ID NO 65  
LENGTH: 16  
TYPE: PRT  
ORGANISM: Salmonella enterica  
US-10-946-647-65

Query Match 34.6%; Score 27; DB 5; Length 16;  
Best Local Similarity 57.1%; Pred. No. 1.4e+03;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 6 HNDYSKN 12  
|:|:|:|  
Db 1 HNDFDLN 7

## RESULT 48

US-10-946-647-368  
Sequence 368, Application US/10946647  
Publication No. US20050186217A1  
GENERAL INFORMATION:  
APPLICANT: EMERY, DARYL A.  
APPLICANT: STRAUB, DARREN E.  
APPLICANT: WONDERLING, LAURA  
TITLE OF INVENTION: COMPOSITIONS PRODUCED USING ENTERIC PATHOGENS AND METHODS OF USE  
FILE REFERENCE: 293.00340101  
CURRENT APPLICATION NUMBER: US/10/946,647  
CURRENT FILING DATE: 2004-09-20  
PRIOR APPLICATION NUMBER: 60/504,119  
PRIOR FILING DATE: 2003-09-19  
NUMBER OF SEQ ID NOS: 1448  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 368  
LENGTH: 16  
TYPE: PRT  
ORGANISM: Salmonella enteritidis  
US-10-946-647-368

Query Match 34.6%; Score 27; DB 5; Length 16;  
Best Local Similarity 57.1%; Pred. No. 1.4e+03;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 6 HNDYSKN 12  
|:|:|:|  
Db 1 HNDFDLN 7

## RESULT 49

US-10-946-647-517  
Sequence 517, Application US/10946647  
Publication No. US20050186217A1  
GENERAL INFORMATION:  
APPLICANT: EMERY, DARYL A.  
APPLICANT: STRAUB, DARREN E.  
APPLICANT: WONDERLING, LAURA  
TITLE OF INVENTION: COMPOSITIONS PRODUCED USING ENTERIC PATHOGENS AND METHODS OF USE  
FILE REFERENCE: 293.00340101  
CURRENT APPLICATION NUMBER: US/10/946,647  
CURRENT FILING DATE: 2004-09-20  
PRIOR APPLICATION NUMBER: 60/504,119  
PRIOR FILING DATE: 2003-09-19  
NUMBER OF SEQ ID NOS: 1448  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 517  
LENGTH: 16  
TYPE: PRT  
ORGANISM: Salmonella enteritidis  
US-10-946-647-517

Query Match 34.6%; Score 27; DB 5; Length 16;  
Best Local Similarity 57.1%; Pred. No. 1.4e+03;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 6 HNDYSKN 12

Db 1 HNDPDLN 7

RESULT 50  
US-10-946-647-635  
Sequence 635, Application US/10946647  
Publication No. US20050186217A1  
GENERAL INFORMATION:  
APPLICANT: EMERY, DARYL A.  
APPLICANT: STRAUB, DARREN E.  
APPLICANT: MONDEBLING, LAURA  
TITLE OF INVENTION: COMPOSITIONS PRODUCED USING ENTERIC PATHOGENS AND METHODS OF USE  
FILE REFERENCE: 293.00340101  
CURRENT APPLICATION NUMBER: US/10/946,647  
CURRENT FILING DATE: 2004-09-20  
PRIOR APPLICATION NUMBER: 60/504,119  
PRIOR FILING DATE: 2003-09-19  
NUMBER OF SEQ ID NOS: 1448  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 635  
LENGTH: 16  
TYPE: PRT  
ORGANISM: Salmonella enteritidis  
US-10-946-647-635

Query Match 34.6%; Score 27; DB 5; Length 16;  
Best Local Similarity 57.1%; Pred. No. 1.4e+03;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 6 HNDYSKN 12  
Db 1 HNDPDLN 7

RESULT 51  
US-09-731-221-57  
Sequence 57, Application US/09731221  
Patent No. US20020018778A1  
GENERAL INFORMATION:  
APPLICANT: Caplan, Michael  
TITLE OF INVENTION: Passive Desensitization  
FILE REFERENCE: 2002834-0103  
CURRENT APPLICATION NUMBER: US/09/731,221  
CURRENT FILING DATE: 2001-12-06  
NUMBER OF SEQ ID NOS: 79  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 57  
LENGTH: 20  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURES:  
OTHER INFORMATION: Description of Artificial Sequence: Atachis  
US-09-731-221-57

Query Match 34.6%; Score 27; DB 3; Length 20;  
Best Local Similarity 36.4%; Pred. No. 1.7e+03;  
Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 2 IKRDHNDYSKN 12  
Db 10 IORDEDSYERD 20

RESULT 52  
US-09-864-761-39698  
Sequence 39698, Application US/09864761  
Patent No. US20020048763A1  
GENERAL INFORMATION:  
APPLICANT: Penn, Sharon G.  
APPLICANT: Rank, David R.  
APPLICANT: Hanzel, David K.

APPLICANT: Chen, Wenheng  
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
FILE REFERENCE: Aecomica-X-1  
CURRENT APPLICATION NUMBER: US/09/864,761  
CURRENT FILING DATE: 2001-05-23

PRIOR APPLICATION NUMBER: US 60/180,312  
PRIOR FILING DATE: 2000-02-04  
PRIOR APPLICATION NUMBER: US 60/207,456  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: US 09/632,366  
PRIOR FILING DATE: 2000-08-03  
PRIOR APPLICATION NUMBER: GB 24263,6  
PRIOR FILING DATE: 2000-10-04  
PRIOR APPLICATION NUMBER: US 60/236,359  
PRIOR FILING DATE: 2000-09-27  
PRIOR APPLICATION NUMBER: PCT/US01/00666  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00667  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00664  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00669  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00665  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00668  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00663  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00662  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00661  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00670  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: US 60/234,687  
PRIOR FILING DATE: 2000-09-21  
PRIOR APPLICATION NUMBER: US 09/608,408  
PRIOR FILING DATE: 2000-06-30  
PRIOR APPLICATION NUMBER: US 09/774,203  
PRIOR FILING DATE: 2001-01-29  
NUMBER OF SEQ ID NOS: 49117  
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1  
SEQ ID NO 39698  
LENGTH: 20  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURES:  
OTHER INFORMATION: MAP TO AC002127.1  
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.3  
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.4  
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3.8  
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 3.8  
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 3.4  
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.4  
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.5  
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 3  
US-09-864-761-39698

Query Match 34.6%; Score 27; DB 3; Length 20;  
Best Local Similarity 40.0%; Pred. No. 1.7e+03;  
Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 SIKRDHNDYS 10  
Db 11 TFKKRNNDYT 20

RESULT 53  
US-10-931-260-41  
Sequence 41, Application US/10931260  
Publication No. US20050152927A1

GENERAL INFORMATION:  
APPLICANT: Griffith, Irwin J.;  
Pollock, Joanne;  
Bond, Julian P.;  
Gaman, Richard D;  
Kuo, Wei-Chang;  
Powers, Stephen P.;  
Exley, Mark A.;  
Shen, Xian;  
Shaked, Ze'ev

TITLE OF INVENTION: Allergenic Proteins And Peptides From  
Japanese Cedar Pollen

NUMBER OF SEQUENCES: 283

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lathive & Cockfield, LLP  
STREET: 28 State St  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/931,260  
FILING DATE: 30-Aug-2004

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/240,203  
FILING DATE: 29-Jan-1999

APPLICATION NUMBER: 08/467,023  
FILING DATE: 1995-JUN-06

APPLICATION NUMBER: 08/350,225  
FILING DATE: 1994-DEC-06

APPLICATION NUMBER: 08/226,248  
FILING DATE: 1994-APR-08

APPLICATION NUMBER: PCT/US93/00139  
FILING DATE: 1993-JAN-15

APPLICATION NUMBER: 07/938,990  
FILING DATE: 1992-SEP-01

APPLICATION NUMBER: 07/730,452  
FILING DATE: 1991-JUL-15

APPLICATION NUMBER: 07/729,134  
FILING DATE: 1991-JUL-12

APPLICATION NUMBER: 07/975,179  
FILING DATE: 1992-NOV-12

APPLICATION NUMBER: PCT/US92/05661  
FILING DATE: 1992-JUL-10

ATTORNEY/AGENT INFORMATION:  
NAME: Amy E. Mandragouras, Esq.  
REGISTRATION NUMBER: 36,207  
REFERENCE/DOCKET NUMBER: IMI-028CD2CCPA2

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 227-7400  
TELEFAX: (617) 742-4214

INFORMATION FOR SEQ ID NO: 41:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: internal

SEQUENCE DESCRIPTION: SEQ ID NO: 41:  
US-10-931-260-41

Query Match  
Best Local Similarity 66.7%; Score 27; DB 5; Length 20;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 DHNDYS 10  
|||:|

Db 14 DHNSFS 19

RESULT 54  
US-10-089-549-12  
Sequence 12, Application US/10089549  
Publication No. US20030194762A1

GENERAL INFORMATION:  
APPLICANT: KUBOTA, Michio  
APPLICANT: TSUSAKI, Keiji  
APPLICANT: HIGASHIYAMA, Takanobu  
APPLICANT: FUKUDA, Shigeharu  
APPLICANT: MIYAKE, Toshio

TITLE OF INVENTION: ALPHA-1SOMALYOSYLGLUCOSACCHARIDE-FORMING ENZYME, PROCESS AND USE  
TITLE OF INVENTION: SAME

FILE REFERENCE: KUBOTA=9

CURRENT APPLICATION NUMBER: US/10/089,549  
CURRENT FILING DATE: 2002-12-13

PRIOR APPLICATION NUMBER: JP 233364/2000  
PRIOR FILING DATE: 2000-08-01

PRIOR APPLICATION NUMBER: JP 234937/2000  
PRIOR FILING DATE: 2000-08-02

PRIOR APPLICATION NUMBER: PCT/JP01/06412  
PRIOR FILING DATE: 2001-07-25

NUMBER OF SEQ ID NOS: 19

SOFTWARE: Patent In Version 3.1

SEQ ID NO 12

LENGTH: 8

TYPE: PRT

ORGANISM: Bacillus globisporus

US-10-089-549-12

Query Match  
Best Local Similarity 66.7%; Score 26; DB 4; Length 8;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 DYKNP 13  
|:|

Db 1 DRSNP 6

RESULT 55  
US-10-245-871-459  
Sequence 459, Application US/10245871  
Publication No. US20030235594A1

GENERAL INFORMATION:  
APPLICANT: HUMPHREYS, ROBERT  
APPLICANT: XU, MINZHEN

TITLE OF INVENTION: 11-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES  
FILE REFERENCE: REH-2013

CURRENT APPLICATION NUMBER: US/10/245,871  
CURRENT FILING DATE: 2003-01-09

PRIOR APPLICATION NUMBER: 10/197,000  
PRIOR FILING DATE: 2002-07-17

PRIOR APPLICATION NUMBER: 09/396,813  
PRIOR FILING DATE: 1999-09-14

NUMBER OF SEQ ID NOS: 905

SOFTWARE: Patent In Ver. 2.1

SEQ ID NO 459

LENGTH: 9

TYPE: PRT

ORGANISM: Homo sapiens

US-10-245-871-459

Query Match  
Best Local Similarity 71.4%; Score 26; DB 4; Length 9;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 KRDNHY 9  
|||

Db 1 KRVPDY 7



## RESULT 56

US-10-253-286-459  
; Sequence 459, Application US/10253286  
; Publication No. US20040058681A1  
; GENERAL INFORMATION:  
; APPLICANT: HUMPHREYS, ROBERT  
; APPLICANT: XU, MINZHEN  
; TITLE OF INVENTION: 11-KEY/ANTIGENIC EPIOTOPE HYBRID PEPTIDE VACCINES  
; FILE REFERENCE: RH-2015  
; CURRENT APPLICATION NUMBER: US/10/253, 286  
; CURRENT FILING DATE: 2003-01-13  
; PRIOR APPLICATION NUMBER: 10/197,000  
; PRIOR FILING DATE: 2002-07-17  
; PRIOR APPLICATION NUMBER: 09/396,813  
; PRIOR FILING DATE: 1999-09-14  
; NUMBER OF SEQ ID NOS: 905  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 459  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-253-286-459

Query Match 33.3%; Score 26; DB 4; Length 10;  
Best Local Similarity 71.4%; Pred. No. 1.7e+06;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 KRHDNDY 9  
|||  
Db 1 KRVPDPY 7

## RESULT 57

US-09-894-018-263  
; Sequence 263, Application US/09894018  
; Patent No. US20020119127A1  
; GENERAL INFORMATION:  
; APPLICANT: EPIMUNE, Inc.  
; APPLICANT: Sette, Alessandro  
; APPLICANT: Chestnut, Robert  
; APPLICANT: Livingston, Brian  
; APPLICANT: Baker, Denise  
; APPLICANT: Newman, Mark  
; APPLICANT: Brown, David  
; TITLE OF INVENTION: METHODS AND SYSTEM FOR OPTIMIZING  
; FILE REFERENCE: 39963-20033, 00  
; CURRENT APPLICATION NUMBER: US/09/894, 018  
; CURRENT FILING DATE: 2001-06-27  
; PRIOR APPLICATION NUMBER: PCT/US00/35568  
; PRIOR FILING DATE: 2000-12-28  
; PRIOR APPLICATION NUMBER: US 60/173,390  
; PRIOR FILING DATE: 1999-12-28  
; PRIOR APPLICATION NUMBER: US 60/284,221  
; PRIOR FILING DATE: 2001-04-16  
; NUMBER OF SEQ ID NOS: 368  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 263  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: P. falciparum  
US-09-894-018-263

Query Match 33.3%; Score 26; DB 3; Length 10;  
Best Local Similarity 66.7%; Pred. No. 1.2e+03;  
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 HNDYSK 11  
|||  
Db 5 HNSYK 10

## RESULT 58

## US-10-360-836-33

; Sequence 33, Application US/10360836  
; Publication No. US20030185854A1  
; GENERAL INFORMATION:  
; APPLICANT: Zavala, Fidel  
; APPLICANT: Birkett, Ashley  
; TITLE OF INVENTION: USE OF RECOMBINANT HEPATITIS B CORE  
; TITLE OF INVENTION: PARTICLES TO DEVELOP VACCINES AGAINST INFECTIOUS PATHOGENS  
; FILE REFERENCE: 5986/1J876  
; CURRENT APPLICATION NUMBER: US/10/360, 836  
; CURRENT FILING DATE: 2003-02-07  
; PRIOR APPLICATION NUMBER: 60/354,963  
; PRIOR FILING DATE: 2002-02-08  
; NUMBER OF SEQ ID NOS: 86  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 33  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Plasmodium  
US-10-360-836-33

Query Match 33.3%; Score 26; DB 4; Length 10;  
Best Local Similarity 66.7%; Pred. No. 1.2e+03;  
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 HNDYSK 11  
|||  
Db 5 HNSYK 10

## RESULT 59

US-10-371-525-441  
; Sequence 441, Application US/10371525  
; Publication No. US20030203869A1  
; GENERAL INFORMATION:  
; APPLICANT: Fikes, John D.  
; APPLICANT: Hermanson, Gary G.  
; APPLICANT: Sette, Alessandro  
; APPLICANT: Ishioka, Glenn Y.  
; APPLICANT: Livingston, Brian  
; APPLICANT: Chestnut, Robert W.  
; APPLICANT: Epimune Inc.  
; TITLE OF INVENTION: Expression Vectors for Stimulating an  
; TITLE OF INVENTION: Immune Response and Methods of Using the Same  
; FILE REFERENCE: 39963-20022, 01  
; CURRENT APPLICATION NUMBER: US/10/371,525  
; CURRENT FILING DATE: 2003-02-21  
; PRIOR APPLICATION NUMBER: US 03/311,784  
; PRIOR FILING DATE: 1999-05-13  
; PRIOR APPLICATION NUMBER: US 60/085,751  
; PRIOR FILING DATE: 1998-05-15  
; NUMBER OF SEQ ID NOS: 463  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 441  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Pf LSA1 59 (peptide 1167.47)  
US-10-371-525-441

Query Match 33.3%; Score 26; DB 4; Length 10;  
Best Local Similarity 66.7%; Pred. No. 1.2e+03;  
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 HNDYSK 11  
|||  
Db 5 HNSYK 10

## RESULT 60

US-10-371-069-441

```
/ Sequence 441, Application US/10371069
/ Publication No. US20030216342A1
/ GENERAL INFORMATION:
/ APPLICANT: EPIMUNE Inc.
/ APPLICANT: Fikes, John D.
/ APPLICANT: Hermanson, Gary G.
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Ishioka, Glenn Y.
/ APPLICANT: Livingston, Brian
/ APPLICANT: Chesnut, Robert W.
/ APPLICANT: Epimmune Inc.
/ TITLE OF INVENTION: Expression Vectors for Stimulating an
/ FILE REFERENCE: 39963-20022.10
/ CURRENT APPLICATION NUMBER: US/10/371,069
/ CURRENT FILING DATE: 2003-02-21
/ PRIOR APPLICATION NUMBER: US 09/078,904
/ PRIOR FILING DATE: 1998-05-13
/ PRIOR APPLICATION NUMBER: US 60/085,751
/ PRIOR FILING DATE: 1998-05-15
/ NUMBER OF SEQ ID NOS: 463
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 441
/ LENGTH: 10
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Pf LSA1 59 (peptide 1167.47)
US-10-371-069-441
```

```
Query Match 33.3%; Score 26; DB 4; Length 10;
Best Local Similarity 66.7%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 6 HNDYSK 11
DB 5 HNSYK 10
```

```
RESULT 61
US-10-371-645-441
/ Sequence 441, Application US/10371645
/ Publication No. US20030216343A1
/ GENERAL INFORMATION:
/ APPLICANT: EPIMUNE Inc.
/ APPLICANT: Fikes, John D.
/ APPLICANT: Hermanson, Gary G.
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Ishioka, Glenn Y.
/ APPLICANT: Livingston, Brian
/ APPLICANT: Chesnut, Robert W.
/ APPLICANT: Epimmune Inc.
/ TITLE OF INVENTION: Expression Vectors for Stimulating an
/ FILE REFERENCE: 39963-20022.11
/ CURRENT APPLICATION NUMBER: US/10/371,645
/ CURRENT FILING DATE: 2003-06-20
/ PRIOR APPLICATION NUMBER: US 09/078,904
/ PRIOR FILING DATE: 1998-05-13
/ PRIOR APPLICATION NUMBER: US 60/085,751
/ PRIOR FILING DATE: 1998-05-15
/ NUMBER OF SEQ ID NOS: 463
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 441
/ LENGTH: 10
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Pf LSA1 59 (peptide 1167.47)
US-10-371-645-441
```

```
Query Match 33.3%; Score 26; DB 4; Length 10;
Best Local Similarity 66.7%; Pred. No. 1.2e+03;
```

```
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 6 HNDYSK 11
DB 5 HNSYK 10
```

```
RESULT 62
US-10-371-260-441
/ Sequence 441, Application US/10371260
/ Publication No. US20030220285A1
/ GENERAL INFORMATION:
/ APPLICANT: EPIMUNE Inc.
/ APPLICANT: Fikes, John D.
/ APPLICANT: Hermanson, Gary G.
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Ishioka, Glenn Y.
/ APPLICANT: Livingston, Brian
/ APPLICANT: Chesnut, Robert W.
/ APPLICANT: Epimmune Inc.
/ TITLE OF INVENTION: Expression Vectors for Stimulating an
/ FILE REFERENCE: 39963-20022.13
/ CURRENT APPLICATION NUMBER: US/10/371,260
/ CURRENT FILING DATE: 2003-02-21
/ PRIOR APPLICATION NUMBER: US 09/078,904
/ PRIOR FILING DATE: 1998-05-13
/ PRIOR APPLICATION NUMBER: US 60/085,751
/ PRIOR FILING DATE: 1998-05-15
/ NUMBER OF SEQ ID NOS: 463
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 441
/ LENGTH: 10
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Pf LSA1 59 (peptide 1167.47)
US-10-371-260-441
```

```
Query Match 33.3%; Score 26; DB 4; Length 10;
Best Local Similarity 66.7%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 6 HNDYSK 11
DB 5 HNSYK 10
```

```
RESULT 63
US-10-474-960A-263
/ Sequence 263, Application US/10474960A
/ Publication No. US20040248113A1
/ GENERAL INFORMATION:
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Livingston, Brian
/ APPLICANT: Baker, Denise
/ APPLICANT: Newman, Mark
/ APPLICANT: Brown, David
/ TITLE OF INVENTION: Methods and System for Optimizing Multi-epitope Nucleic
/ FILE REFERENCE: 2060.0320004
/ CURRENT APPLICATION NUMBER: US/10/474,960A
/ CURRENT FILING DATE: 2003-10-16
/ PRIOR APPLICATION NUMBER: PCT/US02/09877
/ PRIOR FILING DATE: 2002-03-28
/ PRIOR APPLICATION NUMBER: US 09/894,018
/ PRIOR FILING DATE: 2001-06-27
/ PRIOR APPLICATION NUMBER: US 60/284,221
/ PRIOR FILING DATE: 2001-04-16
/ NUMBER OF SEQ ID NOS: 419
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 263
```

LENGTH: 10  
TYPE: PRT  
ORGANISM: P. falciparum  
US-10-474-960A-263

Query Match 33.3%; Score 26; DB 5; Length 10;  
Best Local Similarity 66.7%; Pred. No. 1.2e+03;  
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 HNDYSK 11  
DB 5 HNSYK 10

RESULT 64  
US-10-697-399-9  
Sequence 9, Application US/10697399  
Publication No. US20040162413A1  
GENERAL INFORMATION:  
APPLICANT: Watkins, Jeffrey D.  
APPLICANT: Huse, William D.  
APPLICANT: Vaesset, Alain P.  
APPLICANT: Margulis, David P.  
APPLICANT: Smith, Eric P.  
TITLE OF INVENTION: Methods of Optimizing Antibody Variable Region Binding Affinity  
FILE REFERENCE: AME-08122  
CURRENT APPLICATION NUMBER: US/10/697,399  
CURRENT FILING DATE: 2003-10-30  
NUMBER OF SEQ ID NOS: 50  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 9  
LENGTH: 11  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic  
US-10-697-399-9

Query Match 33.3%; Score 26; DB 4; Length 11;  
Best Local Similarity 55.6%; Pred. No. 1.3e+03;  
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 SIKRDNDY 9  
DB 1 SASQDINDY 9

RESULT 65  
US-10-930-300-129  
Sequence 129, Application US/10930300  
Publication No. US20050014138A1  
GENERAL INFORMATION:  
APPLICANT: Rath, Mathias  
TITLE OF INVENTION: METHOD OF PRODUCING VACCINES FROM PROTEIN SIGNAL  
OLIGOPEPTIDES  
NUMBER OF SEQUENCES: 360  
CORRESPONDENCE ADDRESS:  
ADDRESSER: INHOUSE IP MANAGEMENT  
STREET: 280 Colorado Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94301  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy Disk, 3.50 inch, 1.44MB Storage  
OPERATING SYSTEM: WINDOWS 95  
SOFTWARE: MS WORD 6.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/930,300  
FILING DATE: 30-Aug-2004  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/182,248  
FILING DATE: 14-JAN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: ALI KAMAREI  
REGISTRATION NUMBER: 37000  
REFERENCE/DOCKET NUMBER: 10262-1US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-322-7371  
TELEFAX: 650-322-7389  
INFORMATION FOR SEQ ID NO: 129:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 129:  
US-10-930-300-129

Query Match 33.3%; Score 26; DB 5; Length 11;  
Best Local Similarity 40.0%; Pred. No. 1.3e+03;  
Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 2 IKRDNDYSK 11  
DB 1 VKRRNRNIK 10

RESULT 66  
US-10-193-460A-16  
Sequence 16, Application US/10193460A  
Publication No. US20030082769A1  
GENERAL INFORMATION:  
APPLICANT: BOEHRINGER INGELHEIM (CANADA) LTD.  
TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS E2 TRANSACTIVATION  
DOMAIN/INHIBITOR CO-CRYSTAL AND X-RAY COORDINATES DEFINING  
TITLE OF INVENTION: THE INHIBITOR-BINDING POCKET  
FILE REFERENCE: 13/100  
CURRENT APPLICATION NUMBER: US/10/193,460A  
CURRENT FILING DATE: 2002-07-11  
PRIOR APPLICATION NUMBER: 60/304,412  
PRIOR FILING DATE: 2001-07-12  
NUMBER OF SEQ ID NOS: 22  
SOFTWARE: PatsSeq for Windows Version 4.0  
SEQ ID NO 16  
LENGTH: 12  
TYPE: PRT  
ORGANISM: HPV16  
US-10-193-460A-16

Query Match 33.3%; Score 26; DB 4; Length 12;  
Best Local Similarity 71.4%; Pred. No. 1.5e+03;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 DNRDYSK 11  
DB 1 DHIDYWK 7

RESULT 67  
US-10-652-407-44  
Sequence 44, Application US/10652407  
Publication No. US20040180823A1  
GENERAL INFORMATION:  
APPLICANT: Pasquale, Elena B.  
APPLICANT: Koolpe, Mitchell  
APPLICANT: Murali, Keith K.  
TITLE OF INVENTION: NOVEL AGENTS THAT MODULATE EPH RECEPTOR ACTIVITY  
FILE REFERENCE: BURHAM-003A  
CURRENT APPLICATION NUMBER: US/10/652,407  
CURRENT FILING DATE: 2003-08-29  
PRIOR APPLICATION NUMBER: US 60/413,242  
PRIOR FILING DATE: 2002-09-24  
NUMBER OF SEQ ID NOS: 71

/ SOFTWARE: FastSeq for Windows Version 4.0  
/ SEQ ID NO 44  
/ LENGTH: 12  
/ TYPE: PRT  
/ ORGANISM: Artificial Sequence  
/ FEATURE:  
/ OTHER INFORMATION: EphA4-binding peptide  
US-10-652-407-44

Query Match 33.3%; Score 26; DB 4; Length 12;  
Best Local Similarity 55.6%; Pred. No. 1.5e+03;  
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 DHNDYSKP 13  
Db 1 DHNHNLNP 9

RESULT 68  
US-10-958-765-35  
/ Sequence 35, Application US/10958765  
/ Publication No. US20050191296A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Yissum Research and Development Company of the Hebrew  
/ APPLICANT: University of Jerusalem  
/ TITLE OF INVENTION: Broad Spectrum in vivo effective Superantigen Toxin Antagonists  
/ TITLE OF INVENTION: based on the interaction between CD28 and the Superantigen and  
/ TITLE OF INVENTION: uses thereof  
/ FILE REFERENCE: 1396-16824-17428US+  
/ CURRENT APPLICATION NUMBER: US/10/958,765  
/ PRIOR FILING DATE: 2004-10-04  
/ PRIOR APPLICATION NUMBER: IL 148993  
/ PRIOR FILING DATE: 2002-04-04  
/ PRIOR APPLICATION NUMBER: PCT/IL03/00278  
/ PRIOR FILING DATE: 2003-04-03  
/ NUMBER OF SEQ ID NOS: 63  
/ SOFTWARE: PatentIn version 3.3  
/ SEQ ID NO 35  
/ LENGTH: 12  
/ TYPE: PRT  
/ ORGANISM: Artificial Sequence  
/ FEATURE:  
/ OTHER INFORMATION: Synthetic peptide pbs  
US-10-958-765-35

Query Match 33.3%; Score 26; DB 5; Length 12;  
Best Local Similarity 66.7%; Pred. No. 1.5e+03;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 6 HNDYSK 11  
Db 4 HHDSK 9

RESULT 69  
US-09-992-665-15  
/ Sequence 15, Application US/09992665  
/ Publication No. US20030092009A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Kala Palm  
/ TITLE OF INVENTION: PROFILING TUMOR SPECIFIC MARKERS FOR THE  
/ TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF NEOPLASTIC DISEASE  
/ FILE REFERENCE: CEMTNS.002A  
/ CURRENT APPLICATION NUMBER: US/09/992,665  
/ PRIOR FILING DATE: 2001-11-13  
/ PRIOR APPLICATION NUMBER: 60/249,508  
/ PRIOR FILING DATE: 2000-11-16  
/ NUMBER OF SEQ ID NOS: 380  
/ SOFTWARE: FastSeq for Windows Version 4.0  
/ SEQ ID NO 15  
/ LENGTH: 13  
/ TYPE: PRT  
/ ORGANISM: Artificial Sequence

/ FEATURE:  
/ OTHER INFORMATION: Probe  
US-09-992-665-15

Query Match 33.3%; Score 26; DB 3; Length 13;  
Best Local Similarity 66.7%; Pred. No. 1.6e+03;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 HNDYSK 11  
Db 3 HDYYSK 8

RESULT 70  
US-09-391-104-15  
/ Sequence 15, Application US/09391104  
/ Publication No. US20020031817A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Abbott Laboratories  
/ APPLICANT: Falduto, Michael T.  
/ APPLICANT: Magnuson, Scott R.  
/ APPLICANT: Morgan, Douglas W.  
/ TITLE OF INVENTION: HUMAN MATRIX METALLOPROTEINASE GENE,  
/ TITLE OF INVENTION: PROTEINS ENCODED THEREFROM AND METHODS  
/ FILE REFERENCE: 6073 US P1  
/ CURRENT APPLICATION NUMBER: US/09/391,104  
/ PRIOR FILING DATE: 1999-09-07  
/ PRIOR APPLICATION NUMBER: US 08/814,394  
/ PRIOR FILING DATE: 1997-03-11  
/ NUMBER OF SEQ ID NOS: 35  
/ SOFTWARE: FastSeq for Windows Version 3.0  
/ SEQ ID NO 15  
/ LENGTH: 15  
/ TYPE: PRT  
/ ORGANISM: Artificial Sequence  
/ FEATURE:  
/ OTHER INFORMATION: Synthetic peptides  
US-09-391-104-15

Query Match 33.3%; Score 26; DB 3; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.9e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 DHND 8  
Db 4 DHND 7

RESULT 71  
US-10-124-986-33  
/ Sequence 33, Application US/10124986  
/ Publication No. US20030036508A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Ford et al.  
/ TITLE OF INVENTION: EGF MOTIF PROTEIN, EGF16, MATERIALS AND METHODS  
/ FILE REFERENCE: 28110/37958  
/ CURRENT APPLICATION NUMBER: US/10/124,986  
/ PRIOR FILING DATE: 2002-04-17  
/ PRIOR APPLICATION NUMBER: US 09/981,649  
/ PRIOR FILING DATE: 2001-10-15  
/ PRIOR APPLICATION NUMBER: US 09/687,860  
/ PRIOR FILING DATE: 2000-10-13  
/ PRIOR APPLICATION NUMBER: US 09/620,312  
/ PRIOR FILING DATE: 2000-07-19  
/ PRIOR APPLICATION NUMBER: US 09/363,316  
/ PRIOR FILING DATE: 1999-07-28  
/ NUMBER OF SEQ ID NOS: 36  
/ SOFTWARE: FastSeq for Windows Version 3.0  
/ SEQ ID NO 33  
/ LENGTH: 15  
/ TYPE: PRT  
/ ORGANISM: Artificial Sequence

```
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: EGFL6 peptide
US-10-124-986-33

Query Match      33.3%; Score 26; DB 4; Length 15;
Best Local Similarity 40.0%; Pred. No. 1.9e+03;
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 4 RDHNDYSKNP 13
   :|:|:|
DB 3 REDDDPDWNP 12

RESULT 72
US-10-116-275-44
Sequence 44, Application US/10116275
Publication No. US20030211476A1
GENERAL INFORMATION:
APPLICANT: Elian Pharmaceutical Technology
APPLICANT: O'Mahony, Daniel J.
APPLICANT: Brayden, David
APPLICANT: Byrne, Daragh
APPLICANT: Lambkin, Imelda
APPLICANT: Higgins, Lisa
TITLE OF INVENTION: Genetic Analysis of Peyer's Patches and M Cells and Methods and
FILE REFERENCE: E1067/20087
CURRENT APPLICATION NUMBER: US/10/116, 275
CURRENT FILING DATE: 2002-10-04
NUMBER OF SEQ ID NOS: 349
SOFTWARE: PatentIn version 3.1
SEQ ID NO 44
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Listed in Table titled "Peptides that Target to and/or Enhance Up
US-10-116-275-44

Query Match      33.3%; Score 26; DB 4; Length 15;
Best Local Similarity 27.3%; Pred. No. 1.9e+03;
Matches 3; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 2 IKRDNDYSKN 12
   :|:|:|
DB 4 LRRNHSKKN 14

RESULT 73
US-10-475-104-129
Sequence 129, Application US/10475104
Publication No. US20040171097A1
GENERAL INFORMATION:
APPLICANT: Schneider-Mergener, Jens
APPLICANT: Schuckowski, Mike
APPLICANT: Reimer, Ulf
APPLICANT: Dong, Liyang
APPLICANT: Panse, Soren
APPLICANT: Scharn, Dirk
APPLICANT: Oesterkamp, Frank
APPLICANT: Hummel, Gerd
APPLICANT: Jodion, Laurence
TITLE OF INVENTION: Method for Determining the Substrate Specificity of an Enzymatic
FILE REFERENCE: 2918-0102
CURRENT APPLICATION NUMBER: US/10/475, 104
PRIOR FILING DATE: 2003-10-17
CURRENT APPLICATION NUMBER: PCT/EP02/04265
PRIOR FILING DATE: 2002-04-17
NUMBER OF SEQ ID NOS: 144
SOFTWARE: PatentIn version 3.2
SEQ ID NO 129
```

```
LENGTH: 15
TYPE: PRT
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: synthesized peptide sequence
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (14)-(14)
OTHER INFORMATION: Xaa = beta-alanine
FEATURE:
NAME/KEY: MOD RES
LOCATION: (15)-(15)
OTHER INFORMATION: amino group
US-10-475-104-129

Query Match      33.3%; Score 26; DB 4; Length 15;
Best Local Similarity 36.4%; Pred. No. 1.9e+03;
Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 2 IKRDNDYSKN 12
   :|:|:|
DB 3 ISKNDPDYQDD 13

RESULT 74
US-10-126-845-53
Sequence 53, Application US/10126845
Publication No. US20030181367A1
GENERAL INFORMATION:
APPLICANT: O'Mahony, Daniel J.
APPLICANT: Lambkin, Imelda J.
APPLICANT: Phyllis, Clemencia
APPLICANT: Houghten, Richard
TITLE OF INVENTION: MEMBRANE TRANSLOCATING PEPTIDE DRUG DELIVERY SYSTEM
FILE REFERENCE: E1067/20058
CURRENT APPLICATION NUMBER: US/10/126, 845
CURRENT FILING DATE: 2002-10-15
NUMBER OF SEQ ID NOS: 119
SOFTWARE: PatentIn version 3.1
SEQ ID NO 53
LENGTH: 16
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: D form retroinversion peptide
FEATURE:
NAME/KEY: MOD RES
LOCATION: (1)-(1)
OTHER INFORMATION: dansylated
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (2)-(16)
OTHER INFORMATION: D form amino acid
US-10-126-845-53

Query Match      33.3%; Score 26; DB 4; Length 16;
Best Local Similarity 27.3%; Pred. No. 2e+03;
Matches 3; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 2 IKRDNDYSKN 12
   :|:|:|
DB 5 LRRNHSKKN 15

RESULT 75
US-10-764-235-53
Sequence 53, Application US/10764235
Publication No. US20040138132A1
GENERAL INFORMATION:
APPLICANT: O'Mahony, Daniel J.
APPLICANT: Lambkin, Imelda J.
TITLE OF INVENTION: MEMBRANE TRANSLOCATING PEPTIDE DRUG DELIVERY SYSTEM
FILE REFERENCE: P26,479-B USA
```

1 CURRENT APPLICATION NUMBER: US/10/764,235  
2 CURRENT FILING DATE: 2004-01-23  
3 PRIOR APPLICATION NUMBER: 09/671,089  
4 PRIOR FILING DATE: 2000-09-27  
5 PRIOR APPLICATION NUMBER: 60/156,246  
6 PRIOR FILING DATE: 1999-09-27  
7 NUMBER OF SEQ ID NOS: 59  
8 SOFTWARE: PatentIn version 3.1  
9 SEQ ID NO 53  
10 LENGTH: 16  
11 TYPE: PRT  
12 ORGANISM: Artificial Sequence  
13 FEATURE:  
14 OTHER INFORMATION: D form retroinversion peptide  
15 NAME/KEY: MOD\_RES  
16 LOCATION: (1)..(1)  
17 OTHER INFORMATION: danylated  
18 FEATURE:  
19 NAME/KEY: MISC\_FEATURE  
20 LOCATION: (2)..(16)  
21 OTHER INFORMATION: D form amino acid  
22 US-10-764-235-53

Query Match 33.3%; Score 26; DB 4; Length 16;  
Best Local Similarity 27.3%; Pred. No. 2e+03;  
Matches 3; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 2 IKRDNDYSKN 12  
DB 5 LRRNHSHKAN 15

RESULT 76  
US-10-955-656-53  
1 Sequence 53, Application US/10955656  
2 Publication No. US20050101762A1  
3 GENERAL INFORMATION:  
4 APPLICANT: O'Mahony, Daniel J.  
5 APPLICANT: Lambkin, Imelda J.  
6 APPLICANT: Pinilla, Clemencia  
7 APPLICANT: Houghten, Richard  
8 TITLE OF INVENTION: CONJUGATES OF MEMBRANE TRANSLOCATING AGENTS AND PHARMACEUTICALLY  
9 FILE REFERENCE: P26, 481-A USA  
10 CURRENT APPLICATION NUMBER: US/10/955,656  
11 CURRENT FILING DATE: 2004-09-30  
12 PRIOR APPLICATION NUMBER: 10/126,845  
13 PRIOR FILING DATE: 2002-04-19  
14 PRIOR APPLICATION NUMBER: 09/671,089  
15 PRIOR FILING DATE: 2000-09-27  
16 PRIOR APPLICATION NUMBER: 60/156,246  
17 PRIOR FILING DATE: 1999-09-27  
18 NUMBER OF SEQ ID NOS: 119  
19 SOFTWARE: PatentIn version 3.1  
20 SEQ ID NO 53  
21 LENGTH: 16  
22 TYPE: PRT  
23 ORGANISM: Artificial Sequence  
24 FEATURE:  
25 OTHER INFORMATION: D form retroinversion peptide  
26 NAME/KEY: MOD\_RES  
27 LOCATION: (1)..(1)  
28 OTHER INFORMATION: danylated  
29 FEATURE:  
30 NAME/KEY: MISC\_FEATURE  
31 LOCATION: (2)..(16)  
32 OTHER INFORMATION: D form amino acid  
33 US-10-955-656-53

Query Match 33.3%; Score 26; DB 5; Length 16;  
Best Local Similarity 27.3%; Pred. No. 2e+03;

Matches 3; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 2 IKRDNDYSKN 12  
DB 5 LRRNHSHKAN 15

RESULT 77  
US-10-660-370-87  
1 Sequence 87, Application US/10660370  
2 Publication No. US20050064507A1  
3 GENERAL INFORMATION:  
4 APPLICANT: Shaw, J. Stephen  
5 APPLICANT: National Institutes of Health  
6 TITLE OF INVENTION: Determining Kinase Specificity  
7 FILE REFERENCE: 1662.009US2  
8 CURRENT APPLICATION NUMBER: US/10/660,370  
9 CURRENT FILING DATE: 2003-09-11  
10 NUMBER OF SEQ ID NOS: 640  
11 SOFTWARE: FastSeq for Windows Version 4.0  
12 SEQ ID NO 87  
13 LENGTH: 17  
14 TYPE: PRT  
15 ORGANISM: Artificial Sequence  
16 FEATURE:  
17 OTHER INFORMATION: A synthetic peptide  
18 US-10-660-370-87

Query Match 33.3%; Score 26; DB 5; Length 17;  
Best Local Similarity 50.0%; Pred. No. 2.1e+03;  
Matches 7; Conservative 2; Mismatches 1; Indels 4; Gaps 1;

QY 1 SIKRDNDYSKNPM 14  
DB 8 SIKRD---TVNPL 17

RESULT 78  
US-09-839-884-6  
1 Sequence 6, Application US/09839884  
2 Patent No. US20020076739A1  
3 GENERAL INFORMATION:  
4 APPLICANT: Aebersold, Rudolf H.  
5 APPLICANT: Gelb, Michael H.  
6 APPLICANT: Gygi, Steven  
7 APPLICANT: Scott, C R  
8 APPLICANT: Turecek, Frantisek  
9 APPLICANT: Gerber, Scott A  
10 APPLICANT: Rist, Beate  
11 TITLE OF INVENTION: Rapid Quantitative Analysis of Proteins or Protein  
12 FILE REFERENCE: 64-98A  
13 CURRENT APPLICATION NUMBER: US/09/839,884  
14 CURRENT FILING DATE: 2001-04-20  
15 PRIOR APPLICATION NUMBER: 09/383,062  
16 PRIOR FILING DATE: 1999-08-25  
17 PRIOR APPLICATION NUMBER: 60/097,788  
18 PRIOR FILING DATE: 1998-08-25  
19 NUMBER OF SEQ ID NOS: 64  
20 SOFTWARE: PatentIn Ver. 2.0  
21 SEQ ID NO 6  
22 LENGTH: 18  
23 TYPE: PRT  
24 ORGANISM: Artificial Sequence  
25 FEATURE:  
26 OTHER INFORMATION: Description of Artificial Sequence: Test peptide  
27 US-09-839-884-6

Query Match 33.3%; Score 26; DB 3; Length 18;  
Best Local Similarity 50.0%; Pred. No. 2.3e+03;  
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 3 KRDNDYSKN 12

Db 1 KDDONPHSN 10

RESULT 79  
US-09-371-900-50  
Sequence 50, Application US/09371900  
Patent No. US20020137700A1  
GENERAL INFORMATION:  
APPLICANT: FALB, DEAN A  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE  
TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE  
NUMBER OF SEQUENCES: 54  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PENNIE & EDMONDS LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/371,900  
FILING DATE: 11-Aug-1999  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/599,654  
FILING DATE: 09-FEB-1996  
APPLICATION NUMBER: US 08/485,573  
FILING DATE: 07-JUN-1995  
APPLICATION NUMBER: US 08/386,844  
FILING DATE: 10-FEB-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: CORUZZI, LAURA A  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7853-104  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 50:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 50:  
US-09-371-900-50  
Query Match 33.3%; Score 26; DB 3; Length 18;  
Best Local Similarity 66.7%; Pred. No. 2.3e+03;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 8 DYSKNP 13  
: |||  
Db 5 EYKNP 10

RESULT 80  
US-09-924-417-16  
Sequence 16, Application US/09924417  
Patent No. US2002014241A1  
GENERAL INFORMATION:  
APPLICANT: FALB, DEAN  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR  
THE TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR  
DISEASE  
NUMBER OF SEQUENCES: 67

CORRESPONDENCE ADDRESS:  
ADDRESSEE: PENNIE & EDMONDS LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: diskette  
COMPUTER: IBM compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/924,417  
FILING DATE: 07-Aug-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/034,286  
FILING DATE: 04-MAR-1998  
APPLICATION NUMBER: 08/870,434  
FILING DATE: 06-JUN-1997  
APPLICATION NUMBER: 08/799,910  
FILING DATE: 13-FEB-1997  
APPLICATION NUMBER: 60/011,787  
FILING DATE: 16-FEB-1996  
APPLICATION NUMBER: 08/599,654  
FILING DATE: 09-FEB-1996  
APPLICATION NUMBER: 08/485,573  
FILING DATE: 07-JUN-1995  
APPLICATION NUMBER: 08/386,844  
FILING DATE: 10-FEB-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7853-114-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 7909090  
TELEFAX: (212) 8699741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 16:  
US-09-924-417-16  
Query Match 33.3%; Score 26; DB 3; Length 18;  
Best Local Similarity 66.7%; Pred. No. 2.3e+03;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 8 DYSKNP 13  
: |||  
Db 5 EYKNP 10

RESULT 81  
US-09-839-884-6  
Sequence 6, Application US/09839884  
Publication No. US20030087322A9  
GENERAL INFORMATION:  
APPLICANT: Aedersold, Rudolf H.  
APPLICANT: Gelb, Michael H  
APPLICANT: Gysl, Steven  
APPLICANT: Scott, C R  
APPLICANT: turecek, Frantisek  
APPLICANT: Gerber, Scott A  
APPLICANT: Rist, Beate  
TITLE OF INVENTION: Rapid Quantitative Analysis of Proteins or Protein  
FUNCTION: Function in Complex Mixture  
FILE REFERENCE: 64-98A

1 CURRENT APPLICATION NUMBER: US/09/839,884  
2 CURRENT FILING DATE: 2001-04-20  
3 PRIOR APPLICATION NUMBER: 09/383,062  
4 PRIOR FILING DATE: 1999-08-25  
5 PRIOR APPLICATION NUMBER: 60/097,788  
6 PRIOR FILING DATE: 1998-08-25  
7 NUMBER OF SEQ ID NOS: 64  
8 SOFTWARE: PatentIn Ver. 2.0  
9 SEQ ID NO 6  
10 LENGTH: 18  
11 TYPE: PRT  
12 ORGANISM: Artificial Sequence  
13 FEATURE:  
14 OTHER INFORMATION: Description of Artificial Sequence: Test peptide  
15 US-09-839-884-6

Query Match 33.3%; Score 26; DB 3; Length 18;  
Best Local Similarity 50.0%; Pred. No. 2.3e+03;  
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 3 KRDNYSKN 12  
DB 1 KDDQNPSSN 10

RESULT 82  
US-10-225-567A-1380  
1 Sequence 1380, Application US/10225567A  
2 Publication No. US20030113798A1  
3 GENERAL INFORMATION:  
4 APPLICANT: Lifespan Biosciences  
5 APPLICANT: Brown, Joseph P.  
6 APPLICANT: Burnett, Christine L.  
7 APPLICANT: Roush, Christine L.  
8 TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS  
9 FILE REFERENCE: 1920-4-4  
10 CURRENT APPLICATION NUMBER: US/10/225,567A  
11 CURRENT FILING DATE: 2001-12-19  
12 PRIOR APPLICATION NUMBER: 60/257,144  
13 PRIOR FILING DATE: 2000-12-19  
14 NUMBER OF SEQ ID NOS: 2292  
15 SOFTWARE: PatentIn version 3.1  
16 SEQ ID NO 1380  
17 LENGTH: 18  
18 TYPE: PRT  
19 ORGANISM: Homo sapiens  
20 US-10-225-567A-1380

Query Match 33.3%; Score 26; DB 4; Length 18;  
Best Local Similarity 40.0%; Pred. No. 2.3e+03;  
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 5 DHNDYSKNPM 14  
DB 3 DFRDHAKNAL 12

RESULT 83  
US-10-186-950-50  
1 Sequence 50, Application US/10186950  
2 Publication No. US20030188327A1  
3 GENERAL INFORMATION:  
4 APPLICANT: FALB, DEAN A  
5 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE  
6 TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE  
7 NUMBER OF SEQUENCES: 54  
8 CORRESPONDENCE ADDRESS:  
9 ADDRESSEE: PENNIE & EDMONDS LLP  
10 STREET: 1155 Avenue of the Americas  
11 CITY: New York  
12 STATE: New York  
13 COUNTRY: USA  
14 ZIP: 10036-2711

1 COMPUTER READABLE FORM:  
2 MEDIUM TYPE: floppy disk  
3 COMPUTER: IBM PC compatible  
4 OPERATING SYSTEM: PC-DOS/MS-DOS  
5 SOFTWARE: PatentIn Release #1.0, Version #1.30  
6 CURRENT APPLICATION DATA:  
7 APPLICATION NUMBER: US/10/186,950  
8 FILING DATE: 02-Jul-2002  
9 CLASSIFICATION: <Unknown>  
10 PRIOR APPLICATION DATA:  
11 APPLICATION NUMBER: US/08/944,496  
12 FILING DATE: <Unknown>  
13 APPLICATION NUMBER: US 08/599,654  
14 FILING DATE: 09-FEB-1996  
15 APPLICATION NUMBER: US 08/485,573  
16 FILING DATE: 07-JUN-1995  
17 APPLICATION NUMBER: US 08/386,844  
18 FILING DATE: 10-FEB-1995  
19 ATTORNEY/AGENT INFORMATION:  
20 NAME: CORUZZI, LAURA A  
21 REGISTRATION NUMBER: 30,742  
22 REFERENCE/DOCKET NUMBER: 7853-104  
23 TELECOMMUNICATION INFORMATION:  
24 TELEPHONE: (212) 790-9090  
25 TELEFAX: (212) 869-8864  
26 TELEX: 66141 PENNIE  
27 INFORMATION FOR SEQ ID NO: 50:  
28 SEQUENCE CHARACTERISTICS:  
29 LENGTH: 18 amino acids  
30 TYPE: amino acid  
31 STRANDEDNESS: <Unknown>  
32 TOPOLOGY: unknown  
33 MOLECULE TYPE: peptide  
34 SEQUENCE DESCRIPTION: SEQ ID NO: 50:  
35 US-10-186-950-50

Query Match 33.3%; Score 26; DB 4; Length 18;  
Best Local Similarity 66.7%; Pred. No. 2.3e+03;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 DYKNP 13  
DB 5 BYKNP 10

RESULT 84  
US-10-653-872-16  
1 Sequence 16, Application US/10653872  
2 Publication No. US2004008192A1  
3 GENERAL INFORMATION:  
4 APPLICANT: FALB, DEAN  
5 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR  
6 THE TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR  
7 DISEASE  
8 NUMBER OF SEQUENCES: 67  
9 CORRESPONDENCE ADDRESS:  
10 ADDRESSEE: PENNIE & EDMONDS LLP  
11 STREET: 1155 Avenue of the Americas  
12 CITY: New York  
13 STATE: NY  
14 COUNTRY: USA  
15 ZIP: 10036-2711  
16 COMPUTER READABLE FORM:  
17 MEDIUM TYPE: Diskette  
18 COMPUTER: IBM Compatible  
19 OPERATING SYSTEM: DOS  
20 SOFTWARE: FastSeq Version 2.0  
21 CURRENT APPLICATION DATA:  
22 APPLICATION NUMBER: US/10/653,872  
23 FILING DATE: 03-Sep-2003  
24 CLASSIFICATION: <Unknown>  
25 PRIOR APPLICATION DATA:  
26 APPLICATION NUMBER: US/09/924,417



FILING DATE: 07-AUG-2001  
APPLICATION NUMBER: US/09/034,286  
FILING DATE: 04-MAR-1998  
APPLICATION NUMBER: 08/870,434  
FILING DATE: 06-JUN-1997  
APPLICATION NUMBER: 08/799,910  
FILING DATE: 13-FEB-1997  
APPLICATION NUMBER: 60/011,787  
FILING DATE: 16-FEB-1996  
APPLICATION NUMBER: 08/599,654  
FILING DATE: 09-FEB-1996  
APPLICATION NUMBER: 08/485,573  
FILING DATE: 07-JUN-1995  
APPLICATION NUMBER: 08/386,844  
FILING DATE: 10-FEB-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7853-114-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)7909090  
TELEFAX: (212)8699741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 16:  
US-10-653-872-16

Query Match 33.3%; Score 26; DB 4; Length 18;  
Best Local Similarity 66.7%; Pred. No. 2.3e+03;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 DYKRP 13  
| : : :  
Db 5 EYRNP 10

RESULT 85  
US-10-994-815-6  
Sequence 6, Application US/10994815  
Publication No. US20050233399A1  
GENERAL INFORMATION:  
APPLICANT: Aebersold, Rudolf H.  
APPLICANT: Gelb, Michael H.  
APPLICANT: Gysli, Steven  
APPLICANT: Scott, C R  
APPLICANT: Turecek, Frantisek  
APPLICANT: Gerber, Scott A  
APPLICANT: Rist, Beate  
TITLE OF INVENTION: Rapid Quantitative Analysis of Proteins or Protein  
FILE REFERENCE: 64-98A  
CURRENT APPLICATION NUMBER: US/10/994,815  
CURRENT FILING DATE: 2004-11-23  
PRIORITY APPLICATION NUMBER: US/09/839,884  
PRIORITY FILING DATE: 2001-04-20  
PRIORITY APPLICATION NUMBER: 09/383,062  
PRIORITY FILING DATE: 1999-08-25  
PRIORITY APPLICATION NUMBER: 60/097,788  
PRIORITY FILING DATE: 1998-08-25  
NUMBER OF SEQ ID NOS: 64  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 6  
LENGTH: 18  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Test peptide

US-10-994-815-6

Query Match 33.3%; Score 26; DB 5; Length 18;  
Best Local Similarity 50.0%; Pred. No. 2.3e+03;  
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 3 KRDNDSKN 12  
| : : :  
Db 1 KDDQNPSSN 10

RESULT 86  
US-10-225-567A-2058  
Sequence 2058, Application US/10225567A  
Publication No. US2003013798A1  
GENERAL INFORMATION:  
APPLICANT: Lifespan Biosciences  
APPLICANT: Brown, Joseph P.  
APPLICANT: Burnet, Glenn C.  
APPLICANT: Roush, Christine L.  
TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTOR  
FILE REFERENCE: 1920-4-4  
CURRENT APPLICATION NUMBER: US/10/225,567A  
CURRENT FILING DATE: 2001-12-19  
PRIORITY APPLICATION NUMBER: 60/257,144  
PRIORITY FILING DATE: 2000-12-19  
NUMBER OF SEQ ID NOS: 2292  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 2058  
LENGTH: 20  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-225-567A-2058

Query Match 33.3%; Score 26; DB 4; Length 20;  
Best Local Similarity 40.0%; Pred. No. 2.5e+03;  
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 SIKRDNDYS 10  
| : : :  
Db 2 SVSEYEGDYS 11

RESULT 87  
US-10-378-173-190  
Sequence 190, Application US/10378173  
Publication No. US20030232014A1  
GENERAL INFORMATION:  
APPLICANT: Burke et al.  
TITLE OF INVENTION: PHOSPHORYLATED PROTEINS AND USES RELATED THERETO  
FILE REFERENCE: MDSP-P01-023  
CURRENT APPLICATION NUMBER: US/10/378,173  
CURRENT FILING DATE: 2003-03-03  
PRIORITY APPLICATION NUMBER: 60/360787  
PRIORITY FILING DATE: 2002-03-01  
NUMBER OF SEQ ID NOS: 231  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 190  
LENGTH: 20  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: phosphorylated peptide  
NAME/KEY: MISC FEATURE  
LOCATION: (14)-(14)  
OTHER INFORMATION: phosphorylation  
NAME/KEY: MISC FEATURE  
LOCATION: (16)-(16)  
OTHER INFORMATION: phosphorylation  
US-10-378-173-190

Query Match 33.3%; Score 26; DB 4; Length 20;  
Best Local Similarity 66.7%; Pred. No. 2.5e+03;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 9 YSKNPM 14  
DB 2 YSKNPM 7

## RESULT 88

US-10-466-085A-21  
; Sequence 21, Application US/10466085A  
; Publication No. US20040161835A1  
; GENERAL INFORMATION:  
; APPLICANT: KUBOTA, Michio  
; APPLICANT: MARUTA, Kazuhiko  
; APPLICANT: YAMAMOTO, Takuo  
; APPLICANT: FUKUDA, Shigeharu  
; TITLE OF INVENTION: POLYPEPTIDE HAVING -ISOMALTOXYLGLUCOSACCHARIDE-FORMING ENZYME  
; FILE REFERENCE: KUBOTA=14  
; CURRENT APPLICATION NUMBER: US/10/466,085A  
; CURRENT FILING DATE: 2003-07-11  
; PRIOR FILING DATE: 2001-01-12  
; PRIOR APPLICATION NUMBER: JP 5441/2001  
; PRIOR FILING DATE: 2001-01-12  
; PRIOR APPLICATION NUMBER: PCT/JP02/00052  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 21  
; LENGTH: 20  
; TYPE: PRT  
; ORGANISM: Bacillus globisporus N75  
US-10-466-085A-21

Query Match 33.3%; Score 26; DB 4; Length 20;  
Best Local Similarity 66.7%; Pred. No. 2.5e+03;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 DYSKNP 13  
DB 1 DYSKNP 6

## RESULT 89

US-10-025-222A-36  
; Sequence 36, Application US/10025222A  
; Publication No. US2003003444A1  
; GENERAL INFORMATION:  
; APPLICANT: PELLETIER, JERRY  
; APPLICANT: GROS, PHILIPPE  
; APPLICANT: DUBOW, MICHAEL  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS INVOLVING AN ESSENTIAL  
; TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS GENE AND ITS ENCODED PROTEIN  
; FILE REFERENCE: 073406-0701  
; CURRENT APPLICATION NUMBER: US/10/025,222A  
; CURRENT FILING DATE: 2001-12-19  
; PRIOR APPLICATION NUMBER: 60/256,349  
; PRIOR FILING DATE: 2000-12-19  
; NUMBER OF SEQ ID NOS: 41  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 36  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Staphylococcus aureus  
US-10-025-222A-36

Query Match 32.7%; Score 25.5; DB 4; Length 17;  
Best Local Similarity 53.8%; Pred. No. 2.6e+03;  
Matches 7; Conservative 1; Mismatches 2; Indels 3; Gaps 1;

QY 1 SIKRD--HNDYS 10

DB 2 SIKRDEIHNDLS 14

## RESULT 90

US-09-834-765-658  
; Sequence 658, Application US/09834765  
; Patent No. US20020055478A1  
; GENERAL INFORMATION:  
; APPLICANT: Mary Paris  
; APPLICANT: Pia M. Challita-Eid  
; APPLICANT: Arthur B. Raitano  
; APPLICANT: Steve Chappell Mitchell  
; APPLICANT: Daniel B.H. Afar  
; APPLICANT: Aya Jakobovits  
; TITLE OF INVENTION: GTP-BINDING PROTEIN USEFUL IN TREATMENT  
; TITLE OF INVENTION: AND DETECTION OF CANCER  
; FILE REFERENCE: 129,6USU1  
; CURRENT APPLICATION NUMBER: US/09/834,765  
; CURRENT FILING DATE: 2001-09-21  
; PRIOR APPLICATION NUMBER: 60/197,647  
; PRIOR FILING DATE: 2000-04-12  
; NUMBER OF SEQ ID NOS: 770  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 658  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-834-765-658

Query Match 32.1%; Score 25; DB 3; Length 9;  
Best Local Similarity 55.6%; Pred. No. 1.7e+06;  
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 SIKRDNDY 9  
DB 1 STLRDPNEY 9

## RESULT 91

US-09-938-864-180  
; Sequence 180, Application US/09938864  
; Publication No. US20030072767A1  
; GENERAL INFORMATION:  
; APPLICANT: Gaiger, Alexander  
; APPLICANT: McNeill, Patricia D.  
; APPLICANT: Smithgall, Molly  
; APPLICANT: Moulton, Gus  
; APPLICANT: Vedvick, Thomas S.  
; APPLICANT: Sleath, Paul R.  
; APPLICANT: Moseman, Sally  
; APPLICANT: Evans, Lawrence  
; APPLICANT: Spies, A. Gregory  
; APPLICANT: Boydston, Jeremy  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1  
; TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY  
; FILE REFERENCE: 210121,465C5  
; CURRENT APPLICATION NUMBER: US/09/938,864  
; CURRENT FILING DATE: 2001-08-24  
; NUMBER OF SEQ ID NOS: 413  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 180  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-09-938-864-180

Query Match 32.1%; Score 25; DB 3; Length 9;  
Best Local Similarity 44.4%; Pred. No. 1.7e+06;  
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 4 RDNDYSKN 12

Db 1 RHHNMHQRN 9

RESULT 92  
US-09-791-477-180  
; Sequence 180, Application US/09791477  
; Publication No. US20030082194A1  
; GENERAL INFORMATION:  
; APPLICANT: Gaiger, Alexander  
; APPLICANT: Cheever, Martin A.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSIS  
; FILE REFERENCE: 2077.000200  
; CURRENT APPLICATION NUMBER: US/09/791,477  
; PRIOR APPLICATION NUMBER: 2001-02-22  
; PRIOR FILING DATE: 2000-02-22  
; NUMBER OF SEQ ID NOS: 326  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 180  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-791-477-180

Query Match 32.1%; Score 25; DB 3; Length 9;  
Best Local Similarity 44.4%; Pred. No. 1.7e+06;  
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 4 RDHNDYSKN 12  
| | | : |  
| | | : |  
Db 1 RHHNMHQRN 9

RESULT 93  
US-09-785-019-180  
; Sequence 180, Application US/09785019  
; Publication No. US20030082196A1  
; GENERAL INFORMATION:  
; APPLICANT: Gaiger, Alexander  
; APPLICANT: Cheever, Martin A.  
; APPLICANT: McNeill, Patricia D.  
; APPLICANT: Smithgall, Molly  
; APPLICANT: Moulton, Gus  
; APPLICANT: Vedvick, Thomas S.  
; APPLICANT: Sleath, Paul  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1  
; FILE REFERENCE: 210121.465C4  
; CURRENT APPLICATION NUMBER: US/09/785,019  
; CURRENT FILING DATE: 2001-02-15  
; NUMBER OF SEQ ID NOS: 376  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 180  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-785-019-180

Query Match 32.1%; Score 25; DB 3; Length 9;  
Best Local Similarity 44.4%; Pred. No. 1.7e+06;  
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 4 RDHNDYSKN 12  
| | | : |  
| | | : |  
Db 1 RHHNMHQRN 9

RESULT 94  
US-10-125-635A-180  
; Sequence 180, Application US/10125635A  
; Publication No. US20030039635A1  
; GENERAL INFORMATION:

; APPLICANT: Gaiger, Alexander  
; APPLICANT: Smithgall, Molly D.  
; APPLICANT: Carter, Darrick  
; APPLICANT: Cheever, Martin A.  
; APPLICANT: McNeill, Patricia D.  
; APPLICANT: Sutherland, R. Alec  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1  
; FILE REFERENCE: 210121.465C7  
; CURRENT APPLICATION NUMBER: US/10/125,635A  
; CURRENT FILING DATE: 2002-07-19  
; NUMBER OF SEQ ID NOS: 461  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 180  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-125-635A-180

Query Match 32.1%; Score 25; DB 4; Length 9;  
Best Local Similarity 44.4%; Pred. No. 1.7e+06;  
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 4 RDHNDYSKN 12  
| | | : |  
| | | : |  
Db 1 RHHNMHQRN 9

RESULT 95  
US-10-002-603-180  
; Sequence 180, Application US/10002603  
; Publication No. US20030095971A1  
; GENERAL INFORMATION:  
; APPLICANT: Gaiger, Alexander  
; APPLICANT: McNeill, Patricia D.  
; APPLICANT: Smithgall, Molly  
; APPLICANT: Moulton, Gus  
; APPLICANT: Vedvick, Thomas S.  
; APPLICANT: Sleath, Paul R.  
; APPLICANT: Mossman, Sally  
; APPLICANT: Evans, Lawrence  
; APPLICANT: Spies, A. Gregory  
; APPLICANT: Boydston, Jeremy  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1  
; FILE REFERENCE: 210121.465C6  
; CURRENT APPLICATION NUMBER: US/10/002,603  
; CURRENT FILING DATE: 2001-10-30  
; NUMBER OF SEQ ID NOS: 413  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 180  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-002-603-180

Query Match 32.1%; Score 25; DB 4; Length 9;  
Best Local Similarity 44.4%; Pred. No. 1.7e+06;  
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 4 RDHNDYSKN 12  
| | | : |  
| | | : |  
Db 1 RHHNMHQRN 9

RESULT 96  
US-10-195-835-180  
; Sequence 180, Application US/10195835  
; Publication No. US20030198622A1  
; GENERAL INFORMATION:  
; APPLICANT: Gaiger, Alexander  
; APPLICANT: Smithgall, Molly D.  
; APPLICANT: Carter, Darrick

```

/ APPLICANT: Cheever, Martin A.
/ APPLICANT: McNeill, Patricia D.
/ APPLICANT: Sutherland, R. Alec
/ APPLICANT: Moesman, Sally P.
/ APPLICANT: Evans, Lawrence S.
/ APPLICANT: Swanson, Ryan M.
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
/ FILE REFERENCE: 210121.465C8
/ CURRENT APPLICATION NUMBER: US/10/195.835
/ CURRENT FILING DATE: 2002-07-12
/ NUMBER OF SEQ ID NOS: 461
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 180
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Homo sapien
US-10-195-835-180

```

```

Query Match      32.1% Score 25; DB 4; Length 9;
Best Local Similarity 44.4%; Pred. No. 1.7e+06;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

```

```

QY      4 RDHNDYSK 12
      ||| : |
      1 RHHNMHQRN 9

```

```

RESULT 97
US-10-286-333-180
/ Sequence 180, Application US/10286333
/ Publication No. US20030215458A1
/ GENERAL INFORMATION:
/ APPLICANT: Gaiger, Alexander
/ APPLICANT: McNeill, Patricia D.
/ APPLICANT: Jaya, No. US20030215458A1a1e
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
/ FILE REFERENCE: 210121.465C10
/ CURRENT APPLICATION NUMBER: US/10/286.333
/ CURRENT FILING DATE: 2002-10-30
/ NUMBER OF SEQ ID NOS: 506
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 180
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Homo sapien
US-10-286-333-180

```

```

Query Match      32.1% Score 25; DB 4; Length 9;
Best Local Similarity 44.4%; Pred. No. 1.7e+06;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

```

```

QY      4 RDHNDYSK 12
      ||| : |
      1 RHHNMHQRN 9

```

```

RESULT 98
US-10-244-830-180
/ Sequence 180, Application US/10244830
/ Publication No. US20030235557A1
/ GENERAL INFORMATION:
/ APPLICANT: Gaiger, Alexander
/ APPLICANT: Cheever, Martin A.
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
/ FILE REFERENCE: 210121.465C9
/ CURRENT APPLICATION NUMBER: US/10/244.830
/ CURRENT FILING DATE: 2002-09-16
/ NUMBER OF SEQ ID NOS: 468
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 180

```

```

/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Homo sapien
US-10-244-830-180

```

```

Query Match      32.1% Score 25; DB 4; Length 9;
Best Local Similarity 44.4%; Pred. No. 1.7e+06;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

```

```

QY      4 RDHNDYSK 12
      ||| : |
      1 RHHNMHQRN 9

```

```

RESULT 99
US-10-427-717-180
/ Sequence 180, Application US/10427717
/ Publication No. US20040018204A1
/ GENERAL INFORMATION:
/ APPLICANT: Gaiger, Alexander
/ APPLICANT: McNeill, Patricia D.
/ APPLICANT: Jaya, No. US20040018204A1a1e
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
/ FILE REFERENCE: 210121.465C11
/ CURRENT APPLICATION NUMBER: US/10/427.717
/ CURRENT FILING DATE: 2003-04-30
/ NUMBER OF SEQ ID NOS: 508
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 180
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Homo sapien
US-10-427-717-180

```

```

Query Match      32.1% Score 25; DB 4; Length 9;
Best Local Similarity 44.4%; Pred. No. 1.7e+06;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

```

```

QY      4 RDHNDYSK 12
      ||| : |
      1 RHHNMHQRN 9

```

```

RESULT 100
US-10-363-791-11
/ Sequence 11, Application US/10363791
/ Publication No. US20040029197A1
/ GENERAL INFORMATION:
/ APPLICANT: TAKIMOTO, Masato
/ APPLICANT: KUZIMAKI, No. US20040029197A1i1yuki
/ APPLICANT: SATO, No. US20040029197A1i1yuki
/ APPLICANT: SAHARA, Hiroeki
/ TITLE OF INVENTION: A novel human cancer/testis-associated gene thereof
/ FILE REFERENCE: 4439-4006
/ CURRENT APPLICATION NUMBER: US/10/363.791
/ CURRENT FILING DATE: 2003-03-07
/ PRIOR APPLICATION NUMBER: JP 2000-274218
/ PRIOR FILING DATE: 2000-09-08
/ NUMBER OF SEQ ID NOS: 227
/ SOFTWARE: Patentin version 3.2
/ SEQ ID NO 11
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-363-791-11

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Query Match      32.1% Score 25; DB 4; Length 9;
Best Local Similarity 55.6%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

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```

QY      3 KRDNHYSK 11
      ||| : |

```

Db 1 KIDNDFIK 9

Search completed: January 20, 2006, 19:45:35  
Job time : 52.4808 secs

**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: January 20, 2006, 19:12:21 ; Search time 5.65385 Seconds

(without alignments)  
25.093 Million cell updates/sec

Title: US-09-662-293-1

Perfect score: 78

Sequence: 1 SIKRDHNDYSKNPM 14

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 70606 seqs, 10133881 residues

Total number of hits satisfying chosen parameters: 34662

Minimum DB seq length: 0

Maximum DB seq length: 20

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Published Applications AA New:\*

1: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*

2: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep:\*

3: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep:\*

4: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*

5: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep:\*

6: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep:\*

7: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep:\*

8: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30.5	20	6	US-10-485-788A-542	Sequence 542, App
2	33.3	9	7	US-11-033-039-459	Sequence 459, App
3	33.3	11	6	US-10-925-366A-90	Sequence 90, Appl
4	32.1	9	7	US-11-045-024-5857	Sequence 5857, App
5	32.1	14	6	US-10-467-657-8922	Sequence 8922, App
6	32.1	16	6	US-10-834-397-338	Sequence 238, App
7	32.1	18	7	US-11-033-039-1157	Sequence 1157, App
8	32.1	18	7	US-11-033-039-1180	Sequence 1180, App
9	32.1	18	7	US-11-033-039-1186	Sequence 1186, App
10	32.1	18	7	US-11-033-039-1206	Sequence 1206, App
11	32.1	20	6	US-10-485-788A-589	Sequence 589, App
12	32.1	20	7	US-11-023-562-128	Sequence 128, App
13	30.8	9	6	US-10-665-658-15	Sequence 15, Appl
14	30.8	9	6	US-10-665-658-56	Sequence 66, Appl
15	30.8	10	7	US-11-033-039-488	Sequence 88, Appl
16	30.8	11	7	US-11-045-024-427	Sequence 427, Appl
17	30.8	11	7	US-11-045-024-428	Sequence 428, App
18	30.8	11	7	US-11-045-024-5104	Sequence 5104, App
19	30.8	11	7	US-11-045-024-5105	Sequence 5105, App
20	30.8	11	7	US-11-045-024-8154	Sequence 8154, App
21	30.8	11	7	US-11-045-024-8155	Sequence 8155, App
22	30.8	11	7	US-11-045-024-10738	Sequence 10738, A
23	30.8	11	7	US-11-045-024-10739	Sequence 10739, A
24	30.8	11	7	US-11-045-024-12504	Sequence 12504, A
25	30.8	11	7	US-11-045-024-12505	Sequence 12505, A

26	30.8	12	7	US-11-058-727-104	Sequence 104, App
27	30.8	12	7	US-11-108-389-104	Sequence 104, App
28	30.8	12	7	US-11-069-834-28	Sequence 28, Appl
29	30.8	16	6	US-10-467-657-8683	Sequence 8683, App
30	30.8	16	7	US-11-054-515-2918	Sequence 2918, App
31	30.8	18	7	US-11-033-039-1169	Sequence 1169, App
32	30.8	18	7	US-11-033-039-1196	Sequence 1196, App
33	30.8	20	7	US-11-033-039-55	Sequence 55, Appl
34	29.5	10	7	US-11-057-708-32	Sequence 32, Appl
35	29.5	11	7	US-11-045-024-933	Sequence 933, App
36	29.5	14	7	US-11-054-315-3215	Sequence 315, App
37	29.5	15	7	US-11-106-932-106	Sequence 106, App
38	29.5	17	6	US-10-467-657-8975	Sequence 8975, App
39	28.8	20	7	US-11-094-142-31	Sequence 31, Appl
40	28.2	8	7	US-11-054-515-3179	Sequence 3179, App
41	28.2	10	6	US-10-859-643-628	Sequence 628, App
42	28.2	10	6	US-10-973-977-66	Sequence 66, Appl
43	28.2	10	7	US-11-097-864-628	Sequence 628, App
44	28.2	10	7	US-11-097-912-628	Sequence 628, App
45	28.2	12	7	US-11-058-727-105	Sequence 105, App
46	28.2	12	7	US-11-108-389-105	Sequence 105, App
47	28.2	13	6	US-10-511-559-554	Sequence 554, App
48	28.2	13	6	US-10-511-559-555	Sequence 555, App
49	28.2	14	7	US-11-116-144-258	Sequence 258, App
50	28.2	15	6	US-10-939-890-199	Sequence 199, App
51	28.2	15	7	US-11-045-024-13269	Sequence 13269, A
52	28.2	16	6	US-10-939-890-11	Sequence 11, Appl
53	28.2	16	6	US-10-939-890-205	Sequence 205, App
54	28.2	19	7	US-11-152-846-2	Sequence 2, Appl1
55	28.2	19	6	US-10-503-575-173	Sequence 173, App
56	26.9	7	7	US-11-129-104-12	Sequence 12, Appl
57	26.9	8	7	US-11-045-024-7497	Sequence 7497, App
58	26.9	8	7	US-11-045-024-8233	Sequence 8233, App
59	26.9	9	6	US-10-473-037-8	Sequence 8, Appl1
60	26.9	9	6	US-10-859-643-482	Sequence 482, App
61	26.9	9	7	US-11-021-441-102	Sequence 102, App
62	26.9	9	7	US-11-097-864-482	Sequence 482, App
63	26.9	9	7	US-11-097-912-482	Sequence 482, App
64	26.9	9	7	US-11-045-024-5858	Sequence 5858, App
65	26.9	9	7	US-11-041-893-66	Sequence 66, Appl
66	26.9	10	7	US-11-010-748A-522	Sequence 522, App
67	26.9	10	7	US-11-156-843-119	Sequence 119, App
68	26.9	10	7	US-11-129-104-54	Sequence 54, Appl
69	26.9	10	7	US-11-129-104-55	Sequence 55, Appl
70	26.9	11	7	US-11-156-843-30	Sequence 30, Appl
71	26.9	11	7	US-11-156-843-37	Sequence 37, Appl
72	26.9	11	7	US-11-127-877-88	Sequence 88, Appl
73	26.9	11	7	US-11-127-877-90	Sequence 90, Appl
74	26.9	12	7	US-11-110-274-321	Sequence 321, App
75	26.9	13	6	US-10-511-559-475	Sequence 475, App
76	26.9	13	6	US-10-511-559-476	Sequence 476, App
77	26.9	13	7	US-11-054-515-3172	Sequence 3172, App
78	26.9	13	7	US-11-054-515-3187	Sequence 3187, App
79	26.9	13	7	US-11-078-469-109	Sequence 109, App
80	26.9	13	7	US-11-078-469-111	Sequence 111, App
81	26.9	13	7	US-11-078-469-113	Sequence 113, App
82	26.9	13	7	US-11-078-469-117	Sequence 117, App
83	26.9	14	7	US-11-129-104-51	Sequence 51, Appl
84	26.9	14	6	US-10-989-326-52	Sequence 52, Appl
85	26.9	14	6	US-10-632-654-15	Sequence 15, Appl
86	26.9	14	7	US-11-054-515-3218	Sequence 3218, App
87	26.9	15	6	US-10-952-535A-29	Sequence 29, Appl
88	26.9	15	7	US-11-045-024-13379	Sequence 13379, A
89	26.9	16	7	US-11-108-185-39	Sequence 39, Appl
90	26.9	16	7	US-11-108-185-42	Sequence 42, Appl
91	26.9	16	7	US-11-108-185-67	Sequence 67, Appl
92	26.9	17	6	US-10-201-825-23	Sequence 23, Appl
93	26.9	17	7	US-11-038-880-165	Sequence 165, App
94	26.9	18	6	US-10-503-575-177	Sequence 177, Appl
95	26.9	18	6	US-10-485-788A-5536	Sequence 556, App
96	26.9	18	6	US-10-500-878-18	Sequence 18, Appl
97	26.9	18	7	US-11-033-039-1304	Sequence 1304, App
98	26.9	20	6	US-10-956-155A-5	Sequence 5, Appl1

99 21 26.9 20 7 US-11-054-515-2131  
100 21 26.9 20 7 US-11-078-469-55

Sequence 2131, Ap  
Sequence 55, Appl

## ALIGNMENTS

## RESULT 1

US-10-485-788A-542  
; Sequence 542, Application US/10485788A  
; Publication No. US20050282743A1  
; GENERAL INFORMATION:  
; APPLICANT: Lu, Peter S.  
; APPLICANT: Rabinowitz, Joshua D.  
; APPLICANT: Schweitzer, Johannes  
; APPLICANT: Carrick, Deanna Marie  
; APPLICANT: Arbor Vita Corporation  
; TITLE OF INVENTION: Molecular Interactions in Cells  
; FILE REFERENCE: 20054-003320US  
; CURRENT APPLICATION NUMBER: US/10/485,788A  
; CURRENT FILING DATE: 2004-02-03  
; PRIOR APPLICATION NUMBER: US 60/309,841  
; PRIOR FILING DATE: 2001-08-03  
; PRIOR APPLICATION NUMBER: US 60/360,061  
; PRIOR FILING DATE: 2002-02-25  
; PRIOR APPLICATION NUMBER: WO PCT/US02/24655  
; PRIOR FILING DATE: 2002-08-02  
; NUMBER OF SEQ ID NOS: 841  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 542  
; LENGTH: 20  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-485-788A-542

## Query Match

Best Local Similarity 38.5%; Score 30; DB 6; Length 20;  
Best Local Similarity 57.1%; Pred. No. 14;

Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 7 NDYSKXP 13

DB 9 NDETPNP 15

## RESULT 2

US-11-033-039-459  
; Sequence 459, Application US/11033039  
; Publication No. US20060002947A1  
; GENERAL INFORMATION:  
; APPLICANT: HUMPHREYS, ROBERT  
; APPLICANT: XU, MINZHEN  
; TITLE OF INVENTION: LI-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES  
; FILE REFERENCE: RSH-2011US01  
; CURRENT APPLICATION NUMBER: US/11/033,039  
; PRIOR FILING DATE: 2005-01-11  
; PRIOR APPLICATION NUMBER: 10/245,871  
; PRIOR FILING DATE: 2002-09-17  
; PRIOR APPLICATION NUMBER: 10/197,000  
; PRIOR FILING DATE: 2002-07-17  
; PRIOR APPLICATION NUMBER: 09/396,813  
; PRIOR FILING DATE: 1999-09-14  
; NUMBER OF SEQ ID NOS: 1452  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 459  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-033-039-459

Query Match 33.3%; Score 26; DB 7; Length 9;  
Best Local Similarity 71.4%; Pred. No. 5.5e+04;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 KRDPNDY 9  
DB 1 KRVPDPY 7

## RESULT 3

US-10-925-366A-90  
; Sequence 90, Application US/10925366A  
; Publication No. US20050271663A1  
; GENERAL INFORMATION:  
; APPLICANT: Ignatovich, Olga  
; APPLICANT: Demildt, Rudolph M.T.  
; APPLICANT: Benjamin, Woolven  
; APPLICANT: Grant, Steven  
; APPLICANT: Jones, Philip  
; APPLICANT: Basran, Amrik  
; APPLICANT: Brewis, Neil  
; TITLE OF INVENTION: Compositions and Methods for Treating Inflammatory Disorders  
; FILE REFERENCE: 8039/2105  
; CURRENT APPLICATION NUMBER: US/10/925,366A  
; CURRENT FILING DATE: 2004-08-24  
; PRIOR APPLICATION NUMBER: US 10/744,774  
; PRIOR FILING DATE: 2003-12-23  
; PRIOR APPLICATION NUMBER: PCT/GB2003/002804  
; PRIOR FILING DATE: 2003-06-30  
; PRIOR APPLICATION NUMBER: PCT/GB2002/03014  
; PRIOR FILING DATE: 2002-06-28  
; PRIOR APPLICATION NUMBER: GB 0230202.4  
; PRIOR FILING DATE: 2002-12-27  
; PRIOR APPLICATION NUMBER: GB 115841.9  
; PRIOR FILING DATE: 2001-06-28  
; PRIOR APPLICATION NUMBER: PCT/GB2004/002829  
; PRIOR FILING DATE: 2004-06-30  
; PRIOR APPLICATION NUMBER: US 60/535,076  
; PRIOR FILING DATE: 2004-01-08  
; PRIOR APPLICATION NUMBER: PCT/GB2003/005646  
; PRIOR FILING DATE: 2003-12-24  
; PRIOR APPLICATION NUMBER: GB 0327706.8  
; PRIOR FILING DATE: 2003-11-28  
; PRIOR APPLICATION NUMBER: US 60/509,613  
; PRIOR FILING DATE: 2003-10-08  
; NUMBER OF SEQ ID NOS: 368  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 90  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Artificial CDR3 sequence  
US-10-925-366A-90

Query Match 33.3%; Score 26; DB 6; Length 11;  
Best Local Similarity 60.0%; Pred. No. 35;  
Matches 6; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

QY 4 RDNH---DY 9  
DB 2 RDNHSLFDY 11

## RESULT 4

US-11-045-024-5857  
; Sequence 5857, Application US/11045024  
; Publication No. US20050271676A1  
; GENERAL INFORMATION:  
; APPLICANT: Sette, Alessandro  
; APPLICANT: Sidney, John  
; APPLICANT: Southwood, Scott  
; APPLICANT: Livingston, Brian  
; APPLICANT: Chesnut, Robert  
; APPLICANT: Baker, Denise Marie  
; APPLICANT: Celis, Eteban  
; APPLICANT: Kubo, Ralph



```
APPLICANT: Grey, Howard M.
APPLICANT: Bplimmune Inc.
TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
FILE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
FILE REFERENCE: 2060.0040007
CURRENT APPLICATION NUMBER: US/11/045,024
CURRENT FILING DATE: 2005-01-28
PRIOR APPLICATION NUMBER: US 09/412,863
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: US 08/027,146
PRIOR FILING DATE: 1993-03-05
PRIOR APPLICATION NUMBER: US 08/073,205
PRIOR FILING DATE: 1993-06-04
PRIOR APPLICATION NUMBER: US 08/103,396
PRIOR FILING DATE: 1993-08-06
PRIOR APPLICATION NUMBER: US 08/159,184
PRIOR FILING DATE: 1993-11-29
PRIOR APPLICATION NUMBER: US 08/159,339
PRIOR FILING DATE: 1993-11-29
PRIOR APPLICATION NUMBER: US 08/205,713
PRIOR FILING DATE: 1994-03-04
PRIOR APPLICATION NUMBER: US 08/347,610
PRIOR FILING DATE: 1994-12-01
NUMBER OF SEQ ID NOS: 14528
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5857
LENGTH: 9
TYPE: PRT
ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-5857
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```
Query Match 32.1% Score 25; DB 7; Length 9;
Best Local Similarity 50.0%; Pred. No. 5.5e+04;
Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
Qy 5 DHNDYSKN 12
Db 1 DHEKHSN 8
```

```
RESULT 5
US-10-467-657-8922
Sequence 8922, Application US/10467657
Publication No. US20050260581A1
GENERAL INFORMATION:
APPLICANT: CHIRON SPA
APPLICANT: FONTANA Maria Rita
APPLICANT: PIZZA Mariagrazia
APPLICANT: MASTIGNANI Vega
APPLICANT: MONACI Elisabetta
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/467,657
CURRENT FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: GB-0103424.8
PRIOR FILING DATE: 2001-02-12
NUMBER OF SEQ ID NOS: 9218
SOFTWARE: Seqwin99, version 1.04
SEQ ID NO 8922
LENGTH: 14
TYPE: PRT
ORGANISM: Neisseria gonorrhoeae
US-10-467-657-8922
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```
Query Match 32.1% Score 25; DB 6; Length 14;
Best Local Similarity 66.7%; Pred. No. 69;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy 6 HNDYK 11
Db 4 HNSYK 9
```

```
RESULT 6
US-10-834-397-238
Sequence 238, Application US/10834397
Publication No. US2006000334A1
GENERAL INFORMATION:
```

APPLICANT: Knappik, Achim

Pack, Peter

Ilaq, Yic

Ge, Liming

Moroney, Simon

Plueckhuhn, Andreas

TITLE OF INVENTION: Protein/(Poly)peptide libraries

NUMBER OF SEQUENCES: 373

CORRESPONDENCE ADDRESS:

ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave

STREET: 1251 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10021

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/834,397

FILING DATE: 29-Apr-2004

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/490,324

FILING DATE: 24-Jan-2000

APPLICATION NUMBER: US/09/025,769

FILING DATE: 18-FEB-1998

APPLICATION NUMBER: EP 95 11 3021.0

FILING DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:

NAME: James F. Haley, Jr., Esq.

REGISTRATION NUMBER: 27,794

REFERENCE/DOCKET NUMBER: MORPHO/5

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212)596-9000

TELEFAX: (212)596-9090

INFORMATION FOR SEQ ID NO: 238:

SEQUENCE CHARACTERISTICS:

LENGTH: 16 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: linear

MOLECULE TYPE: protein

FRAGMENT TYPE: internal

SEQUENCE DESCRIPTION: SEQ ID NO: 238:

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US-10-834-397-238
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Query Match 32.1% Score 25; DB 6; Length 16;
Best Local Similarity 54.5%; Pred. No. 80;
Matches 6; Conservative 1; Mismatches 2; Indels 2; Gaps 1;
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```
Qy 4 RDHNDYSKNPM 14
Db 5 RDNFSY--DFM 13
```

```
RESULT 7
US-11-033-039-1157
```

Sequence 1157, Application US/11033039

Publication No. US20060002947A1

GENERAL INFORMATION:

APPLICANT: HUMPHREYS, ROBERT

APPLICANT: XU, MINZHEN

TITLE OF INVENTION: LI-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES

FILE REFERENCE: RH-2017US01

CURRENT APPLICATION NUMBER: US/11/033,039

CURRENT FILING DATE: 2005-01-11

```
/ PRIOR APPLICATION NUMBER: 10/245,871
/ PRIOR FILING DATE: 2002-09-17
/ PRIOR APPLICATION NUMBER: 10/197,000
/ PRIOR FILING DATE: 2002-07-17
/ PRIOR APPLICATION NUMBER: 09/396,813
/ PRIOR FILING DATE: 1999-09-14
/ NUMBER OF SEQ ID NOS: 1452
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 1157
/ LENGTH: 18
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic
/ OTHER INFORMATION: hybrid peptide
/ FEATURE:
/ NAME/KEY: MOD_RES
/ LOCATION: (5)..(5)
/ OTHER INFORMATION: Ava
US-11-033-039-1157
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Query Match      32.1%; Score 25; DB 7; Length 18;
Best Local Similarity 57.1%; Pred. No. 91;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
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```
QY      5 DHNDYSK 11
      | | | | :
Db      7 DFNDYEE 13
```

```
RESULT 8
US-11-033-039-1180
/ Sequence 1180, Application US/11033039
/ Publication No. US20060002947A1
/ GENERAL INFORMATION:
/ APPLICANT: HUMPHREYS, ROBERT
/ TITLE OF INVENTION: LI-KEY/ANTIGENIC EPIOTOPE HYBRID PEPTIDE VACCINES
/ FILE REFERENCE: REH-2017US01
/ CURRENT APPLICATION NUMBER: US/11/033,039
/ CURRENT FILING DATE: 2005-01-11
/ PRIOR APPLICATION NUMBER: 10/245,871
/ PRIOR FILING DATE: 2002-09-17
/ PRIOR APPLICATION NUMBER: 10/197,000
/ PRIOR FILING DATE: 2002-07-17
/ PRIOR APPLICATION NUMBER: 09/396,813
/ PRIOR FILING DATE: 1999-09-14
/ NUMBER OF SEQ ID NOS: 1452
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 1180
/ LENGTH: 18
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic
/ OTHER INFORMATION: hybrid peptide
/ FEATURE:
/ NAME/KEY: MOD_RES
/ LOCATION: (5)..(5)
/ OTHER INFORMATION: Ava
US-11-033-039-1180
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```
Query Match      32.1%; Score 25; DB 7; Length 18;
Best Local Similarity 57.1%; Pred. No. 91;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
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```
QY      5 DHNDYSK 11
      | | | | :
Db      10 DFNDYEE 16
```

```
RESULT 9
US-11-033-039-1186
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/ Sequence 1186, Application US/11033039
/ Publication No. US20060002947A1
/ GENERAL INFORMATION:
/ APPLICANT: HUMPHREYS, ROBERT
/ TITLE OF INVENTION: LI-KEY/ANTIGENIC EPIOTOPE HYBRID PEPTIDE VACCINES
/ FILE REFERENCE: REH-2017US01
/ CURRENT APPLICATION NUMBER: US/11/033,039
/ CURRENT FILING DATE: 2005-01-11
/ PRIOR APPLICATION NUMBER: 10/245,871
/ PRIOR FILING DATE: 2002-09-17
/ PRIOR APPLICATION NUMBER: 10/197,000
/ PRIOR FILING DATE: 2002-07-17
/ PRIOR APPLICATION NUMBER: 09/396,813
/ PRIOR FILING DATE: 1999-09-14
/ NUMBER OF SEQ ID NOS: 1452
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 1186
/ LENGTH: 18
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic
/ OTHER INFORMATION: hybrid peptide
/ FEATURE:
/ NAME/KEY: MOD_RES
/ LOCATION: (5)..(5)
/ OTHER INFORMATION: Ava
US-11-033-039-1186
```

```
Query Match      32.1%; Score 25; DB 7; Length 18;
Best Local Similarity 57.1%; Pred. No. 91;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      5 DHNDYSK 11
      | | | | :
Db      7 DFNDYEE 13
```

```
RESULT 10
US-11-033-039-1206
/ Sequence 1206, Application US/11033039
/ Publication No. US20060002947A1
/ GENERAL INFORMATION:
/ APPLICANT: HUMPHREYS, ROBERT
/ TITLE OF INVENTION: LI-KEY/ANTIGENIC EPIOTOPE HYBRID PEPTIDE VACCINES
/ FILE REFERENCE: REH-2017US01
/ CURRENT APPLICATION NUMBER: US/11/033,039
/ CURRENT FILING DATE: 2005-01-11
/ PRIOR APPLICATION NUMBER: 10/245,871
/ PRIOR FILING DATE: 2002-09-17
/ PRIOR APPLICATION NUMBER: 10/197,000
/ PRIOR FILING DATE: 2002-07-17
/ PRIOR APPLICATION NUMBER: 09/396,813
/ PRIOR FILING DATE: 1999-09-14
/ NUMBER OF SEQ ID NOS: 1452
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 1206
/ LENGTH: 18
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic
/ OTHER INFORMATION: hybrid peptide
/ FEATURE:
/ NAME/KEY: MOD_RES
/ LOCATION: (5)..(5)
/ OTHER INFORMATION: Ava
US-11-033-039-1206
```

```
Query Match      32.1%; Score 25; DB 7; Length 18;
Best Local Similarity 57.1%; Pred. No. 91;
```

Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
Qy 5 DHNDYSK 11  
Db 10 DFNDYER 16

## RESULT 11

US-10-485-788A-589  
; Sequence 589, Application US/10485788A  
; Publication No. US20050282743A1  
; GENERAL INFORMATION:  
; APPLICANT: Lu, Peter S.  
; APPLICANT: Rabinowitz, Joshua D.  
; APPLICANT: Schmeizler, Johannes  
; APPLICANT: Carrick, Deanna Marie  
; APPLICANT: Arbor Vita Corporation  
; TITLE OF INVENTION: Molecular Interactions in Cells  
; FILE REFERENCE: 20054-003320US  
; CURRENT APPLICATION NUMBER: US/10/485,788A  
; CURRENT FILING DATE: 2004-02-03  
; PRIOR APPLICATION NUMBER: US 60/309,841  
; PRIOR FILING DATE: 2001-08-03  
; PRIOR APPLICATION NUMBER: US 60/360,061  
; PRIOR FILING DATE: 2002-02-25  
; PRIOR APPLICATION NUMBER: NO PCT/US02/24655  
; NUMBER OF SEQ ID NOS: 841  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 589  
; LENGTH: 20  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-485-788A-589

Query Match 32.1%; Score 25; DB 6; Length 20;  
Best Local Similarity 44.4%; Pred. No. 1e+02;  
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 IKRDNDYS 10  
Db 7 VKSEFNSYS 15

RESULT 12  
US-11-022-562-128  
; Sequence 128, Application US/11022562  
; Publication No. US20050249742A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruprecht, Ruth M.  
; APPLICANT: Shisong, JIANG  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING  
; FILE REFERENCE: DFN-043CN  
; CURRENT APPLICATION NUMBER: US/11/022,562  
; PRIOR APPLICATION NUMBER: PCT/US03/20322  
; PRIOR FILING DATE: 2003-06-27  
; PRIOR APPLICATION NUMBER: 60/392718  
; PRIOR FILING DATE: 2002-06-27  
; NUMBER OF SEQ ID NOS: 340  
; SOFTWARE: PatsSeq for Windows Version 4.0  
; SEQ ID NO 128  
; LENGTH: 20  
; TYPE: PRT  
; ORGANISM: Simian Immunodeficiency Virus  
US-11-022-562-128

Query Match 32.1%; Score 25; DB 7; Length 20;  
Best Local Similarity 57.1%; Pred. No. 1e+02;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
Qy 5 DHNDYSK 11

Db 10 DNGDYER 16

RESULT 13  
US-10-665-658-15  
; Sequence 15, Application US/10665658  
; Publication No. US20050276801A1  
; GENERAL INFORMATION:  
; APPLICANT: Jardieu, Paula M.  
; APPLICANT: Presta, Leonard G.  
; TITLE OF INVENTION: Humanized Anti-CD11a Antibodies  
; NUMBER OF SEQUENCES: 71  
; CORRESPONDENCE ADDRESS:  
; ADDRESSER: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/665,658  
; FILING DATE: 19-Sep-2003  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/031971  
; FILING DATE: 27-NOV-1996  
; APPLICATION NUMBER: 08/974899  
; FILING DATE: 20-NOV-1997  
; APPLICATION NUMBER: 09/420745  
; FILING DATE: 20-OCT-1999  
; APPLICATION NUMBER: 09/975798  
; FILING DATE: 28-FEB-2001  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Tan, Lee K.  
; REGISTRATION NUMBER: 39,447  
; REFERENCE/DOCKET NUMBER: P1014R1C1D1C1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-4462  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 15:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
; SEQUENCE DESCRIPTION: SEQ ID NO: 15:  
US-10-665-658-15

Query Match 30.8%; Score 24; DB 6; Length 9;  
Best Local Similarity 50.0%; Pred. No. 5.5e+04;  
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
Qy 4 RDNDY 9  
Db 1 QCHNEY 6

RESULT 14  
US-10-665-658-66  
; Sequence 66, Application US/10665658  
; Publication No. US20050276801A1  
; GENERAL INFORMATION:  
; APPLICANT: Jardieu, Paula M.  
; APPLICANT: Presta, Leonard G.  
; TITLE OF INVENTION: Humanized Anti-CD11a Antibodies  
; NUMBER OF SEQUENCES: 71  
; CORRESPONDENCE ADDRESS:  
; ADDRESSER: Genentech, Inc.

```
/ STREET: 1 DNA Way
/ CITY: South San Francisco
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94080
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 3.5 inch, 1.44 mb floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Winpatin (Genentech)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/665,658
/ FILING DATE: 19-Sep-2003
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 60/031971
/ FILING DATE: 27-NOV-1996
/ APPLICATION NUMBER: 08/974899
/ FILING DATE: 20-NOV-1997
/ APPLICATION NUMBER: 09/420745
/ FILING DATE: 20-OCT-1999
/ APPLICATION NUMBER: 09/975798
/ FILING DATE: 28-FEB-2001
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Tan, Lee K.
/ REGISTRATION NUMBER: 39,447
/ REFERENCE/DOCKET NUMBER: P1014R1C1D1C1
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 650/225-4462
/ TELEFAX: 650/952-9881
/ INFORMATION FOR SEQ ID NO: 66:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 9 amino acids
/ TYPE: Amino Acid
/ TOPOLOGY: <Unknown>
/ SEQUENCE DESCRIPTION: SEQ ID NO: 66:
US-10-665-658-66

Query Match      30.8%; Score 24; DB 6; Length 9;
Best Local Similarity 50.0%; Pred. No. 5.5e+04;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      4 RDHNDY 9
       : ||:|
Db      1 QQHNEY 6

RESULT 15
US-11-033-039-88
/ Sequence 88, Application US/11033039
/ Publication No. US20060002947A1
/ GENERAL INFORMATION:
/ APPLICANT: HUMPHREYS, ROBERT
/ APPLICANT: XU, MINZHEN
/ TITLE OF INVENTION: LI-KEY/ANTIGENIC EPIOTOPE HYBRID PEPTIDE VACCINES
/ FILE REFERENCE: REH-2017US01
/ CURRENT APPLICATION NUMBER: US/11/033,039
/ PRIOR APPLICATION NUMBER: 2005-01-11
/ PRIOR FILING DATE: 2002-09-17
/ PRIOR APPLICATION NUMBER: 10/245,871
/ PRIOR FILING DATE: 2002-09-17
/ PRIOR APPLICATION NUMBER: 10/197,000
/ PRIOR FILING DATE: 2002-07-17
/ PRIOR APPLICATION NUMBER: 09/336,813
/ PRIOR FILING DATE: 1999-09-14
/ NUMBER OF SEQ ID NOS: 1452
/ SOFTWARE: Patentin version 3.3
/ SEQ ID NO 88
/ LENGTH: 10
/ TYPE: PRT
/ ORGANISM: Arachis hypogaea
US-11-033-039-88

Query Match      30.8%; Score 24; DB 7; Length 10;
```

```
Best Local Similarity 50.0%; Pred. No. 70;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      2 IRRDNDY 9
       : ||:|
Db      2 IORDSDY 9

RESULT 16
US-11-045-024-427
/ Sequence 427, Application US/11045024
/ Publication No. US20050271676A1
/ GENERAL INFORMATION:
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Livingston, Brian
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Baker, Denise Marie
/ APPLICANT: Cells, Esteban
/ APPLICANT: Kubo, Ralph
/ APPLICANT: Grey, Howard M.
/ TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
/ FILE REFERENCE: 2060,0040007
/ CURRENT APPLICATION NUMBER: US/11/045,024
/ PRIOR FILING DATE: 2005-01-28
/ PRIOR APPLICATION NUMBER: US 09/412,863
/ PRIOR FILING DATE: 1999-10-05
/ PRIOR APPLICATION NUMBER: US 08/027,146
/ PRIOR FILING DATE: 1993-03-05
/ PRIOR APPLICATION NUMBER: US 08/073,205
/ PRIOR FILING DATE: 1993-06-04
/ PRIOR APPLICATION NUMBER: US 08/103,396
/ PRIOR FILING DATE: 1993-08-06
/ PRIOR APPLICATION NUMBER: US 08/159,184
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/159,339
/ PRIOR FILING DATE: 1994-03-04
/ PRIOR APPLICATION NUMBER: US 08/205,713
/ PRIOR FILING DATE: 1994-12-01
/ PRIOR APPLICATION NUMBER: US 08/347,610
/ NUMBER OF SEQ ID NOS: 14528
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 427
/ LENGTH: 11
/ TYPE: PRT
/ ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-427

Query Match      30.8%; Score 24; DB 7; Length 11;
Best Local Similarity 66.7%; Pred. No. 78;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      4 RDHNDY 9
       : ||:|
Db      6 RDDSXY 11

RESULT 17
US-11-045-024-428
/ Sequence 428, Application US/11045024
/ Publication No. US20050271676A1
/ GENERAL INFORMATION:
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Livingston, Brian
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Baker, Denise Marie
/ APPLICANT: Cells, Esteban
```

```
APPLICANT: Kubo, Ralph
APPLICANT: Grey, Howard M.
TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
FILE REFERENCE: 2060.0040007
CURRENT APPLICATION NUMBER: US/11/045,024
PRIOR APPLICATION NUMBER: US 09/412,863
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: US 08/027,146
PRIOR FILING DATE: 1993-03-05
PRIOR APPLICATION NUMBER: US 08/073,205
PRIOR FILING DATE: 1993-06-04
PRIOR APPLICATION NUMBER: US 08/103,396
PRIOR FILING DATE: 1993-08-06
PRIOR APPLICATION NUMBER: US 08/159,184
PRIOR FILING DATE: 1993-11-29
PRIOR APPLICATION NUMBER: US 08/159,339
PRIOR FILING DATE: 1993-11-29
PRIOR APPLICATION NUMBER: US 08/205,713
PRIOR FILING DATE: 1994-03-04
PRIOR APPLICATION NUMBER: US 08/347,610
PRIOR FILING DATE: 1994-12-01
NUMBER OF SEQ ID NOS: 14528
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 428
LENGTH: 11
TYPE: PRT
ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-428
```

```
Query Match 30.8% Score 24; DB 7; Length 11;
Best Local Similarity 66.7% Pred. No. 78;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
Oy 4 RDHNDY 9
||:|
Db 6 RDSDSY 11
```

```
RESULT 18
US-11-045-024-5104
Sequence 5104, Application US/11045024
Publication No. US20050271676A1
GENERAL INFORMATION:
APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
APPLICANT: Livingston, Brian
APPLICANT: Chesnut, Robert
APPLICANT: Baker, Denise Marie
APPLICANT: Cells, Esteban
APPLICANT: Kubo, Ralph
APPLICANT: Grey, Howard M.
APPLICANT: EpiImmune Inc.
TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
FILE REFERENCE: 2060.0040007
CURRENT APPLICATION NUMBER: US/11/045,024
PRIOR APPLICATION NUMBER: US 09/412,863
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: US 08/027,146
PRIOR FILING DATE: 1993-03-05
PRIOR APPLICATION NUMBER: US 08/073,205
PRIOR FILING DATE: 1993-06-04
PRIOR APPLICATION NUMBER: US 08/103,396
PRIOR FILING DATE: 1993-08-06
PRIOR APPLICATION NUMBER: US 08/159,184
PRIOR FILING DATE: 1993-11-29
PRIOR APPLICATION NUMBER: US 08/159,339
PRIOR FILING DATE: 1993-11-29
```

```
PRIOR APPLICATION NUMBER: US 08/205,713
PRIOR FILING DATE: 1994-03-04
PRIOR APPLICATION NUMBER: US 08/347,610
PRIOR FILING DATE: 1994-12-01
NUMBER OF SEQ ID NOS: 14528
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5104
LENGTH: 11
TYPE: PRT
ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-5104
```

```
Query Match 30.8% Score 24; DB 7; Length 11;
Best Local Similarity 66.7% Pred. No. 78;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
Oy 4 RDHNDY 9
||:|
Db 6 RDSDSY 11
```

```
RESULT 19
US-11-045-024-5105
Sequence 5105, Application US/11045024
Publication No. US20050271676A1
GENERAL INFORMATION:
APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
APPLICANT: Livingston, Brian
APPLICANT: Chesnut, Robert
APPLICANT: Baker, Denise Marie
APPLICANT: Cells, Esteban
APPLICANT: Kubo, Ralph
APPLICANT: Grey, Howard M.
APPLICANT: EpiImmune Inc.
TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
FILE REFERENCE: 2060.0040007
CURRENT APPLICATION NUMBER: US/11/045,024
PRIOR APPLICATION NUMBER: US 09/412,863
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: US 08/027,146
PRIOR FILING DATE: 1993-03-05
PRIOR APPLICATION NUMBER: US 08/073,205
PRIOR FILING DATE: 1993-06-04
PRIOR APPLICATION NUMBER: US 08/103,396
PRIOR FILING DATE: 1993-08-06
PRIOR APPLICATION NUMBER: US 08/159,184
PRIOR FILING DATE: 1993-11-29
PRIOR APPLICATION NUMBER: US 08/159,339
PRIOR FILING DATE: 1994-03-04
PRIOR APPLICATION NUMBER: US 08/347,610
PRIOR FILING DATE: 1994-12-01
NUMBER OF SEQ ID NOS: 14528
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5105
LENGTH: 11
TYPE: PRT
ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-5105
```

```
Query Match 30.8% Score 24; DB 7; Length 11;
Best Local Similarity 66.7% Pred. No. 78;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
Oy 4 RDHNDY 9
||:|
Db 6 RDSDSY 11
```

```
RESULT 20
US-11-045-024-8154
; Sequence 8154, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: Eplimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; PRIOR FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8154
; LENGTH: 11
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-8154

Query Match          30.8%; Score 24; DB 7; Length 11;
Best Local Similarity 66.7%; Pred. No. 78;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 RDNDY 9
Db 6 RDSDY 11

RESULT 21
US-11-045-024-8155
; Sequence 8155, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: Eplimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
```

```
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8155
; LENGTH: 11
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-8155

Query Match          30.8%; Score 24; DB 7; Length 11;
Best Local Similarity 66.7%; Pred. No. 78;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 RDNDY 9
Db 6 RDSDY 11

RESULT 22
US-11-045-024-10738
; Sequence 10738, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: Eplimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10738
```

```

: LENGTH: 11
: TYPE: PRT
: ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-10738

Query Match      30.8%; Score 24; DB 7; Length 11;
Best Local Similarity 66.7%; Pred. No. 78;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      4 RDNDY 9
      ||:|
Db      6 RDDSdy 11

RESULT 23
US-11-045-024-10739
: Sequence 10739, Application US/11045024
: Publication No. US20050271676A1
: GENERAL INFORMATION:
: APPLICANT: Sette, Alessandro
: APPLICANT: Sidney, John
: APPLICANT: Southwood, Scott
: APPLICANT: Livingston, Brian
: APPLICANT: Chesnut, Robert
: APPLICANT: Baker, Denise Marie
: APPLICANT: Celis, Basteen
: APPLICANT: Kubo, Ralph
: APPLICANT: Grey, Howard M.
: APPLICANT: Eptimmune Inc.
: TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
: TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
: FILE REFERENCE: 2060.0040007
: CURRENT APPLICATION NUMBER: US/11/045,024
: CURRENT FILING DATE: 2005-01-28
: PRIOR APPLICATION NUMBER: US 09/412,863
: PRIOR FILING DATE: 1999-10-05
: PRIOR APPLICATION NUMBER: US 08/027,146
: PRIOR FILING DATE: 1993-03-05
: PRIOR APPLICATION NUMBER: US 08/073,205
: PRIOR FILING DATE: 1993-06-04
: PRIOR APPLICATION NUMBER: US 08/103,396
: PRIOR FILING DATE: 1993-08-06
: PRIOR APPLICATION NUMBER: US 08/159,184
: PRIOR FILING DATE: 1993-11-29
: PRIOR APPLICATION NUMBER: US 08/159,339
: PRIOR FILING DATE: 1993-11-29
: PRIOR APPLICATION NUMBER: US 08/205,713
: PRIOR FILING DATE: 1994-03-04
: PRIOR APPLICATION NUMBER: US 08/347,610
: PRIOR FILING DATE: 1994-12-01
: NUMBER OF SEQ ID NOS: 14528
: SOFTWARE: PaSeq for Windows Version 4.0
: SEQ ID NO 10739
: LENGTH: 11
: TYPE: PRT
: ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-10739

Query Match      30.8%; Score 24; DB 7; Length 11;
Best Local Similarity 66.7%; Pred. No. 78;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      4 RDNDY 9
      ||:|
Db      6 RDDSdy 11

RESULT 24
US-11-045-024-12504
: Sequence 12504, Application US/11045024
: Publication No. US20050271676A1
: GENERAL INFORMATION:
: APPLICANT: Sette, Alessandro
```

```

: APPLICANT: Sidney, John
: APPLICANT: Southwood, Scott
: APPLICANT: Livingston, Brian
: APPLICANT: Chesnut, Robert
: APPLICANT: Baker, Denise Marie
: APPLICANT: Celis, Basteen
: APPLICANT: Kubo, Ralph
: APPLICANT: Grey, Howard M.
: APPLICANT: Eptimmune Inc.
: TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
: TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
: FILE REFERENCE: 2060.0040007
: CURRENT APPLICATION NUMBER: US/11/045,024
: CURRENT FILING DATE: 2005-01-28
: PRIOR APPLICATION NUMBER: US 09/412,863
: PRIOR FILING DATE: 1999-10-05
: PRIOR APPLICATION NUMBER: US 08/027,146
: PRIOR FILING DATE: 1993-03-05
: PRIOR APPLICATION NUMBER: US 08/073,205
: PRIOR FILING DATE: 1993-06-04
: PRIOR APPLICATION NUMBER: US 08/103,396
: PRIOR FILING DATE: 1993-08-06
: PRIOR APPLICATION NUMBER: US 08/159,184
: PRIOR FILING DATE: 1993-11-29
: PRIOR APPLICATION NUMBER: US 08/159,339
: PRIOR FILING DATE: 1993-11-29
: PRIOR APPLICATION NUMBER: US 08/205,713
: PRIOR FILING DATE: 1994-03-04
: PRIOR APPLICATION NUMBER: US 08/347,610
: PRIOR FILING DATE: 1994-12-01
: NUMBER OF SEQ ID NOS: 14528
: SOFTWARE: PaSeq for Windows Version 4.0
: SEQ ID NO 12504
: LENGTH: 11
: TYPE: PRT
: ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-12504

Query Match      30.8%; Score 24; DB 7; Length 11;
Best Local Similarity 66.7%; Pred. No. 78;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      4 RDNDY 9
      ||:|
Db      6 RDDSdy 11

RESULT 25
US-11-045-024-12505
: Sequence 12505, Application US/11045024
: Publication No. US20050271676A1
: GENERAL INFORMATION:
: APPLICANT: Sette, Alessandro
: APPLICANT: Sidney, John
: APPLICANT: Southwood, Scott
: APPLICANT: Livingston, Brian
: APPLICANT: Chesnut, Robert
: APPLICANT: Baker, Denise Marie
: APPLICANT: Celis, Basteen
: APPLICANT: Kubo, Ralph
: APPLICANT: Grey, Howard M.
: APPLICANT: Eptimmune Inc.
: TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
: TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
: FILE REFERENCE: 2060.0040007
: CURRENT APPLICATION NUMBER: US/11/045,024
: CURRENT FILING DATE: 2005-01-28
: PRIOR APPLICATION NUMBER: US 09/412,863
: PRIOR FILING DATE: 1999-10-05
: PRIOR APPLICATION NUMBER: US 08/027,146
: PRIOR FILING DATE: 1993-03-05
: PRIOR APPLICATION NUMBER: US 08/073,205
: PRIOR FILING DATE: 1993-06-04
```

```
/ PRIOR APPLICATION NUMBER: US 08/103,396
/ PRIOR FILING DATE: 1993-08-06
/ PRIOR APPLICATION NUMBER: US 08/159,184
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/159,339
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/205,713
/ PRIOR FILING DATE: 1994-03-04
/ PRIOR APPLICATION NUMBER: US 08/347,610
/ PRIOR FILING DATE: 1994-12-01
/ NUMBER OF SEQ ID NOS: 14528
/ SOFTWARE: FaastSeq for Windows Version 4.0
/ SEQ ID NO 12505
/ LENGTH: 11
/ TYPE: PRT
/ ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-12505
```

```
Query Match          30.8%; Score 24; DB 7; Length 11;
Best Local Similarity 66.7%; Pred. No. 78;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 4 RDNDYK 9
    | | |
    | | |
Db 6 RDDSDY 11
```

```
RESULT 26
US-11-058-727-104
/ Sequence 104, Application US/11058727
/ Publication No. US20050261483A1
/ GENERAL INFORMATION:
/ APPLICANT: Andre R. Abad
/ APPLICANT: Ronald D. Flannagan
/ APPLICANT: Rafael Herrmann
/ APPLICANT: Theodore W. Kahn
/ APPLICANT: Albert L. Lu
/ APPLICANT: Billy Fred McCutchen
/ APPLICANT: James K. Presnall
/ APPLICANT: James F.H. Wong
/ APPLICANT: Cao-Guo Yu
/ TITLE OF INVENTION: Genes Encoding Proteins with Pesticidal
/ FILE REFERENCE: 35718/287809
/ CURRENT APPLICATION NUMBER: US/11/058,727
/ PRIOR FILING DATE: 2005-02-15
/ PRIOR APPLICATION NUMBER: 60/391,786
/ PRIOR FILING DATE: 2002-06-26
/ PRIOR APPLICATION NUMBER: 60/460,787
/ PRIOR FILING DATE: 2003-04-04
/ PRIOR APPLICATION NUMBER: 10/606,320
/ PRIOR FILING DATE: 2003-06-25
/ NUMBER OF SEQ ID NOS: 134
/ SOFTWARE: FaastSeq for Windows Version 4.0
/ SEQ ID NO 104
/ LENGTH: 12
/ TYPE: PRT
/ ORGANISM: Bacillus thuringiensis
US-11-058-727-104
```

```
Query Match          30.8%; Score 24; DB 7; Length 12;
Best Local Similarity 57.1%; Pred. No. 86;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 5 DHNDYSK 11
    | | |
    | | |
Db 1 DYKDYLK 7
```

```
RESULT 27
US-11-108-389-104
/ Sequence 104, Application US/11108389
/ Publication No. US20050261188A1
```

```
/ GENERAL INFORMATION:
/ APPLICANT: Andre R. Abad
/ APPLICANT: Ronald D. Flannagan
/ APPLICANT: Rafael Herrmann
/ APPLICANT: Theodore W. Kahn
/ APPLICANT: Albert L. Lu
/ APPLICANT: Billy Fred McCutchen
/ APPLICANT: James K. Presnall
/ APPLICANT: James F.H. Wong
/ APPLICANT: Cao-Guo Yu
/ TITLE OF INVENTION: Genes Encoding Proteins with Pesticidal
/ FILE REFERENCE: 35718/291049
/ CURRENT APPLICATION NUMBER: US/11/108,389
/ PRIOR FILING DATE: 2005-04-18
/ PRIOR APPLICATION NUMBER: 60/391,786
/ PRIOR FILING DATE: 2002-06-26
/ PRIOR APPLICATION NUMBER: 60/460,787
/ PRIOR FILING DATE: 2003-04-04
/ PRIOR APPLICATION NUMBER: 10/606,320
/ PRIOR FILING DATE: 2003-06-25
/ NUMBER OF SEQ ID NOS: 134
/ SOFTWARE: FaastSeq for Windows Version 4.0
/ SEQ ID NO 104
/ LENGTH: 12
/ TYPE: PRT
/ ORGANISM: Bacillus thuringiensis
US-11-108-389-104
```

```
Query Match          30.8%; Score 24; DB 7; Length 12;
Best Local Similarity 57.1%; Pred. No. 86;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 5 DHNDYSK 11
    | | |
    | | |
Db 1 DYKDYLK 7
```

```
RESULT 28
US-11-069-834-28
/ Sequence 28, Application US/11069834
/ Publication No. US20050276811A1
/ GENERAL INFORMATION:
/ APPLICANT: CARROLL, MICHAEL C.
/ APPLICANT: MOORE JR., FRANCIS D.
/ APPLICANT: HECHTMAN, HERBERT B.
/ TITLE OF INVENTION: NATURAL IGM ANTIBODIES AND INHIBITORS THEREOF
/ FILE REFERENCE: CRA-002.01
/ CURRENT APPLICATION NUMBER: US/11/069,834
/ PRIOR FILING DATE: 2005-03-01
/ PRIOR APPLICATION NUMBER: 60/588,648
/ PRIOR FILING DATE: 2004-07-16
/ PRIOR APPLICATION NUMBER: 60/549,123
/ PRIOR FILING DATE: 2004-03-01
/ NUMBER OF SEQ ID NOS: 65
/ SOFTWARE: PatentIn Ver. 3.3
/ SEQ ID NO 28
/ LENGTH: 12
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic
/ OTHER INFORMATION: peptide
US-11-069-834-28
```

```
Query Match          30.8%; Score 24; DB 7; Length 12;
Best Local Similarity 20.0%; Pred. No. 86;
Matches 2; Conservative 7; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 3 KRDNDYSKN 12
    | | |
    | | |
Db 2 RNNNNNNHNS 11
```



## RESULT 29

```

US-10-467-657-8683
: Sequence 8683, Application US/10467657
: Publication NO. US20050260581A1
: GENERAL INFORMATION:
: APPLICANT: CHIRON SPA
: APPLICANT: FONTANA Maria Rita
: APPLICANT: PIZZA Mariagrazia
: APPLICANT: MASTIGNANI Veges
: APPLICANT: MONACI Elisabetta
: TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
: FILE REFERENCE:
: CURRENT APPLICATION NUMBER: US/10/467,657
: CURRENT FILING DATE: 2003-08-11
: PRIOR APPLICATION NUMBER: GB-0103424.8
: PRIOR FILING DATE: 2001-02-12
: NUMBER OF SEQ ID NOS: 9218
: SOFTWARE: SeqwIn99, version 1.04
: SEQ ID NO 8683
: LENGTH: 16
: TYPE: PR1
: ORGANISM: Neisseria gonorrhoeae
US-10-467-657-8683

```

Query Match	30.8%	Score 24	DB 6	Length 16
Best Local Similarity	36.4%	Pred. No.	1.2e+02	
Match 4, Conservative		4, Mismatches	3,	Indels 0, Gaps 0,

Qy	3	KRDHNDYSKNP	13
Db	6	KQDDADITQHP	16

RESULT 30

```

US-11-054-515-2918
1 Sequence 2918, Application US/11/054515
2 Publication No. US20050255532n1
3 GENERAL INFORMATION:
4 APPLICANT: Ruben et al.
5 TITLE OR INVENTION: Antibodies that Immunospecifically Bind Bly5
6 FILE REFERENCE: PP523p3
7 CURRENT APPLICATION NUMBER: US/11/054,515
8 PRIOR FILING DATE: 2005-02-10
9 PRIOR APPLICATION NUMBER: 60/543,296
10 PRIOR FILING DATE: 2004-02-11
11 PRIOR APPLICATION NUMBER: 60/580,347
12 PRIOR FILING DATE: 2004-06-18
13 PRIOR APPLICATION NUMBER: 10/293,418
14 PRIOR FILING DATE: 2002-11-14
15 PRIOR APPLICATION NUMBER: 60/331,469
16 PRIOR FILING DATE: 2001-11-16
17 PRIOR APPLICATION NUMBER: 60/340,817
18 PRIOR FILING DATE: 2001-12-19
19 PRIOR APPLICATION NUMBER: 09/080,748
20 PRIOR FILING DATE: 2001-06-15
21 PRIOR APPLICATION NUMBER: 60/293,439
22 PRIOR FILING DATE: 2001-05-25
23 PRIOR APPLICATION NUMBER: 60/277,379
24 PRIOR FILING DATE: 2001-03-21
25 PRIOR APPLICATION NUMBER: 60/276,248
26 PRIOR FILING DATE: 2001-03-16
27 PRIOR APPLICATION NUMBER: 60/240,816
28 PRIOR FILING DATE: 2000-10-17
29 Remaining Prior Application data removed - See File Wrapper or PALM.
30 NUMBER OF SEQ ID NOS: 3247
31 SEQ ID NO 2918

```

Query match	30.8%	Score 24;	DB 7;	Length 16;
-------------	-------	-----------	-------	------------

Best Local Similarity	80.0%	Pred. No.	1.2e+02;
Matches	4;	Conservative	0;
		Mismatches	1;
		Indels	0;
		Gaps	0;

QY	5	DHNDY	9
Db	9	DHNYY	13

RESULT 31  
11-032

```

US-11-033-039-1169
? Sequence 1169, Application US/11033039
? Publication No. US2006002947A1
? GENERAL INFORMATION:
? APPLICANT: HUMPEREYS, ROBERT
? APPLICANT: XU, MINZHEN
? TITLE OF INVENTION: LI-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
? FILE REFERENCE: REF-2017HS01
? CURRENT APPLICATION NUMBER: US/11/033,039
? CURRENT FILING DATE: 2005-01-11
? PRIOR APPLICATION NUMBER: 10/245,871
? PRIOR FILING DATE: 2002-09-17
? PRIOR APPLICATION NUMBER: 10/197,000
? PRIOR FILING DATE: 2002-07-17
? PRIOR APPLICATION NUMBER: 09/396,813
? PRIOR FILING DATE: 1999-09-14
? NUMBER OF SEQ ID NOS: 1452
? SOFTWARE: PatentIn version 3.3
? SEQ ID NO 1169
? LENGTH: 18
? TYPE: PRT
? ORGANISM: Artificial Sequence
? FEATURE:
? OTHER INFORMATION: Description of Artificial Sequence: Synthetic
? OTHER INFORMATION: hybrid peptide
? FEATURE:
? NAME/KEY: MOD RES
? LOCATION: (5)..(5)
? OTHER INFORMATION: Ava
? US-11-033-039-1169

```

Query Match Similarity	30.8%;	Score 24;	DB 7;	Length 18;
Best Local Similarity	50.0%;	Pred. No. 1.4e+02;		
Matches 4; Conservative	3;	Mismatches 1;	Indels 0;	Gaps 0;

Qy	1	SIKRDHND	8
		:	: :
Db	6	TIKRSYNN	13

RESULT 32

```

US-11-033-039-1196
: Sequence 1196, Application US/11033039
: Publication No. US20060002947A1
: GENERAL INFORMATION:
: APPLICANT: HUMPHREYS, ROBERT
: APPLICANT: XU, MINZHEN
: TITLE OF INVENTION: LI-KEY/ANTIGENIC EPIOTOPE HYBRID PEPTIDE VACCINES
: FILE REFERENCE: REF-2017US01
: CURRENT APPLICATION NUMBER: US/11/033, 039
: CURRENT FILING DATE: 2005-01-11
: PRIOR APPLICATION NUMBER: 10/245, 871
: PRIOR FILING DATE: 2002-09-17
: PRIOR APPLICATION NUMBER: 10/197, 000
: PRIOR FILING DATE: 2002-07-17
: PRIOR APPLICATION NUMBER: 09/396, 813
: PRIOR FILING DATE: 1999-09-14
: NUMBER OF SEQ ID NOS: 1452
: SOFTWARE: PatentIn version 3.3
: SEQ ID NO 1196
: LENGTH: 18
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:

```

/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
/ OTHER INFORMATION: hybrid peptide  
/ FEATURE:  
/ NAME/KEY: MOD\_RES  
/ LOCATION: (5)..(5)  
/ OTHER INFORMATION: Ava  
US-11-033-039-1196

Query Match 30.8%; Score 24; DB 7; Length 18;  
Best Local Similarity 50.0%; Pred. No. 1.4e+02;  
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 SIKRDHND 8  
|:|:|:  
Db 6 TIKRSTYNN 13

RESULT 33  
US-11-033-039-55  
/ Sequence 55, Application US/11033039  
/ Publication No. US2006002947A1  
/ GENERAL INFORMATION:  
/ APPLICANT: HUMPHREYS, ROBERT  
/ APPLICANT: XU, MINZHEN  
/ TITLE OF INVENTION: LI-KEY/ANTIGENIC EPIOTOPE HYBRID PEPTIDE VACCINES  
/ FILE REFERENCE: REH-2017US01  
/ CURRENT APPLICATION NUMBER: US/11/033,039  
/ CURRENT FILING DATE: 2005-01-11  
/ PRIOR APPLICATION NUMBER: 10/245,871  
/ PRIOR FILING DATE: 2002-09-17  
/ PRIOR APPLICATION NUMBER: 10/197,000  
/ PRIOR FILING DATE: 2002-07-17  
/ PRIOR APPLICATION NUMBER: 09/396,813  
/ PRIOR FILING DATE: 1999-09-14  
/ NUMBER OF SEQ ID NOS: 1452  
/ SOFTWARE: PatentIn version 3.3  
/ SEQ ID NO 55  
/ LENGTH: 20  
/ TYPE: PRT  
/ ORGANISM: Arachis hypogaea  
US-11-033-039-55

Query Match 30.8%; Score 24; DB 7; Length 20;  
Best Local Similarity 50.0%; Pred. No. 1.5e+02;  
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 IKRDHNDY 9  
|:|:|:  
Db 12 IQRDEDSY 19

RESULT 34  
US-11-057-708-32  
/ Sequence 32, Application US/11057708  
/ Publication No. US20050250702A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Universiteit Utrecht  
/ APPLICANT: Strous, Gerardus  
/ APPLICANT: Van Kerkhof, Petrus  
/ APPLICANT: Govers, Roland  
/ TITLE OF INVENTION: CONTROLLING AVAILABILITY OR ACTIVITY OF PROTEINS BY USE OF PROTEIN  
/ FILE REFERENCE: 2183-4525US  
/ CURRENT APPLICATION NUMBER: US/11/057,708  
/ CURRENT FILING DATE: 2005-02-14  
/ PRIOR APPLICATION NUMBER: US/09/660,302  
/ PRIOR FILING DATE: 2000-09-12  
/ PRIOR APPLICATION NUMBER: PCT/NL99/00136  
/ PRIOR FILING DATE: 1999-03-12  
/ PRIOR APPLICATION NUMBER: EP98200799.9  
/ PRIOR FILING DATE: 1998-03-12  
/ NUMBER OF SEQ ID NOS: 51  
/ SOFTWARE: PatentIn version 3.0

/ SEQ ID NO 32  
/ LENGTH: 10  
/ TYPE: PRT  
/ ORGANISM: Unknown  
/ FEATURE:  
/ OTHER INFORMATION: Unnaure, RHESUS BLOOD GROUP-ASSOCIATED GLYCOPROTEIN  
US-11-057-708-32

Query Match 29.5%; Score 23; DB 7; Length 10;  
Best Local Similarity 75.0%; Pred. No. 1e+02;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 HNDY 9  
|:|:|:  
Db 2 HNEY 5

RESULT 35  
US-11-045-024-933  
/ Sequence 933, Application US/11045024  
/ Publication No. US20050271676A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Sette, Alessandro  
/ APPLICANT: Sidney, John  
/ APPLICANT: Southwood, Scott  
/ APPLICANT: Livingston, Brian  
/ APPLICANT: Chesnut, Robert  
/ APPLICANT: Baker, Denise Marie  
/ APPLICANT: Celis, Esteban  
/ APPLICANT: Kubo, Ralph  
/ APPLICANT: Grey, Howard M.  
/ APPLICANT: Eplimmune Inc.  
/ TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency  
/ TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions  
/ FILE REFERENCE: 2060.0040007  
/ CURRENT APPLICATION NUMBER: US/11/045,024  
/ CURRENT FILING DATE: 2005-01-28  
/ PRIOR APPLICATION NUMBER: US 09/412,863  
/ PRIOR FILING DATE: 1999-10-05  
/ PRIOR APPLICATION NUMBER: US 08/027,146  
/ PRIOR FILING DATE: 1993-03-05  
/ PRIOR APPLICATION NUMBER: US 08/073,205  
/ PRIOR FILING DATE: 1993-06-04  
/ PRIOR APPLICATION NUMBER: US 08/103,396  
/ PRIOR FILING DATE: 1993-08-06  
/ PRIOR APPLICATION NUMBER: US 08/159,184  
/ PRIOR FILING DATE: 1993-11-29  
/ PRIOR APPLICATION NUMBER: US 08/159,339  
/ PRIOR FILING DATE: 1993-11-29  
/ PRIOR APPLICATION NUMBER: US 08/205,713  
/ PRIOR FILING DATE: 1994-03-04  
/ PRIOR APPLICATION NUMBER: US 08/347,610  
/ PRIOR FILING DATE: 1994-12-01  
/ NUMBER OF SEQ ID NOS: 14528  
/ SOFTWARE: FastSeq for Windows Version 4.0  
/ SEQ ID NO 933  
/ LENGTH: 11  
/ TYPE: PRT  
/ ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS  
US-11-045-024-933

Query Match 29.5%; Score 23; DB 7; Length 11;  
Best Local Similarity 42.9%; Pred. No. 1.2e+02;  
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 6 HNDYSKN 12  
|:|:|:  
Db 3 HTNYTSN 9

RESULT 36  
US-11-054-515-3215  
/ Sequence 3215, Application US/11054515

Publication No. US20050255532A1  
 GENERAL INFORMATION:  
 APPLICANT: Ruben et al.  
 TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys  
 FILE REFERENCE: PFS23P3  
 CURRENT APPLICATION NUMBER: US/11/054,515  
 CURRENT FILING DATE: 2005-02-10  
 PRIOR APPLICATION NUMBER: 60/543,296  
 PRIOR FILING DATE: 2004-02-11  
 PRIOR APPLICATION NUMBER: 60/580,347  
 PRIOR FILING DATE: 2004-06-18  
 PRIOR APPLICATION NUMBER: 10/293,418  
 PRIOR FILING DATE: 2002-11-14  
 PRIOR APPLICATION NUMBER: 60/331,469  
 PRIOR FILING DATE: 2001-11-16  
 PRIOR APPLICATION NUMBER: 60/340,817  
 PRIOR FILING DATE: 2001-12-19  
 PRIOR APPLICATION NUMBER: 09/880,748  
 PRIOR FILING DATE: 2001-06-15  
 PRIOR APPLICATION NUMBER: 60/293,499  
 PRIOR FILING DATE: 2001-05-25  
 PRIOR APPLICATION NUMBER: 60/277,379  
 PRIOR FILING DATE: 2001-03-21  
 PRIOR APPLICATION NUMBER: 60/276,248  
 PRIOR FILING DATE: 2001-03-16  
 PRIOR APPLICATION NUMBER: 60/240,816  
 PRIOR FILING DATE: 2000-10-17  
 Remaining Prior Application data removed - See File Wrapper or PALM.  
 NUMBER OF SEQ ID NOS: 3247  
 SEQ ID NO 3215  
 LENGTH: 14  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-11-054-515-3215

Query Match 29.5%; Score 23; DB 7; Length 14;  
 Best Local Similarity 55.6%; Pred. No. 1.5e+02;  
 Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 DHNDYSKRP 13  
 DB 4 DHNDGSGPP 12

RESULT 37  
 US-11-106-932-106  
 Sequence 106, Application US/11106932  
 Publication No. US20050260697A1  
 GENERAL INFORMATION:  
 APPLICANT: WANG, KA-WANG KEVIN  
 APPLICANT: HAYES, RONALD  
 APPLICANT: LIU, MING CHEN  
 APPLICANT: OLI, MONIKA  
 TITLE OF INVENTION: PROTEOLYTIC MARKERS AS DIAGNOSTIC BIOMARKERS FOR CANCER, ORGAN  
 TITLE OF INVENTION: INJURY AND MUSCLE REHABILITATION/EXERCISE OVERTRAINING  
 FILE REFERENCE: 5853-549-1  
 CURRENT APPLICATION NUMBER: US/11/106,932  
 CURRENT FILING DATE: 2005-04-15  
 NUMBER OF SEQ ID NOS: 147  
 SOFTWARE: PatentIn version 3.2  
 SEQ ID NO 106  
 LENGTH: 15  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-11-106-932-106

Query Match 29.5%; Score 23; DB 7; Length 15;  
 Best Local Similarity 37.5%; Pred. No. 1.6e+02;  
 Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 4 RDHNDYSK 11  
 DB 7 KKHEDPDK 14

RESULT 38  
 US-10-467-657-8975  
 Sequence 8975, Application US/10467657  
 Publication No. US20050260581A1  
 GENERAL INFORMATION:  
 APPLICANT: CHIRON SPA  
 APPLICANT: FONTANA Maria Rita  
 APPLICANT: PIZZA Mariagrazia  
 APPLICANT: MASIGNANI Vega  
 APPLICANT: MONACI Elisabetta  
 TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS  
 FILE REFERENCE:  
 CURRENT APPLICATION NUMBER: US/10/467,657  
 CURRENT FILING DATE: 2003-08-11  
 PRIOR APPLICATION NUMBER: GB-0103424.8  
 PRIOR FILING DATE: 2001-02-12  
 NUMBER OF SEQ ID NOS: 9218  
 SOFTWARE: SeqMan99, version 1.04  
 SEQ ID NO 8975  
 LENGTH: 17  
 TYPE: PRT  
 ORGANISM: Neisseria gonorrhoeae  
 US-10-467-657-8975

Query Match 29.5%; Score 23; DB 6; Length 17;  
 Best Local Similarity 58.3%; Pred. No. 1.9e+02;  
 Matches 7; Conservative 0; Mismatches 3; Indels 2; Gaps 1;

QY 2 IKRDHNDYSKRP 13  
 DB 7 IFRRHN-IKRP 16

RESULT 39  
 US-11-094-142-31  
 Sequence 31, Application US/11094142  
 Publication No. US20050260770A1  
 GENERAL INFORMATION:  
 APPLICANT: Cohen, Irun R.  
 APPLICANT: Quintana, Francisco Javier  
 APPLICANT: Doman, Bryan  
 APPLICANT: Elizur, Gad  
 APPLICANT: Hagedorn, Peter H.  
 TITLE OF INVENTION: ANTIGEN ARRAY AND DIAGNOSTIC USES THEREOF  
 FILE REFERENCE: 29462  
 CURRENT APPLICATION NUMBER: US/11/094,142  
 CURRENT FILING DATE: 2005-03-31  
 NUMBER OF SEQ ID NOS: 47  
 SOFTWARE: PatentIn version 3.3  
 SEQ ID NO 31  
 LENGTH: 20  
 TYPE: PRT  
 ORGANISM: Artificial sequence  
 OTHER INFORMATION: Synthetic peptide  
 US-11-094-142-31

Query Match 28.8%; Score 22.5; DB 7; Length 20;  
 Best Local Similarity 54.5%; Pred. No. 2.8e+02;  
 Matches 6; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

QY 3 KRDR-NDYSKN 12  
 DB 6 KRKKKDIQSN 16

RESULT 40  
 US-11-054-515-3179  
 Sequence 3179, Application US/11054515  
 Publication No. US20050255532A1  
 GENERAL INFORMATION:

```
/ APPLICANT: Ruben et al.
/ TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
/ FILE REFERENCE: P5523p3
/ CURRENT APPLICATION NUMBER: US/11/054,515
/ PRIOR FILING DATE: 2005-02-10
/ PRIOR APPLICATION NUMBER: 60/543,296
/ PRIOR FILING DATE: 2004-02-11
/ PRIOR APPLICATION NUMBER: 60/580,347
/ PRIOR FILING DATE: 2004-06-18
/ PRIOR APPLICATION NUMBER: 10/293,418
/ PRIOR FILING DATE: 2002-11-14
/ PRIOR APPLICATION NUMBER: 60/331,469
/ PRIOR FILING DATE: 2001-11-16
/ PRIOR APPLICATION NUMBER: 60/340,817
/ PRIOR FILING DATE: 2001-12-19
/ PRIOR APPLICATION NUMBER: 09/880,748
/ PRIOR FILING DATE: 2001-06-15
/ PRIOR APPLICATION NUMBER: 60/293,499
/ PRIOR FILING DATE: 2001-05-25
/ PRIOR APPLICATION NUMBER: 60/277,379
/ PRIOR FILING DATE: 2001-03-21
/ PRIOR APPLICATION NUMBER: 60/276,248
/ PRIOR FILING DATE: 2001-03-16
/ PRIOR APPLICATION NUMBER: 60/240,816
/ PRIOR FILING DATE: 2000-10-17
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 3247
/ SEQ ID NO 3179
/ LENGTH: 8
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-054-515-3179
```

```
Query Match      28.2%  Score 22; DB 7; Length 8;
Best Local Similarity 50.0%; Pred. No. 5.5e+04;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      2 IKRDHNDY 9
        :|||:|
Db      1 VKRYTFDY 8
```

```
RESULT 41
US-10-859-643-628
/ Sequence 628, Application US/10859643
/ Publication No. US20060002993A1
/ GENERAL INFORMATION:
/ APPLICANT: Chailita-Bid, Pia M.
/ APPLICANT: Raitano, Arthur B.
/ APPLICANT: Faris, Mary
/ APPLICANT: Hubert, Rene S.
/ APPLICANT: Morrison, Karen Jane Meyrick
/ TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
/ TITLE OF INVENTION: Encited 161P2F10B Useful in Treatment and Detection of
/ FILE REFERENCE: 511582006203
/ CURRENT APPLICATION NUMBER: US/10/859,643
/ CURRENT FILING DATE: 2004-06-02
/ PRIOR APPLICATION NUMBER: US 10/005,480
/ PRIOR FILING DATE: 2001-11-07
/ NUMBER OF SEQ ID NOS: 765
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 628
/ LENGTH: 10
/ TYPE: PRT
/ ORGANISM: Homo Sapien
US-10-859-643-628
```

```
Query Match      28.2%  Score 22; DB 6; Length 10;
Best Local Similarity 60.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 2; Gaps 1;
```

```
QY      3 KRDHNDYSKN 12
        |||:|
Db      3 KRLH--YAKN 10
```

```
RESULT 42
US-10-973-977-66
/ Sequence 66, Application US/10973977
/ Publication No. US20060008467A1
/ GENERAL INFORMATION:
/ APPLICANT: HAYNES, BARTON F.
/ APPLICANT: LIAO, HUA-XIN
/ APPLICANT: LETVIN, NORMAN
/ TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS VACCINE
/ FILE REFERENCE: 1579-942
/ CURRENT APPLICATION NUMBER: US/10/973,977
/ CURRENT FILING DATE: 2004-10-27
/ PRIOR APPLICATION NUMBER: 09/775,805
/ PRIOR FILING DATE: 2001-02-05
/ PRIOR APPLICATION NUMBER: 09/497,497
/ PRIOR FILING DATE: 2000-02-04
/ NUMBER OF SEQ ID NOS: 107
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 66
/ LENGTH: 10
/ TYPE: PRT
/ ORGANISM: Macaque sp.
US-10-973-977-66
```

```
Query Match      28.2%  Score 22; DB 6; Length 10;
Best Local Similarity 66.7%; Pred. No. 1.6e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      9 YSNMFM 14
        |||||
Db      4 YDKNQM 9
```

```
RESULT 43
US-11-097-864-628
/ Sequence 628, Application US/11097864
/ Publication No. US20050265924A1
/ GENERAL INFORMATION:
/ APPLICANT: Chailita-Bid, Pia M.
/ APPLICANT: Raitano, Arthur B.
/ APPLICANT: Faris, Mary
/ APPLICANT: Hubert, Rene S.
/ APPLICANT: Morrison, Karen Jane Meyrick
/ TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 161P2F10B
/ TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF CANCER
/ FILE REFERENCE: 511582006205
/ CURRENT APPLICATION NUMBER: US/11/097,864
/ CURRENT FILING DATE: 2005-04-01
/ PRIOR APPLICATION NUMBER: US 10/062,109
/ PRIOR FILING DATE: 2002-01-31
/ PRIOR APPLICATION NUMBER: US 10/005,480
/ PRIOR FILING DATE: 2001-11-07
/ NUMBER OF SEQ ID NOS: 765
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 628
/ LENGTH: 10
/ TYPE: PRT
/ ORGANISM: Homo Sapien
US-11-097-864-628
```

```
Query Match      28.2%  Score 22; DB 7; Length 10;
Best Local Similarity 60.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 2; Gaps 1;
```

```
QY      3 KRDHNDYSKN 12
        |||:|
Db      3 KRLH--YAKN 10
```

RESULT 44  
US-11-097-912-628  
Sequence 628, Application US/11097912  
Publication No. US20050265921A1  
GENERAL INFORMATION:  
APPLICANT: Chailita-Bid, Pia M.  
APPLICANT: Raitano, Arthur B.  
APPLICANT: Paris, Mary  
APPLICANT: Hubert, Rene S.  
APPLICANT: Morrison, Karen Jane Meyrick  
APPLICANT: Jakobovits, Aya  
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 161P2F10B  
FILE REFERENCE: 51158206204  
CURRENT APPLICATION NUMBER: US/11/097,912  
PRIOR FILING DATE: 2005-04-01  
PRIOR APPLICATION NUMBER: US 10/062,109  
PRIOR FILING DATE: 2002-01-31  
PRIOR APPLICATION NUMBER: US 10/005,480  
PRIOR FILING DATE: 2001-11-07  
NUMBER OF SEQ ID NOS: 765  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 628  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Homo Sapien  
US-11-097-912-628

Query Match 28.2%; Score 22; DB 7; Length 10;  
Best Local Similarity 60.0%; Pred. No. 1.6e+02;  
Matches 6; Conservative 1; Mismatches 1; Indels 2; Gaps 1;

Cy 3 KRDNDYSKN 12  
|||  
Db 3 KRLH-YAKN 10

RESULT 45  
US-11-058-727-105  
Sequence 105, Application US/11058727  
Publication No. US20050261483A1  
GENERAL INFORMATION:  
APPLICANT: Andre R. Abad  
APPLICANT: Ronald D. Flannagan  
APPLICANT: Rafael Herrmann  
APPLICANT: Theodore W. Kahn  
APPLICANT: Albert L. Lu  
APPLICANT: Billy Fred McCutchen  
APPLICANT: James K. Prensall  
APPLICANT: Cao-Guo Yu  
TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal  
FILE REFERENCE: 35718/287809  
CURRENT APPLICATION NUMBER: US/11/058,727  
CURRENT FILING DATE: 2005-02-15  
PRIOR APPLICATION NUMBER: 60/391,786  
PRIOR FILING DATE: 2002-06-26  
PRIOR APPLICATION NUMBER: 60/460,787  
PRIOR FILING DATE: 2003-04-04  
PRIOR APPLICATION NUMBER: 10/606,320  
NUMBER OF SEQ ID NOS: 134  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 105  
LENGTH: 12  
TYPE: PRT  
ORGANISM: Bacillus thuringiensis (mutated)  
US-11-058-727-105

Query Match 28.2%; Score 22; DB 7; Length 12;

Best Local Similarity 50.0%; Pred. No. 1.9e+02;  
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Cy 5 DHNDYS 10  
|||  
Db 1 DYKDYA 6

RESULT 46  
US-11-108-389-105  
Sequence 105, Application US/11108389  
Publication No. US20050261188A1  
GENERAL INFORMATION:  
APPLICANT: Andre R. Abad  
APPLICANT: Ronald D. Flannagan  
APPLICANT: Rafael Herrmann  
APPLICANT: Theodore W. Kahn  
APPLICANT: Albert L. Lu  
APPLICANT: Billy Fred McCutchen  
APPLICANT: James K. Prensall  
APPLICANT: Cao-Guo Yu  
TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal  
FILE REFERENCE: 35718/291049  
CURRENT APPLICATION NUMBER: US/11/108,389  
CURRENT FILING DATE: 2005-04-18  
PRIOR APPLICATION NUMBER: 60/391,786  
PRIOR FILING DATE: 2002-06-26  
PRIOR APPLICATION NUMBER: 60/460,787  
PRIOR FILING DATE: 2003-04-04  
PRIOR APPLICATION NUMBER: 10/606,320  
PRIOR FILING DATE: 2003-06-25  
NUMBER OF SEQ ID NOS: 134  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 105  
LENGTH: 12  
TYPE: PRT  
ORGANISM: Bacillus thuringiensis (mutated)  
US-11-108-389-105

Query Match 28.2%; Score 22; DB 7; Length 12;  
Best Local Similarity 50.0%; Pred. No. 1.9e+02;  
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Cy 5 DHNDYS 10  
|||  
Db 1 DYKDYA 6

RESULT 47  
US-10-511-559-554  
Sequence 554, Application US/10511559  
Publication No. US20050256304A1  
GENERAL INFORMATION:  
APPLICANT: JONES, Tim  
APPLICANT: BAKER, Matthew  
APPLICANT: CARR, Francis, J.  
TITLE OF INVENTION: MODIFIED FACTOR VIII  
FILE REFERENCE: MER-133  
CURRENT APPLICATION NUMBER: US/10/511,559  
CURRENT FILING DATE: 2004-10-15  
PRIOR APPLICATION NUMBER: PCT/EP03/04063  
PRIOR FILING DATE: 2003-04-17  
PRIOR APPLICATION NUMBER: EP 02008712.8  
PRIOR FILING DATE: 2002-04-18  
PRIOR APPLICATION NUMBER: EP 03006554.4  
PRIOR FILING DATE: 2003-03-24  
NUMBER OF SEQ ID NOS: 1147  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 554  
LENGTH: 13  
TYPE: PRT

```
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Potential Epitope of human Factor VIII
US-10-511-559-554
```

```
Query Match      28.2%; Score 22; DB 6; Length 13;
Best Local Similarity 45.5%; Pred. No. 2.1e+02;
Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
```

```
QY      2 IKRDHNYSKN 12
Db      3 IORTGKNSLN 13
```

## RESULT 48

```
US-10-511-559-555
/ Sequence 555, Application US/10511559
/ Publication No. US20050256304A1
/ GENERAL INFORMATION:
/ APPLICANT: JONES, Tim
/ APPLICANT: BAKER, Matthew
/ APPLICANT: CAR, Francis, J.
/ TITLE OF INVENTION: MODIFIED FACTOR VIII
/ FILE REFERENCE: MER-133
/ CURRENT APPLICATION NUMBER: US/10/511,559
/ CURRENT FILING DATE: 2004-10-15
/ PRIOR APPLICATION NUMBER: PCT/EP03/04063
/ PRIOR FILING DATE: 2003-04-17
/ PRIOR APPLICATION NUMBER: EP 02008712.8
/ PRIOR FILING DATE: 2002-04-18
/ PRIOR APPLICATION NUMBER: EP 03006554.4
/ PRIOR FILING DATE: 2003-03-24
/ NUMBER OF SEQ ID NOS: 1147
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 555
/ LENGTH: 13
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Potential Epitope of human Factor VIII
US-10-511-559-555
```

```
Query Match      28.2%; Score 22; DB 6; Length 13;
Best Local Similarity 45.5%; Pred. No. 2.1e+02;
Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
```

```
QY      2 IKRDHNYSKN 12
Db      1 IORTGKNSLN 11
```

## RESULT 49

```
US-11-116-144-258
/ Sequence 258, Application US/11116144
/ Publication No. US2005027181A1
/ GENERAL INFORMATION:
/ APPLICANT: BERTHE, FRANCOIS XAVIER
/ APPLICANT: CASADEVAL, FRANCESC VAYREDA
/ APPLICANT: SANZ MARIA, MARIA CRUZ
/ APPLICANT: GARCIA, TERESA LLOP
/ APPLICANT: OLE, ANGELS MOR
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETECTING PATHOGEN
/ FILE REFERENCE: INT-084
/ CURRENT APPLICATION NUMBER: US/11/116,144
/ CURRENT FILING DATE: 2005-04-27
/ PRIOR APPLICATION NUMBER: PCT/ES04/000581
/ PRIOR FILING DATE: 2004-12-23
/ PRIOR APPLICATION NUMBER: EP 03380307.3
/ PRIOR FILING DATE: 2003-12-23
/ NUMBER OF SEQ ID NOS: 301
/ SOFTWARE: PatentIn Ver. 3.3
/ SEQ ID NO 258
```

```
/ LENGTH: 14
/ TYPE: PRT
/ ORGANISM: Plasmodium yoelii
US-11-116-144-258
```

```
Query Match      28.2%; Score 22; DB 7; Length 14;
Best Local Similarity 50.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
QY      5 DHNDYSKN 12
Db      5 DHGKSGKN 12
```

## RESULT 50

```
US-10-939-890-199
/ Sequence 199, Application US/10939890
/ Publication No. US20050250700A1
/ GENERAL INFORMATION:
/ APPLICANT: Sato, Aaron K.
/ APPLICANT: Sexton, Daniel J.
/ APPLICANT: Dransfield, Daniel T.
/ APPLICANT: Ladner, Robert C.
/ APPLICANT: Arbogast, Christophe
/ APPLICANT: Busat, Philippe
/ APPLICANT: Pan, Hong
/ APPLICANT: Khurana, Sudha
/ APPLICANT: Linder, Karen B.
/ APPLICANT: Marinelli, Edmund R.
/ APPLICANT: Nanjappan, Palaniappa
/ APPLICANT: Nunn, Adrian D.
/ APPLICANT: Pillai, Radhakrishna
/ APPLICANT: Bochen, Sibylle
/ APPLICANT: Ramalingam, Kondaredi
/ APPLICANT: Shrivastava, Ajay
/ APPLICANT: Swenson, Rolf B.
/ APPLICANT: Von Wronski, Mathew A.
/ TITLE OF INVENTION: KDR AND YGF/KDR BINDING PEPTIDES
/ FILE REFERENCE: D0617.70014US00
/ CURRENT APPLICATION NUMBER: US/10/939,890
/ CURRENT FILING DATE: 2004-09-13
/ PRIOR APPLICATION NUMBER: US 10/661,156
/ PRIOR FILING DATE: 2003-09-11
/ PRIOR APPLICATION NUMBER: US 10/382,082
/ PRIOR FILING DATE: 2003-03-03
/ PRIOR APPLICATION NUMBER: PCT/US03/06731
/ PRIOR FILING DATE: 2003-03-03
/ PRIOR APPLICATION NUMBER: US 60/440,411
/ PRIOR FILING DATE: 2003-01-15
/ PRIOR APPLICATION NUMBER: US 60/360,851
/ PRIOR FILING DATE: 2002-03-01
/ NUMBER OF SEQ ID NOS: 883
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 199
/ LENGTH: 15
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Library Isolate
US-10-939-890-199
```

```
Query Match      28.2%; Score 22; DB 6; Length 15;
Best Local Similarity 42.9%; Pred. No. 2.4e+02;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      2 IKRDHND 8
Db      5 VKRDHND 11
```

## RESULT 51

```
US-11-045-024-13269
```

```

/ Sequence 13269, Application US/11045024
/ Publication No. US2005027676A1
/ GENERAL INFORMATION:
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Livingston, Brian
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Baker, Denise Marie
/ APPLICANT: Cells, Ralph
/ APPLICANT: Kudo, Ralph
/ APPLICANT: Grey, Howard M.
/ APPLICANT: BiImmune Inc.
/ TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
/ TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
/ FILE REFERENCE: 2060.0040007
/ CURRENT APPLICATION NUMBER: US/11/045.024
/ CURRENT FILING DATE: 2005-01-28
/ PRIOR APPLICATION NUMBER: US 09/412,863
/ PRIOR FILING DATE: 1999-10-05
/ PRIOR APPLICATION NUMBER: US 08/027,146
/ PRIOR FILING DATE: 1993-03-05
/ PRIOR APPLICATION NUMBER: US 08/073,205
/ PRIOR FILING DATE: 1993-06-04
/ PRIOR APPLICATION NUMBER: US 08/103,396
/ PRIOR FILING DATE: 1993-08-06
/ PRIOR APPLICATION NUMBER: US 08/159,184
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/159,339
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/205,713
/ PRIOR FILING DATE: 1994-03-04
/ PRIOR APPLICATION NUMBER: US 08/347,610
/ PRIOR FILING DATE: 1994-12-01
/ NUMBER OF SEQ ID NOS: 14528
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 13269
/ LENGTH: 15
/ TYPE: PRT
/ ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
/ US-11-045-024-13269

Query Match      28.2%; Score 22; DB 7; Length 15;
Best Local Similarity 36.4%; Pred. No. 2.4e+02;
Matches 4; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY      2 IKRDNDYSKN 12
Db      4 VKTIHTDNGSN 14

```

```

/ APPLICANT: Swenson, Rolf E.
/ APPLICANT: Von Wronski, Mathew A.
/ TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
/ FILE REFERENCE: D0617.70014US00
/ CURRENT APPLICATION NUMBER: US/10/939,890
/ CURRENT FILING DATE: 2004-09-13
/ PRIOR APPLICATION NUMBER: US 10/661,156
/ PRIOR FILING DATE: 2003-09-11
/ PRIOR APPLICATION NUMBER: US 10/382,082
/ PRIOR FILING DATE: 2003-03-03
/ PRIOR APPLICATION NUMBER: PCT/US03/06731
/ PRIOR FILING DATE: 2003-03-03
/ PRIOR APPLICATION NUMBER: US 60/440,411
/ PRIOR FILING DATE: 2003-01-15
/ PRIOR APPLICATION NUMBER: US 60/360,851
/ PRIOR FILING DATE: 2002-03-01
/ NUMBER OF SEQ ID NOS: 883
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 11
/ LENGTH: 16
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: KDR or VEGF/KDR Binding Polypeptide
/ US-10-939-890-11

Query Match      28.2%; Score 22; DB 6; Length 16;
Best Local Similarity 50.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      5 DHRDYSKN 12
Db      1 DHRCYLHN 8

```

```

RESULT 52
US-10-939-890-11
/ Sequence 11, Application US/10939890
/ Publication No. US20050250700A1
/ GENERAL INFORMATION:
/ APPLICANT: Sato, Aaron K.
/ APPLICANT: Sexton, Daniel J.
/ APPLICANT: Dransfield, Daniel T.
/ APPLICANT: Ledner, Robert C.
/ APPLICANT: Arbogast, Christophe
/ APPLICANT: Bussat, Philippe
/ APPLICANT: Fan, Hong
/ APPLICANT: Khurana, Sudha
/ APPLICANT: Linder, Karen B.
/ APPLICANT: Marinelli, Edmund R.
/ APPLICANT: Nanjappan, Palanlappa
/ APPLICANT: Nunn, Adrian D.
/ APPLICANT: Pilla, Radhakrishna
/ APPLICANT: Pochon, Sibylle
/ APPLICANT: Ramalingam, Kondareddiar
/ APPLICANT: Shrivastava, Ajay
/ APPLICANT: Song, Bo

```

```

RESULT 53
US-10-939-890-205
/ Sequence 205, Application US/10939890
/ Publication No. US20050250700A1
/ GENERAL INFORMATION:
/ APPLICANT: Sato, Aaron K.
/ APPLICANT: Sexton, Daniel J.
/ APPLICANT: Dransfield, Daniel T.
/ APPLICANT: Ledner, Robert C.
/ APPLICANT: Arbogast, Christophe
/ APPLICANT: Bussat, Philippe
/ APPLICANT: Fan, Hong
/ APPLICANT: Khurana, Sudha
/ APPLICANT: Linder, Karen B.
/ APPLICANT: Marinelli, Edmund R.
/ APPLICANT: Nanjappan, Palanlappa
/ APPLICANT: Nunn, Adrian D.
/ APPLICANT: Pilla, Radhakrishna
/ APPLICANT: Pochon, Sibylle
/ APPLICANT: Ramalingam, Kondareddiar
/ APPLICANT: Shrivastava, Ajay
/ APPLICANT: Song, Bo
/ APPLICANT: Swenson, Rolf E.
/ APPLICANT: Von Wronski, Mathew A.
/ TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
/ FILE REFERENCE: D0617.70014US00
/ CURRENT APPLICATION NUMBER: US/10/939,890
/ CURRENT FILING DATE: 2004-09-13
/ PRIOR APPLICATION NUMBER: US 10/661,156
/ PRIOR FILING DATE: 2003-09-11
/ PRIOR APPLICATION NUMBER: US 10/382,082
/ PRIOR FILING DATE: 2003-03-03
/ PRIOR APPLICATION NUMBER: PCT/US03/06731
/ PRIOR FILING DATE: 2003-03-03
/ PRIOR APPLICATION NUMBER: US 60/440,411
/ PRIOR FILING DATE: 2003-01-15
/ PRIOR APPLICATION NUMBER: US 60/360,851
/ PRIOR FILING DATE: 2002-03-01

```

```
/ NUMBER OF SEQ ID NOS: 883
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 205
/ LENGTH: 16
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Library Isolate
US-10-939-890-205
```

```
Query Match      28.2%; Score 22; DB 6; Length 16;
Best Local Similarity 50.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy      5 DHNDYSKN 12
Db      1 DHHCYLMN 8
```

```
RESULT 54
US-11-152-846-2
/ Sequence 2, Application US/11152846
/ Publication No. US20060002862A1
/ GENERAL INFORMATION:
/ APPLICANT: Medimmune Vaccines, Inc.
/ APPLICANT: Truong-Le, Vu
/ APPLICANT: Scherer, Tom
/ TITLE OF INVENTION: HIGH PRESSURE SPRAY-DRY OF ANTIBODIES
/ FILE REFERENCE: 26-000630US
/ CURRENT APPLICATION NUMBER: US/11/152,846
/ CURRENT FILING DATE: 2005-06-13
/ NUMBER OF SEQ ID NOS: 20
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 2
/ LENGTH: 16
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-152-846-2
```

```
Query Match      28.2%; Score 22; DB 7; Length 16;
Best Local Similarity 40.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy      3 KRDNHYSKN 12
Db      7 KKDYNPSLKS 16
```

```
RESULT 55
US-10-503-575-173
/ Sequence 173, Application US/10503575
/ Publication No. US20050244823A1
/ GENERAL INFORMATION:
/ APPLICANT: Drifflinout, Jan Wouter
/ APPLICANT: van Veele, Petrus Antonius
/ APPLICANT: Konig, Frits
/ TITLE OF INVENTION: NOVEL EPITOPES FOR CELIAC DISEASE AND AUTOIMMUNE DISEASES, METHOD
/ FILE REFERENCE: 2799/72843-PCT-US
/ CURRENT APPLICATION NUMBER: US/10/503,575
/ CURRENT FILING DATE: 2004-08-04
/ PRIOR APPLICATION NUMBER: PCT/NL03/00077
/ PRIOR FILING DATE: 2003-02-04
/ PRIOR APPLICATION NUMBER: EP 02075456.0
/ PRIOR FILING DATE: 2002-02-04
/ NUMBER OF SEQ ID NOS: 340
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 173
/ LENGTH: 19
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-503-575-173
```

```
Query Match      28.2%; Score 22; DB 6; Length 19;
Best Local Similarity 33.3%; Pred. No. 3.2e+02;
Matches 3; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy      5 DHNDYSKNP 13
Db      4 DFQNTYNGQP 12
```

```
RESULT 56
US-11-129-104-12
/ Sequence 12, Application US/11129104
/ Publication No. US20050287644A1
/ GENERAL INFORMATION:
/ APPLICANT: CHIU, YI-FANG
/ APPLICANT: CHEN, LEE-HSIUAN
/ APPLICANT: HUANG, JEN-PIN
/ TITLE OF INVENTION: METHODS FOR PRODUCING AND CULTURING RABBIT-MOUSE
/ TITLE OF INVENTION: HYBRIDOMAS AND MONOCLONAL ANTIBODIES SECRETED BY
/ FILE REFERENCE: 09468.0005-00000
/ CURRENT APPLICATION NUMBER: US/11/129,104
/ CURRENT FILING DATE: 2005-05-13
/ PRIOR APPLICATION NUMBER: 60/571,440
/ PRIOR FILING DATE: 2004-05-14
/ NUMBER OF SEQ ID NOS: 100
/ SOFTWARE: PatentIn Ver. 3.3
/ SEQ ID NO 12
/ LENGTH: 7
/ TYPE: PRT
/ ORGANISM: Unknown Organism
/ FEATURE:
/ OTHER INFORMATION: Description of Unknown Organism: Human, Mouse, or
US-11-129-104-12
```

```
Query Match      26.9%; Score 21; DB 7; Length 7;
Best Local Similarity 50.0%; Pred. No. 5.5e+04;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy      9 YSKNPM 14
Db      2 YDKTFL 7
```

```
RESULT 57
US-11-045-024-7497
/ Sequence 7497, Application US/11045024
/ Publication No. US20050271676A1
/ GENERAL INFORMATION:
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Livingston, Brian
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Baker, Denise Marie
/ APPLICANT: Cells, Beate
/ APPLICANT: Kubo, Ralph
/ APPLICANT: Grey, Howard M.
/ APPLICANT: Eplimmune Inc.
/ TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
/ FILE REFERENCE: 2060.0040007
/ CURRENT APPLICATION NUMBER: US/11/045,024
/ CURRENT FILING DATE: 2005-01-28
/ PRIOR APPLICATION NUMBER: US 09/412,863
/ PRIOR FILING DATE: 1999-10-05
/ PRIOR APPLICATION NUMBER: US 08/027,146
/ PRIOR FILING DATE: 1993-03-05
/ PRIOR APPLICATION NUMBER: US 08/073,205
/ PRIOR FILING DATE: 1993-06-04
/ PRIOR APPLICATION NUMBER: US 08/103,396
/ PRIOR FILING DATE: 1993-08-06
```



PRIOR APPLICATION NUMBER: US 08/159,184  
PRIOR FILING DATE: 1993-11-29  
PRIOR APPLICATION NUMBER: US 08/159,339  
PRIOR FILING DATE: 1993-11-29  
PRIOR APPLICATION NUMBER: US 08/205,713  
PRIOR FILING DATE: 1994-03-04  
PRIOR APPLICATION NUMBER: US 08/347,610  
PRIOR FILING DATE: 1994-12-01  
NUMBER OF SEQ ID NOS: 14528  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 7497  
LENGTH: 8  
TYPE: PRT  
ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS  
US-11-045-024-7497

Query Match 26.9%; Score 21; DB 7; Length 8;  
Best Local Similarity 42.9%; Pred. No. 5.5e+04;  
Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 KRDNDY 9  
: |||  
Db 2 QEDHEKY 8

RESULT 58  
US-11-045-024-8233  
Sequence 8233, Application US/11045024  
Publication No. US20050271676A1  
GENERAL INFORMATION:  
APPLICANT: Sette, Alessandro  
APPLICANT: Sidney, John  
APPLICANT: Southwood, Scott  
APPLICANT: Livingston, Brian  
APPLICANT: Chesnut, Robert  
APPLICANT: Baker, Denise Marie  
APPLICANT: Cells, Eberden  
APPLICANT: Kubo, Ralph  
APPLICANT: Grey, Howard M.  
APPLICANT: Epiimmune Inc.  
TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency  
TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions  
FILE REFERENCE: 2060.004007  
CURRENT APPLICATION NUMBER: US/11/045.024  
CURRENT FILING DATE: 2005-01-28  
PRIOR APPLICATION NUMBER: US 09/412,863  
PRIOR FILING DATE: 1999-10-05  
PRIOR APPLICATION NUMBER: US 08/027,146  
PRIOR FILING DATE: 1993-03-05  
PRIOR APPLICATION NUMBER: US 08/073,205  
PRIOR FILING DATE: 1993-06-04  
PRIOR APPLICATION NUMBER: US 08/103,396  
PRIOR FILING DATE: 1993-08-06  
PRIOR APPLICATION NUMBER: US 08/159,184  
PRIOR FILING DATE: 1993-11-29  
PRIOR APPLICATION NUMBER: US 08/159,339  
PRIOR FILING DATE: 1993-11-29  
PRIOR APPLICATION NUMBER: US 08/205,713  
PRIOR FILING DATE: 1994-03-04  
PRIOR APPLICATION NUMBER: US 08/347,610  
PRIOR FILING DATE: 1994-12-01  
NUMBER OF SEQ ID NOS: 14528  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 8233  
LENGTH: 8  
TYPE: PRT  
ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS  
US-11-045-024-8233

Query Match 26.9%; Score 21; DB 7; Length 8;  
Best Local Similarity 42.9%; Pred. No. 5.5e+04;  
Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 KRDNDY 9  
: |||  
Db 2 QEDHEKY 8

RESULT 59  
US-10-473-037-8  
Sequence 8, Application US/10473037  
Publication No. US20050260206A1  
GENERAL INFORMATION:  
APPLICANT: KYOWA HAKKO KOGYO CO., LTD.  
TITLE OF INVENTION: Agents for treatment of cancer using recombinant anti-CD3 antibo  
TITLE OF INVENTION: the antibody fragments  
FILE REFERENCE: 11374W01  
CURRENT APPLICATION NUMBER: US/10/473.037  
CURRENT FILING DATE: 2003-09-26  
PRIOR APPLICATION NUMBER: JP2001-097483  
PRIOR FILING DATE: 2001-03-29  
NUMBER OF SEQ ID NOS: 50  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 8  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Mus musculus  
US-10-473-037-8

Query Match 26.9%; Score 21; DB 6; Length 9;  
Best Local Similarity 57.1%; Pred. No. 5.5e+04;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 7 NDYSKNP 13  
: |||  
Db 1 HOYSKLP 7

RESULT 60  
US-10-859-643-482  
Sequence 482, Application US/10859643  
Publication No. US20060002993A1  
GENERAL INFORMATION:  
APPLICANT: Raitano, Arthur B.  
APPLICANT: Fatis, Mary  
APPLICANT: Hubert, Rene S.  
APPLICANT: Morrison, Karen Jane Meyrick  
APPLICANT: Jakobovits, Aya  
TITLE OF INVENTION: Nucleic Acid and Corresponding Protein  
TITLE OF INVENTION: Entitled 1612P10B Useful in Treatment and Detection of  
FILE REFERENCE: 511582006203  
CURRENT APPLICATION NUMBER: US/10/859.643  
CURRENT FILING DATE: 2004-06-02  
PRIOR APPLICATION NUMBER: US 10/005,480  
PRIOR FILING DATE: 2001-11-07  
NUMBER OF SEQ ID NOS: 765  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 482  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Homo Sapien  
US-10-859-643-482

Query Match 26.9%; Score 21; DB 6; Length 9;  
Best Local Similarity 50.0%; Pred. No. 5.5e+04;  
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 5 DNDYSKN 12  
: |||  
Db 1 DNNMYDVN 8

RESULT 61  
US-11-021-441-102

```
/ Sequence 102, Application US/11021441
/ Publication No. US20050249748A1
/ GENERAL INFORMATION:
/ APPLICANT: DUBENSKY, Thomas W., Jr.
/ APPLICANT: PORTNOY, Daniel A.
/ APPLICANT: LUCKETT, William S., Jr.
/ APPLICANT: COOK, David N.
/ TITLE OF INVENTION: RECOMBINANT NUCLEIC ACID MOLECULES,
/ TITLE OF INVENTION: EXPRESSION CASSETTES, AND BACTERIA, AND METHODS OF USE
/ FILE REFERENCE: 282172003900
/ CURRENT APPLICATION NUMBER: US/11/021,441
/ PRIOR FILING DATE: 2004-12-23
/ PRIOR FILING DATE: 2004-10-06
/ PRIOR FILING DATE: 2004-10-06
/ PRIOR FILING DATE: 2004-10-01
/ PRIOR FILING DATE: 2004-08-05
/ PRIOR FILING DATE: 2004-07-23
/ PRIOR FILING DATE: 2004-06-30
/ PRIOR FILING DATE: 2004-03-26
/ NUMBER OF SEQ ID NOS: 129
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 102
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Listeria monocytogenes
US-11-021-441-102
```

```
Query Match          26.9%; Score 21; DB 7; Length 9;
Best Local Similarity 50.0%; Pred. No. 5.5e+04;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      4 RDHNDY 9
Db      3 KDGNEY 8
```

```
RESULT 62
US-11-097-864-482
/ Sequence 482, Application US/11097864
/ Publication No. US20050265924A1
/ GENERAL INFORMATION:
/ APPLICANT: Chaillita-Bid, Pia M.
/ APPLICANT: Raitano, Arthur B.
/ APPLICANT: Paris, Mary
/ APPLICANT: Hubert, Rene S.
/ APPLICANT: Morrison, Karen Jane Meyrick
/ APPLICANT: Jakobovits, Aya
/ TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 161P2F10B
/ FILE REFERENCE: 511582006205
/ CURRENT APPLICATION NUMBER: US/11/097,864
/ CURRENT FILING DATE: 2005-04-01
/ PRIOR APPLICATION NUMBER: US 10/062,109
/ PRIOR FILING DATE: 2002-01-31
/ PRIOR APPLICATION NUMBER: US 10/005,480
/ PRIOR FILING DATE: 2001-11-07
/ NUMBER OF SEQ ID NOS: 765
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 482
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Homo Saplen
US-11-097-864-482
```

```
Query Match          26.9%; Score 21; DB 7; Length 9;
Best Local Similarity 50.0%; Pred. No. 5.5e+04;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy      5 DHNDYSKN 12
Db      1 DNNMVDVN 8
```

```
RESULT 63
US-11-097-912-482
/ Sequence 482, Application US/11097912
/ Publication No. US20050265921A1
/ GENERAL INFORMATION:
/ APPLICANT: Chaillita-Bid, Pia M.
/ APPLICANT: Raitano, Arthur B.
/ APPLICANT: Paris, Mary
/ APPLICANT: Hubert, Rene S.
/ APPLICANT: Morrison, Karen Jane Meyrick
/ APPLICANT: Jakobovits, Aya
/ TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 161P2F10B
/ FILE REFERENCE: 511582006204
/ CURRENT APPLICATION NUMBER: US/11/097,912
/ CURRENT FILING DATE: 2005-04-01
/ PRIOR APPLICATION NUMBER: US 10/062,109
/ PRIOR FILING DATE: 2002-01-31
/ PRIOR APPLICATION NUMBER: US 10/005,480
/ PRIOR FILING DATE: 2001-11-07
/ NUMBER OF SEQ ID NOS: 765
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 482
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Homo Saplen
US-11-097-912-482
```

```
Query Match          26.9%; Score 21; DB 7; Length 9;
Best Local Similarity 50.0%; Pred. No. 5.5e+04;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy      5 DHNDYSKN 12
Db      1 DNNMVDVN 8
```

```
RESULT 64
US-11-045-024-5858
/ Sequence 5858, Application US/11045024
/ Publication No. US20050271676A1
/ GENERAL INFORMATION:
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Livingston, Brian
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Baker, Denise Marie
/ APPLICANT: Celis, Esben
/ APPLICANT: Kubo, Ralph
/ APPLICANT: Grey, Howard M.
/ APPLICANT: Bpimmune Inc.
/ TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
/ FILE REFERENCE: 2060.0040007
/ CURRENT APPLICATION NUMBER: US/11/045,024
/ CURRENT FILING DATE: 2005-01-28
/ PRIOR APPLICATION NUMBER: US 09/412,863
/ PRIOR FILING DATE: 1999-10-05
/ PRIOR APPLICATION NUMBER: US 08/027,146
/ PRIOR FILING DATE: 1993-03-05
/ PRIOR APPLICATION NUMBER: US 08/073,205
/ PRIOR FILING DATE: 1993-06-04
/ PRIOR APPLICATION NUMBER: US 08/103,396
/ PRIOR FILING DATE: 1993-08-06
/ PRIOR APPLICATION NUMBER: US 08/159,184
/ PRIOR FILING DATE: 1993-11-29
```

```

; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5858
; LENGTH: 9
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-5858

```

```

Query Match      26.9%; Score 21; DB 7; Length 9;
Best Local Similarity 37.5%; Pred. No. 5.5e+04;
Matches 3; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

```

```

QY      5 DHNDYSKN 12
      :|:|:|
Db      1 EHEKTHSN 8

```

```

RESULT 65
US-11-041-893-66
; Sequence 66, Application US/11041893
; Publication No. US2006002941A1
; GENERAL INFORMATION:
; APPLICANT: Mahabirab, Gregory G.
; TITLE OF INVENTION: COMPOSITIONS COMPRISING IMMUNE RESPONSE
; FILE REFERENCE: 100123.401
; CURRENT APPLICATION NUMBER: US/11/041,893
; CURRENT FILING DATE: 2005-01-24
; PRIOR APPLICATION NUMBER: US 60/616,855
; PRIOR FILING DATE: 2004-10-06
; PRIOR APPLICATION NUMBER: US 60/538,713
; PRIOR FILING DATE: 2004-01-23
; NUMBER OF SEQ ID NOS: 295
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 66
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Listeria monocytogenes
US-11-041-893-66

```

```

Query Match      26.9%; Score 21; DB 7; Length 9;
Best Local Similarity 50.0%; Pred. No. 5.5e+04;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```

```

QY      4 RDHNDY 9
      :|:|:|
Db      3 KDGNEY 8

```

```

RESULT 66
US-11-010-748A-522
; Sequence 522, Application US/11010748A
; Publication No. US2005024421A1
; GENERAL INFORMATION:
; APPLICANT: Merck Patent GmbH
; APPLICANT: STRITTMATTER, Wolfgang
; APPLICANT: WOLL, Heidrun
; APPLICANT: SCHIAR, Burkhard
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING IMMUNE RESPONSE
; FILE REFERENCE: MRR-136
; CURRENT APPLICATION NUMBER: US/11/010,748A
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: PCT/EP03/06251
; PRIOR FILING DATE: 2003-06-13
; PRIOR APPLICATION NUMBER: EP02013423.5
; PRIOR FILING DATE: 2002-06-13
; NUMBER OF SEQ ID NOS: 926

```

```

; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 522
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: CD64 peptide fragment
US-11-010-748A-522

```

```

Query Match      26.9%; Score 21; DB 7; Length 10;
Best Local Similarity 50.0%; Pred. No. 2.3e+02;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```

```

QY      1 SIKRDN 6
      :|:|:|
Db      5 SLOEDH 10

```

```

RESULT 67
US-11-156-843-119
; Sequence 119, Application US/11156843
; Publication No. US20050267035A1
; GENERAL INFORMATION:
; APPLICANT: West, Robert R.
; APPLICANT: Shepard, Paul O.
; APPLICANT: Fox, Brian
; TITLE OF INVENTION: Peptide and Polypeptide Inhibitors of
; FILE REFERENCE: 00-33
; CURRENT APPLICATION NUMBER: US/11/156,843
; CURRENT FILING DATE: 2005-06-20
; PRIOR APPLICATION NUMBER: US/09/883,727
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 119
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: C1s exosite binding moiety
US-11-156-843-119

```

```

Query Match      26.9%; Score 21; DB 7; Length 10;
Best Local Similarity 60.0%; Pred. No. 2.3e+02;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

```

QY      5 DHNDY 9
      :|:|:|
Db      3 DYEDY 7

```

```

RESULT 68
US-11-129-104-54
; Sequence 54, Application US/11129104
; Publication No. US20050287644A1
; GENERAL INFORMATION:
; APPLICANT: CHIU, YI-FANG
; APPLICANT: CHEN, LEE-HSIUAN
; APPLICANT: HUANG, JEN-PIN
; TITLE OF INVENTION: METHODS FOR PRODUCING AND CULTURING RABBIT-MOUSE
; TITLE OF INVENTION: HYBRIDOMAS AND MONOCLONAL ANTIBODIES SECRETED BY
; FILE REFERENCE: 09468.0005-00000
; CURRENT APPLICATION NUMBER: US/11/129,104
; CURRENT FILING DATE: 2005-05-13
; PRIOR APPLICATION NUMBER: 60/571,440
; PRIOR FILING DATE: 2004-05-14
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 54
; LENGTH: 10
; TYPE: PRT

```

ORGANISM: Homo sapiens  
US-11-129-104-54

Query Match 26.9%; Score 21; DB 7; Length 10;  
Best Local Similarity 50.0%; Pred. No. 2.3e+02;  
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 YSKNPM 14  
| | | |  
DB 5 YDKTPL 10

RESULT 69  
US-11-129-104-55  
Sequence 55, Application US/11129104  
Publication No. US20050287644A1  
GENERAL INFORMATION:  
APPLICANT: CHIU, YI-PANG  
APPLICANT: CHEN, LEE-HSIUAN  
APPLICANT: HUANG, JEN-PIN  
TITLE OF INVENTION: METHODS FOR PRODUCING AND CULTURING RABBIT-MOUSE  
TITLE OF INVENTION: HYBRIDOMAS AND MONOCLONAL ANTIBODIES SECRETED BY  
TITLE OF INVENTION: RABBIT-MOUSE HYBRIDOMAS  
FILE REFERENCE: 09468.0005-00000  
CURRENT APPLICATION NUMBER: US/11/129,104  
CURRENT FILING DATE: 2005-05-13  
PRIOR APPLICATION NUMBER: 60/571,440  
PRIOR FILING DATE: 2004-05-14  
NUMBER OF SEQ ID NOS: 100  
SOFTWARE: PatentIn Ver. 3.3  
SEQ ID NO 55  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-11-129-104-55

Query Match 26.9%; Score 21; DB 7; Length 10;  
Best Local Similarity 50.0%; Pred. No. 2.3e+02;  
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 YSKNPM 14  
| | | |  
DB 2 YDKTPL 7

RESULT 70  
US-11-156-843-30  
Sequence 30, Application US/11156843  
Publication No. US20050267035A1  
GENERAL INFORMATION:  
APPLICANT: West, Robert R.  
APPLICANT: Shepard, Paul O.  
APPLICANT: Fox, Brian  
TITLE OF INVENTION: Peptide and Polypeptide Inhibitors of  
FILE REFERENCE: 00-33  
CURRENT APPLICATION NUMBER: US/11/156,843  
CURRENT FILING DATE: 2005-06-20  
PRIOR APPLICATION NUMBER: US/09/883,727  
PRIOR FILING DATE: 2001-06-18  
NUMBER OF SEQ ID NOS: 140  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 30  
LENGTH: 11  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: C1s exosite binding moiety  
NAME/KEY: MUTAGEN  
LOCATION: (10)...(10)  
OTHER INFORMATION: Xaa = Phe-(p-CH2)SO3H  
US-11-156-843-30

Query Match 26.9%; Score 21; DB 7; Length 11;  
Best Local Similarity 60.0%; Pred. No. 2.6e+02;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 DHNDY 9  
| | | |  
DB 4 DYEDY 8

RESULT 71  
US-11-156-843-37  
Sequence 37, Application US/11156843  
Publication No. US20050267035A1  
GENERAL INFORMATION:  
APPLICANT: West, Robert R.  
APPLICANT: Shepard, Paul O.  
APPLICANT: Fox, Brian  
TITLE OF INVENTION: Peptide and Polypeptide Inhibitors of  
TITLE OF INVENTION: Complement C1s  
FILE REFERENCE: 00-33  
CURRENT APPLICATION NUMBER: US/11/156,843  
CURRENT FILING DATE: 2005-06-20  
PRIOR APPLICATION NUMBER: US/09/883,727  
PRIOR FILING DATE: 2001-06-18  
NUMBER OF SEQ ID NOS: 140  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 37  
LENGTH: 11  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: C1s exosite binding moiety  
NAME/KEY: MUTAGEN  
LOCATION: (10)...(10)  
OTHER INFORMATION: Xaa = sulfated tyrosine  
US-11-156-843-37

Query Match 26.9%; Score 21; DB 7; Length 11;  
Best Local Similarity 60.0%; Pred. No. 2.6e+02;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 DHNDY 9  
| | | |  
DB 4 DYEDY 8

RESULT 72  
US-11-127-677-88  
Sequence 88, Application US/11127677  
Publication No. US20050272107A1  
GENERAL INFORMATION:  
APPLICANT: Medical Research Council  
APPLICANT: Rabbits, Terence H  
APPLICANT: Tanaka, Tomoyuki  
TITLE OF INVENTION: Intracellular antibodies  
FILE REFERENCE: 18396/2462  
CURRENT APPLICATION NUMBER: US/11/127,677  
CURRENT FILING DATE: 2005-05-12  
PRIOR APPLICATION NUMBER: PCT/GB03/04942  
PRIOR FILING DATE: 2003-11-14  
PRIOR APPLICATION NUMBER: GB 0226729.2  
PRIOR FILING DATE: 2002-11-15  
NUMBER OF SEQ ID NOS: 150  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 88  
LENGTH: 11  
TYPE: PRT  
ORGANISM: Artificial sequence  
FEATURE:  
OTHER INFORMATION: Derived protein sequence of Intracellular Dab  
US-11-127-677-88

Query Match 26.9%; Score 21; DB 7; Length 11;  
Best Local Similarity 60.0%; Pred. No. 2.6e+02;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 5 DHNDY 9  
: || |  
Db 6 NHNTY 10

RESULT 73  
US-11-127-677-90  
; Sequence 90, Application US/11127677  
; Publication No. US20050272107A1  
; GENERAL INFORMATION:  
; APPLICANT: Medical Research Council  
; APPLICANT: Rabbitts, Terence H  
; APPLICANT: Tanaka, Tomoyuki  
; TITLE OF INVENTION: Intracellular antibodies  
; FILE REFERENCE: 18396/2462  
; CURRENT APPLICATION NUMBER: US/11/127,677  
; CURRENT FILING DATE: 2005-05-12  
; PRIOR APPLICATION NUMBER: PCT/GB03/04942  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: GB 0226729.2  
; PRIOR FILING DATE: 2002-11-15  
; NUMBER OF SEQ ID NOS: 150  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 90  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Derived protein sequence of Intracellular Dab  
US-11-127-677-90

Query Match 26.9%; Score 21; DB 7; Length 11;  
Best Local Similarity 60.0%; Pred. No. 2.6e+02;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 5 DHNDY 9  
: || |  
Db 6 NHNTY 10

RESULT 74  
US-11-110-274-321  
; Sequence 321, Application US/11110274  
; Publication No. US20050266502A1  
; GENERAL INFORMATION:  
; APPLICANT: Merchlers, Pascal G.  
; APPLICANT: Hoffmann, Marcel  
; APPLICANT: Spitzels, Koenraad F. F.  
; TITLE OF INVENTION: Methods, Compositions and Compound Assays for Inhibiting  
; TITLE OF INVENTION: Amyloid-Beta Protein Production  
; FILE REFERENCE: P27,657-A USA  
; CURRENT APPLICATION NUMBER: US/11/110,274  
; CURRENT FILING DATE: 2005-04-20  
; PRIOR APPLICATION NUMBER: US 60/563,661  
; PRIOR FILING DATE: 2004-04-20  
; NUMBER OF SEQ ID NOS: 620  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 321  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-110-274-321

Query Match 26.9%; Score 21; DB 7; Length 12;  
Best Local Similarity 44.4%; Pred. No. 2.8e+02;  
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 6 HNDYKPM 14

Db 2 HNSLRAPM 10

RESULT 75  
US-10-511-559-475  
; Sequence 475, Application US/10511559  
; Publication No. US20050256304A1  
; GENERAL INFORMATION:  
; APPLICANT: JONES, Tim  
; APPLICANT: BAKER, Matthew  
; APPLICANT: CARR, Francis, J.  
; TITLE OF INVENTION: MODIFIED FACTOR VIII  
; FILE REFERENCE: MER-133  
; CURRENT APPLICATION NUMBER: US/10/511,559  
; CURRENT FILING DATE: 2004-10-15  
; PRIOR APPLICATION NUMBER: PCT/EP03/04063  
; PRIOR FILING DATE: 2003-04-17  
; PRIOR APPLICATION NUMBER: EP 02008712.8  
; PRIOR FILING DATE: 2002-04-18  
; PRIOR APPLICATION NUMBER: EP 03006554.4  
; PRIOR FILING DATE: 2003-03-24  
; NUMBER OF SEQ ID NOS: 1147  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 475  
; LENGTH: 13  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Potential Epitope of human Factor VIII  
US-10-511-559-475

Query Match 26.9%; Score 21; DB 6; Length 13;  
Best Local Similarity 37.5%; Pred. No. 3.1e+02;  
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 SIKRDND 8  
: : || |  
Db 4 SLSEKND 11

RESULT 76  
US-10-511-559-476  
; Sequence 476, Application US/10511559  
; Publication No. US20050256304A1  
; GENERAL INFORMATION:  
; APPLICANT: JONES, Tim  
; APPLICANT: BAKER, Matthew  
; APPLICANT: CARR, Francis, J.  
; TITLE OF INVENTION: MODIFIED FACTOR VIII  
; FILE REFERENCE: MER-133  
; CURRENT APPLICATION NUMBER: US/10/511,559  
; CURRENT FILING DATE: 2004-10-15  
; PRIOR APPLICATION NUMBER: PCT/EP03/04063  
; PRIOR FILING DATE: 2003-04-17  
; PRIOR APPLICATION NUMBER: EP 02008712.8  
; PRIOR FILING DATE: 2002-04-18  
; PRIOR APPLICATION NUMBER: EP 03006554.4  
; PRIOR FILING DATE: 2003-03-24  
; NUMBER OF SEQ ID NOS: 1147  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 476  
; LENGTH: 13  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Potential Epitope of human Factor VIII  
US-10-511-559-476

Query Match 26.9%; Score 21; DB 6; Length 13;  
Best Local Similarity 37.5%; Pred. No. 3.1e+02;  
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 SIKRDND 8  
|:|:|  
Db 2 SLSENNND 9

RESULT 77  
US-11-054-515-3172

; Sequence 3172, Application US/11054515  
; Publication No. US20050255532A1

; GENERAL INFORMATION:

; APPLICANT: Ruben et al.

; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys

; FILE REFERENCE: PF523P3

; CURRENT APPLICATION NUMBER: US/11/054,515

; PRIOR FILING DATE: 2005-02-10

; PRIOR APPLICATION NUMBER: 60/543,296

; PRIOR FILING DATE: 2004-02-11

; PRIOR APPLICATION NUMBER: 60/580,347

; PRIOR FILING DATE: 2004-06-18

; PRIOR APPLICATION NUMBER: 10/293,418

; PRIOR FILING DATE: 2002-11-14

; PRIOR APPLICATION NUMBER: 60/331,469

; PRIOR FILING DATE: 2001-11-16

; PRIOR APPLICATION NUMBER: 60/340,817

; PRIOR FILING DATE: 2001-12-19

; PRIOR APPLICATION NUMBER: 09/880,748

; PRIOR FILING DATE: 2001-06-15

; PRIOR APPLICATION NUMBER: 60/293,499

; PRIOR FILING DATE: 2001-05-25

; PRIOR APPLICATION NUMBER: 60/277,379

; PRIOR FILING DATE: 2001-03-21

; PRIOR APPLICATION NUMBER: 60/276,248

; PRIOR FILING DATE: 2001-03-16

; PRIOR APPLICATION NUMBER: 60/240,816

; PRIOR FILING DATE: 2000-10-17

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 3247

; SEQ ID NO 3172

; LENGTH: 13

; TYPE: PRT

; ORGANISM: Homo sapiens

US-11-054-515-3172

Query Match 26.9%; Score 21; DB 7; Length 13;  
Best Local Similarity 60.0%; Pred. No. 3.1e+02;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 DHNDY 9  
|:|:|  
Db 2 DYTDDY 6

RESULT 78  
US-11-054-515-3187

; Sequence 3187, Application US/11054515

; Publication No. US20050255532A1

; GENERAL INFORMATION:

; APPLICANT: Ruben et al.

; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys

; FILE REFERENCE: PF523P3

; CURRENT APPLICATION NUMBER: US/11/054,515

; CURRENT FILING DATE: 2005-02-10

; PRIOR APPLICATION NUMBER: 60/543,296

; PRIOR FILING DATE: 2004-02-11

; PRIOR APPLICATION NUMBER: 60/580,347

; PRIOR FILING DATE: 2004-06-18

; PRIOR APPLICATION NUMBER: 10/293,418

; PRIOR FILING DATE: 2002-11-14

; PRIOR APPLICATION NUMBER: 60/331,469

; PRIOR FILING DATE: 2001-11-16

; PRIOR APPLICATION NUMBER: 60/340,817

; PRIOR FILING DATE: 2001-12-19

; PRIOR APPLICATION NUMBER: 09/880,748

; PRIOR FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/293,499  
; PRIOR FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: 60/277,379  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/276,248  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/240,816  
; PRIOR FILING DATE: 2000-10-17  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 3247  
; SEQ ID NO 3187  
; LENGTH: 13  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-054-515-3187

Query Match 26.9%; Score 21; DB 7; Length 13;  
Best Local Similarity 60.0%; Pred. No. 3.1e+02;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 DHNDY 9  
|:|:|  
Db 2 DYTDDY 6

RESULT 79  
US-11-078-469-109

; Sequence 109, Application US/11078469

; Publication No. US20050282755A1

; GENERAL INFORMATION:

; APPLICANT: HART, SCOTT A.

; APPLICANT: ZEH, KARIN

; APPLICANT: MACHEIDT, THOMAS

; APPLICANT: STOLOW, DAVID

; APPLICANT: CONGER, DEE

; TITLE OF INVENTION: COMPOSITIONS HAVING ANTIMICROBIAL ACTIVITY AND USES

; TITLE OF INVENTION: THEREOF

; FILE REFERENCE: ANS-2001-UT

; CURRENT APPLICATION NUMBER: US/11/078,469

; CURRENT FILING DATE: 2005-03-11

; PRIOR APPLICATION NUMBER: 60/554,526

; PRIOR FILING DATE: 2004-03-18

; PRIOR APPLICATION NUMBER: 60/618,948

; PRIOR FILING DATE: 2004-10-15

; NUMBER OF SEQ ID NOS: 294

; SOFTWARE: PatentIn Ver. 3.3

; SEQ ID NO 109

; LENGTH: 13

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

; OTHER INFORMATION: peptide moiety

; FEATURE:

; NAME/KEY: MOD.RES

; LOCATION: (1)\_ARX

; OTHER INFORMATION: Lauryl-ARX

US-11-078-469-109

Query Match 26.9%; Score 21; DB 7; Length 13;  
Best Local Similarity 57.1%; Pred. No. 3.1e+02;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 8 DYSKNPM 14  
|:|:|  
Db 6 DWSRNFWM 12

RESULT 80  
US-11-078-469-111

; Sequence 111, Application US/11078469

; Publication No. US20050282755A1

GENERAL INFORMATION:  
APPLICANT: HART, SCOTT A.  
APPLICANT: ZEH, KARIN  
APPLICANT: MACHLEIDT, THOMAS  
APPLICANT: STOLOV, DAVID  
APPLICANT: CONGER, DEB  
TITLE OF INVENTION: COMPOSITIONS HAVING ANTIMICROBIAL ACTIVITY AND USES  
FILE REFERENCE: ANS-2001-UT  
CURRENT APPLICATION NUMBER: US/11/078,469  
PRIOR FILING DATE: 2005-03-11  
PRIOR APPLICATION NUMBER: 60/554,526  
PRIOR FILING DATE: 2004-03-18  
PRIOR APPLICATION NUMBER: 60/618,948  
PRIOR FILING DATE: 2004-10-15  
NUMBER OF SEQ ID NOS: 294  
SOFTWARE: PatentIn Ver. 3.3  
SEQ ID NO 111  
LENGTH: 13  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
FEATURE:  
OTHER INFORMATION: peptide moiety  
FEATURE:  
OTHER INFORMATION: This sequence is composed of all D-isomers  
FEATURE:  
NAME/KEY: MOD\_RES  
LOCATION: (1)  
OTHER INFORMATION: Lauryl-Arg  
US-11-078-469-111

Query Match 26.9%; Score 21; DB 7; Length 13;  
Best Local Similarity 57.1%; Pred. No. 3.1e+02;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Cy 8 DYSKMP 14  
Db 6 DMSRPM 12

RESULT 81  
US-11-078-469-113  
Sequence 113, Application US/11078469  
Publication No. US20050282755A1  
GENERAL INFORMATION:  
APPLICANT: HART, SCOTT A.  
APPLICANT: ZEH, KARIN  
APPLICANT: MACHLEIDT, THOMAS  
APPLICANT: STOLOV, DAVID  
APPLICANT: CONGER, DEB  
TITLE OF INVENTION: COMPOSITIONS HAVING ANTIMICROBIAL ACTIVITY AND USES  
FILE REFERENCE: ANS-2001-UT  
CURRENT APPLICATION NUMBER: US/11/078,469  
PRIOR FILING DATE: 2005-03-11  
PRIOR APPLICATION NUMBER: 60/554,526  
PRIOR FILING DATE: 2004-03-18  
PRIOR APPLICATION NUMBER: 60/618,948  
PRIOR FILING DATE: 2004-10-15  
NUMBER OF SEQ ID NOS: 294  
SOFTWARE: PatentIn Ver. 3.3  
SEQ ID NO 113  
LENGTH: 13  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
FEATURE:  
OTHER INFORMATION: peptide moiety  
FEATURE:  
NAME/KEY: MOD\_RES  
LOCATION: (1)  
OTHER INFORMATION: Ac-Arg

US-11-078-469-113

Query Match 26.9%; Score 21; DB 7; Length 13;  
Best Local Similarity 57.1%; Pred. No. 3.1e+02;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Cy 8 DYSKMP 14  
Db 6 DMSRPM 12

RESULT 82  
US-11-078-469-117  
Sequence 117, Application US/11078469  
Publication No. US20050282755A1  
GENERAL INFORMATION:  
APPLICANT: HART, SCOTT A.  
APPLICANT: ZEH, KARIN  
APPLICANT: MACHLEIDT, THOMAS  
APPLICANT: STOLOV, DAVID  
APPLICANT: CONGER, DEB  
TITLE OF INVENTION: COMPOSITIONS HAVING ANTIMICROBIAL ACTIVITY AND USES  
FILE REFERENCE: ANS-2001-UT  
CURRENT APPLICATION NUMBER: US/11/078,469  
PRIOR FILING DATE: 2005-03-11  
PRIOR APPLICATION NUMBER: 60/554,526  
PRIOR FILING DATE: 2004-03-18  
PRIOR APPLICATION NUMBER: 60/618,948  
PRIOR FILING DATE: 2004-10-15  
NUMBER OF SEQ ID NOS: 294  
SOFTWARE: PatentIn Ver. 3.3  
SEQ ID NO 117  
LENGTH: 13  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
FEATURE:  
OTHER INFORMATION: peptide moiety  
FEATURE:  
OTHER INFORMATION: This sequence is composed of all D-isomers  
FEATURE:  
NAME/KEY: MOD\_RES  
LOCATION: (1)  
OTHER INFORMATION: Ac-Arg  
US-11-078-469-117

Query Match 26.9%; Score 21; DB 7; Length 13;  
Best Local Similarity 57.1%; Pred. No. 3.1e+02;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Cy 8 DYSKMP 14  
Db 6 DMSRPM 12

RESULT 83  
US-11-129-104-11  
Sequence 11, Application US/11129104  
Publication No. US20050287644A1  
GENERAL INFORMATION:  
APPLICANT: CHIU, YI-PANG  
APPLICANT: CHEN, LEE-HSIUAN  
APPLICANT: HUANG, JEN-PIN  
TITLE OF INVENTION: METHODS FOR PRODUCING AND CULTURING RABBIT-MOUSE  
TITLE OF INVENTION: HYBRIDOMAS AND MONOCLONAL ANTIBODIES SECRETED BY  
FILE REFERENCE: 09468.0005-00000  
CURRENT APPLICATION NUMBER: US/11/129,104  
PRIOR FILING DATE: 2005-05-13  
PRIOR APPLICATION NUMBER: 60/571,440  
PRIOR FILING DATE: 2004-05-14  
NUMBER OF SEQ ID NOS: 100

```
/ SOFTWARE: PatentIn Ver. 3.3
/ SEQ ID NO 11
/ LENGTH: 13
/ TYPE: PRT
/ ORGANISM: Unknown Organism
/ FEATURE:
/ OTHER INFORMATION: Description of Unknown Organism: Human, Mouse, or
/ OTHER INFORMATION: Canine peptide
US-11-129-104-11
```

```
Query Match      26.9%; Score 21; DB 7; Length 13;
Best Local Similarity 50.0%; Pred. No. 3.4e+02;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      9 YSKNPM 14
Db      5 YDKTFL 10
```

```
RESULT 84
US-10-989-226-52
/ Sequence 52; Application US/10989226
/ Publication No. US20050255491A1
/ GENERAL INFORMATION:
/ APPLICANT: Lee, Frank D.
/ APPLICANT: Meng, Xun
/ APPLICANT: Afeyan, Noubar B.
/ APPLICANT: Gordon, Neal P.
/ TITLE OF INVENTION: SMALL MOLECULE AND PEPTIDE ARRAYS AND
/ TITLE OF INVENTION: USES THEREOF
/ FILE REFERENCE: EP7M-P01-005
/ CURRENT APPLICATION NUMBER: US/10/989,226
/ CURRENT FILING DATE: 2004-11-15
/ PRIOR APPLICATION NUMBER: US 60/519,530
/ PRIOR FILING DATE: 2003-11-13
/ PRIOR APPLICATION NUMBER: US 60/532,687
/ PRIOR FILING DATE: 2003-12-24
/ NUMBER OF SEQ ID NOS: 84
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 52
/ LENGTH: 14
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-989-226-52
```

```
Query Match      26.9%; Score 21; DB 6; Length 14;
Best Local Similarity 50.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      7 NDYSKNPM 14
Db      6 NDYGNPI 13
```

```
RESULT 85
US-10-632-645-15
/ Sequence 15; Application US/10632645
/ Publication No. US20050276787A1
/ GENERAL INFORMATION:
/ APPLICANT: Couto, Linda B.
/ APPLICANT: Colosi, Peter C.
/ TITLE OF INVENTION: Adeno-Associated Vectors for Expression of Factor VIII
/ FILE REFERENCE: Avigen-04082
/ CURRENT APPLICATION NUMBER: US/10/632,645
/ CURRENT FILING DATE: 2003-08-01
/ PRIOR APPLICATION NUMBER: US/09/740,211
/ PRIOR FILING DATE: 2000-12-18
/ PRIOR APPLICATION NUMBER: 09/470,618
/ PRIOR FILING DATE: 1999-12-22
/ PRIOR APPLICATION NUMBER: 60/125,974
/ PRIOR FILING DATE: 1999-03-24
/ PRIOR APPLICATION NUMBER: 60/104,994
```

```
/ PRIOR FILING DATE: 1998-10-20
/ NUMBER OF SEQ ID NOS: 15
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 15
/ LENGTH: 14
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-632-645-15
```

```
Query Match      26.9%; Score 21; DB 6; Length 14;
Best Local Similarity 60.0%; Pred. No. 3.4e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      9 YSKNP 13
Db      2 PSCNP 6
```

```
RESULT 86
US-11-054-515-3218
/ Sequence 3218; Application US/11054515
/ Publication No. US2005025532A1
/ GENERAL INFORMATION:
/ APPLICANT: Ruben et al.
/ TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
/ FILE REFERENCE: PFS3P3
/ CURRENT APPLICATION NUMBER: US/11/054,515
/ CURRENT FILING DATE: 2005-02-10
/ PRIOR APPLICATION NUMBER: 60/543,296
/ PRIOR FILING DATE: 2004-02-11
/ PRIOR APPLICATION NUMBER: 60/580,347
/ PRIOR FILING DATE: 2004-06-18
/ PRIOR APPLICATION NUMBER: 10/293,418
/ PRIOR FILING DATE: 2002-11-14
/ PRIOR APPLICATION NUMBER: 60/331,469
/ PRIOR FILING DATE: 2001-11-16
/ PRIOR APPLICATION NUMBER: 60/340,817
/ PRIOR FILING DATE: 2001-12-19
/ PRIOR APPLICATION NUMBER: 09/880,748
/ PRIOR FILING DATE: 2001-06-15
/ PRIOR APPLICATION NUMBER: 60/293,499
/ PRIOR FILING DATE: 2001-05-25
/ PRIOR APPLICATION NUMBER: 60/277,379
/ PRIOR FILING DATE: 2001-03-21
/ PRIOR APPLICATION NUMBER: 60/276,248
/ PRIOR FILING DATE: 2001-03-16
/ PRIOR APPLICATION NUMBER: 60/240,816
/ PRIOR FILING DATE: 2000-10-17
/ Remaining Prior Application data removed - See file wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 3247
/ SEQ ID NO 3218
/ LENGTH: 14
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-054-515-3218
```

```
Query Match      26.9%; Score 21; DB 7; Length 14;
Best Local Similarity 60.0%; Pred. No. 3.4e+02;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      5 DHNDY 9
Db      6 DYGDY 10
```

```
RESULT 87
US-10-952-535A-29
/ Sequence 29; Application US/10952535A
/ Publication No. US20050255113A1
/ GENERAL INFORMATION:
/ APPLICANT: Huston, James S.
```



APPLICANT: Messer, Anne  
TITLE OF INVENTION: Lecetf, Jean-Michel  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING POLYPEPTIDE  
FILE REFERENCE: INR-004CP  
CURRENT APPLICATION NUMBER: US/10/952,535A  
CURRENT FILING DATE: 2004-09-27  
PRIOR APPLICATION NUMBER: 60/146,047  
PRIOR FILING DATE: 1999-07-27  
NUMBER OF SEQ ID NOS: 45  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 29  
LENGTH: 15  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURES:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-10-952-535A-29

Query Match 26.9%; Score 21; DB 6; Length 15;  
Best Local Similarity 40.0%; Pred. No. 3.6e+02;  
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Oy 5 HNDYSKNPM 14  
Db 2 DVPDYATPPL 11

RESULT 88  
US-11-045-024-13379  
Sequence 13379, Application US/11045024  
Publication No. US20050271676A1  
GENERAL INFORMATION:  
APPLICANT: Sette, Alessandro  
APPLICANT: Sidney, John  
APPLICANT: Southwood, Scott  
APPLICANT: Livingston, Brian  
APPLICANT: Chesnut, Robert  
APPLICANT: Baker, Denise Marie  
APPLICANT: Cells, Eteban  
APPLICANT: Kubo, Ralph  
APPLICANT: Grey, Howard M.  
APPLICANT: Eplimmune Inc.  
TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency  
FILE REFERENCE: 2060.0040007  
CURRENT APPLICATION NUMBER: US/11/045,024  
CURRENT FILING DATE: 2005-01-28  
PRIOR APPLICATION NUMBER: US 09/412,863  
PRIOR FILING DATE: 1999-10-05  
PRIOR APPLICATION NUMBER: US 08/027,146  
PRIOR FILING DATE: 1993-03-05  
PRIOR APPLICATION NUMBER: US 08/073,205  
PRIOR FILING DATE: 1993-06-04  
PRIOR APPLICATION NUMBER: US 08/103,396  
PRIOR FILING DATE: 1993-08-06  
PRIOR APPLICATION NUMBER: US 08/159,184  
PRIOR FILING DATE: 1993-11-29  
PRIOR APPLICATION NUMBER: US 08/159,339  
PRIOR FILING DATE: 1993-11-29  
PRIOR APPLICATION NUMBER: US 08/205,713  
PRIOR FILING DATE: 1994-03-04  
PRIOR APPLICATION NUMBER: US 08/347,610  
PRIOR FILING DATE: 1994-12-01  
NUMBER OF SEQ ID NOS: 14528  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 13379  
LENGTH: 15  
TYPE: PRT  
ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS  
US-11-045-024-13379

Query Match 26.9%; Score 21; DB 7; Length 15;  
Best Local Similarity 36.4%; Pred. No. 3.6e+02;  
Matches 4; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Oy 2 IKRDNDYSKN 12  
Db 5 IEESQNOQERN 15

RESULT 89  
US-11-108-185-39  
Sequence 39, Application US/1108185  
Publication No. US20050262591A1  
GENERAL INFORMATION:  
APPLICANT: Debonte, Lorin R.  
APPLICANT: Fan, Zhongong  
APPLICANT: Miao, Guo-Hua  
TITLE OF INVENTION: FATY ACID DESATURASES AND MUTANT SEQUENCES THEREOF  
FILE REFERENCE: 07148-063003  
CURRENT APPLICATION NUMBER: US/11/108,185  
CURRENT FILING DATE: 2005-04-18  
PRIOR APPLICATION NUMBER: US/09/771,904  
PRIOR FILING DATE: 2001-01-29  
PRIOR APPLICATION NUMBER: US 08/874,109  
PRIOR FILING DATE: 1997-06-12  
NUMBER OF SEQ ID NOS: 70  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 39  
LENGTH: 16  
TYPE: PRT  
ORGANISM: Arabidopsis thaliana  
US-11-108-185-39

Query Match 26.9%; Score 21; DB 7; Length 16;  
Best Local Similarity 33.3%; Pred. No. 3.9e+02;  
Matches 3; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Oy 6 HNDYSKNPM 14  
Db 4 YGKTYLNPL 12

RESULT 90  
US-11-108-185-42  
Sequence 42, Application US/1108185  
Publication No. US20050262591A1  
GENERAL INFORMATION:  
APPLICANT: Debonte, Lorin R.  
APPLICANT: Fan, Zhongong  
APPLICANT: Miao, Guo-Hua  
TITLE OF INVENTION: FATY ACID DESATURASES AND MUTANT SEQUENCES THEREOF  
FILE REFERENCE: 07148-063003  
CURRENT APPLICATION NUMBER: US/11/108,185  
CURRENT FILING DATE: 2005-04-18  
PRIOR APPLICATION NUMBER: US/09/771,904  
PRIOR FILING DATE: 2001-01-29  
PRIOR APPLICATION NUMBER: US 08/874,109  
PRIOR FILING DATE: 1997-06-12  
NUMBER OF SEQ ID NOS: 70  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 42  
LENGTH: 16  
TYPE: PRT  
ORGANISM: Ricinus communis  
US-11-108-185-42

Query Match 26.9%; Score 21; DB 7; Length 16;  
Best Local Similarity 40.0%; Pred. No. 3.9e+02;  
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Oy 4 RDNDYSKNP 13  
Db 2 RWISKTYLNPL 11

## RESULT 91

US-11-108-185-67  
 ; Sequence 67, Application US/11108185  
 ; Publication No. US20050262591A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: DeBonte, Lorin R.  
 ; APPLICANT: Fan, Zhegong  
 ; APPLICANT: Miao, Guo-Hua  
 ; TITLE OF INVENTION: FATTY ACID DESATURASES AND MUTANT SEQUENCES THEREOF  
 ; FILE REFERENCE: 07148-063003  
 ; CURRENT APPLICATION NUMBER: US/11/108,185  
 ; CURRENT FILING DATE: 2005-04-18  
 ; PRIOR APPLICATION NUMBER: US/09/771,904  
 ; PRIOR FILING DATE: 2001-01-29  
 ; PRIOR APPLICATION NUMBER: US 08/874,109  
 ; PRIOR FILING DATE: 1997-06-12  
 ; NUMBER OF SEQ ID NOS: 70  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 67  
 ; LENGTH: 16  
 ; TYPE: PRT  
 ; ORGANISM: Brassica napus  
 US-11-108-185-67

Query Match 26.9%; Score 21; DB 7; Length 16;  
 Best Local Similarity 33.3%; Pred. No. 3.9e+02;  
 Matches 3; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 6 HNDYSKNPM 14  
 : | | | |  
 Db 4 YGKXIANPL 12

## RESULT 92

US-10-201-525-23  
 ; Sequence 23, Application US/10201525  
 ; Publication No. US2006009631A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Board of Regents of the University of Oklahoma  
 ; TITLE OF INVENTION: TYROSYLPROTEIN SULFOTRANSFERASES AND METHODS OF USE THEREOF  
 ; FILE REFERENCE: 5827.005  
 ; CURRENT APPLICATION NUMBER: US/10/201,525  
 ; CURRENT FILING DATE: 2002-07-22  
 ; PRIOR APPLICATION NUMBER: 09/785,343  
 ; PRIOR FILING DATE: 2001-02-16  
 ; PRIOR APPLICATION NUMBER: PCT/US99/16750  
 ; PRIOR FILING DATE: 1999-07-23  
 ; NUMBER OF SEQ ID NOS: 45  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 23  
 ; LENGTH: 17  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-201-525-23

Query Match 26.9%; Score 21; DB 6; Length 17;  
 Best Local Similarity 60.0%; Pred. No. 4.2e+02;  
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 5 DHNDY 9  
 | : | | |  
 Db 5 DYEDY 9

RESULT 93  
 US-11-038-980-165  
 ; Sequence 165, Application US/11038980  
 ; Publication No. US2006002893A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Cemellon SAS  
 ; APPLICANT: Emmanuelle Vigne

; APPLICANT: Jean-Francois Dedieu  
 ; APPLICANT: Martine Yach  
 ; APPLICANT: Patrice Yeh  
 ; APPLICANT: Michel Perricaudet  
 ; TITLE OF INVENTION: Targeted Adenovirus Vectors for Delivery Of Heterologous Genes  
 ; FILE REFERENCE: P26, 992-C USA  
 ; CURRENT APPLICATION NUMBER: US/11/038,980  
 ; CURRENT FILING DATE: 2005-01-20  
 ; PRIOR APPLICATION NUMBER: US 09/791,524  
 ; PRIOR FILING DATE: 2001-02-22  
 ; PRIOR APPLICATION NUMBER: PCT/IB99/01524  
 ; PRIOR FILING DATE: 1999-08-27  
 ; PRIOR APPLICATION NUMBER: US 60/098,028  
 ; PRIOR FILING DATE: 1998-08-27  
 ; NUMBER OF SEQ ID NOS: 165  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 165  
 ; LENGTH: 17  
 ; TYPE: PRT  
 ; ORGANISM: Human  
 US-11-038-980-165

Query Match 26.9%; Score 21; DB 7; Length 17;  
 Best Local Similarity 40.0%; Pred. No. 4.2e+02;  
 Matches 4; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 4 RDNDYSKNP 13  
 | : | | |  
 Db 5 RGRNONSRRP 14

## RESULT 94

US-10-503-575-77  
 ; Sequence 77, Application US/10503575  
 ; Publication No. US20050244823A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Drijfhout, Jan Wouter  
 ; APPLICANT: van Veele, Petrus Antonius  
 ; APPLICANT: Konig, Frits  
 ; TITLE OF INVENTION: NOVEL EPTROPS FOR CELIAC DISEASE AND AUTOIMMUNE DISEASES, METHOD  
 ; FILE REFERENCE: 2799/72843-PCT-US  
 ; CURRENT APPLICATION NUMBER: US/10/503,575  
 ; CURRENT FILING DATE: 2004-08-04  
 ; PRIOR APPLICATION NUMBER: PCT/NL03/00077  
 ; PRIOR FILING DATE: 2003-02-04  
 ; PRIOR APPLICATION NUMBER: EP 02075456.0  
 ; PRIOR FILING DATE: 2002-02-04  
 ; NUMBER OF SEQ ID NOS: 340  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 77  
 ; LENGTH: 18  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-503-575-77

Query Match 26.9%; Score 21; DB 6; Length 18;  
 Best Local Similarity 37.5%; Pred. No. 4.5e+02;  
 Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 6 HNDYSKNP 13  
 | : | | |  
 Db 4 HCNVQQQP 11

RESULT 95  
 US-10-485-788A-536  
 ; Sequence 536, Application US/10485788A  
 ; Publication No. US20050282743A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Lu, Peter S.  
 ; APPLICANT: Rabinowitz, Joshua D.  
 ; APPLICANT: Schweizer, Johannes

```

; APPLICANT: Carrick, Deanna Marie
; APPLICANT: Arbor Vita Corporation
; TITLE OF INVENTION: Molecular Interactions in Cells
; FILE REFERENCE: 20054-003320US
; CURRENT APPLICATION NUMBER: US/10/485,788A
; PRIOR FILING DATE: 2004-02-03
; PRIOR APPLICATION NUMBER: US 60/309,841
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 60/360,061
; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: WO PCT/US02/24655
; PRIOR FILING DATE: 2002-08-02
; NUMBER OF SEQ ID NOS: 841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 536
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-485-788A-536

Query Match      26.9%; Score 21; DB 6; Length 18;
Best Local Similarity 60.0%; Pred. No. 4.5e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      5 DHNDY 9
      ||:|
Db      8 DNDY 12

RESULT 96
US-10-500-878-18
; Sequence 18, Application US/10500878
; Publication No. US20050287527A1
; GENERAL INFORMATION:
; APPLICANT: National Research Council of Canada
; APPLICANT: NI, Feng
; APPLICANT: SU, Zhengding
; APPLICANT: XU, Ping
; APPLICANT: TOLKACHEV, Dmitri
; APPLICANT: OSBORNE, Michael J.
; APPLICANT: KOTLYCHENKO, Anatol
; TITLE OF INVENTION: QUANTITATIVE RANKING OF TRANSIENT LIGAND
; TITLE OF INVENTION: BINDING TO TARGET BIOMOLECULES BY USE OF NUCLEAR MAGNETIC
; TITLE OF INVENTION: RESONANCE
; FILE REFERENCE: 2139-24PCT
; CURRENT APPLICATION NUMBER: US/10/500,878
; CURRENT FILING DATE: 2004-07-07
; PRIOR APPLICATION NUMBER: US 60/346,894
; PRIOR FILING DATE: 2002-01-11
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Anti-thrombin peptide
US-10-500-878-18

Query Match      26.9%; Score 21; DB 6; Length 18;
Best Local Similarity 60.0%; Pred. No. 4.5e+02;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      4 RDHND 8
      :|
Db      2 QSHND 6

RESULT 97
US-11-033-039-1304
; Sequence 1304, Application US/11033039
; Publication No. US2006002947A1
; GENERAL INFORMATION:
```

```

; APPLICANT: HIMPHREYS, ROBERT
; APPLICANT: XU, MINZHEN
; TITLE OF INVENTION: LI-KEY/ANTIGENIC EPIOTOPE HYBRID PEPTIDE VACCINES
; FILE REFERENCE: RES-2017US01
; CURRENT APPLICATION NUMBER: US/11/033,039
; PRIOR FILING DATE: 2005-01-11
; PRIOR APPLICATION NUMBER: 10/245,871
; PRIOR FILING DATE: 2002-09-17
; PRIOR APPLICATION NUMBER: 10/197,000
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: 09/396,813
; PRIOR FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 1452
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1304
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; NAME/KEY: MOD RES
; LOCATION: (5)-(5)
; OTHER INFORMATION: Ava
US-11-033-039-1304

Query Match      26.9%; Score 21; DB 7; Length 18;
Best Local Similarity 57.1%; Pred. No. 4.5e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      2 IKRDHND 8
      :|
Db      3 MKXDND 9

RESULT 98
US-10-956-755A-5
; Sequence 5, Application US/10956755A
; Publication No. US20050282747A1
; GENERAL INFORMATION:
; APPLICANT: Clark, Richard A.
; APPLICANT: Prestwich, Glenn
; TITLE OF INVENTION: Methods and Compositions for Wound Healing
; FILE REFERENCE: STONYB-09223
; CURRENT APPLICATION NUMBER: US/10/956,755A
; CURRENT FILING DATE: 2004-10-01
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-956-755A-5

Query Match      26.9%; Score 21; DB 6; Length 20;
Best Local Similarity 41.7%; Pred. No. 5e+02;
Matches 5; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY      2 IKRDHNDYKSNP 13
      :|
Db      9 IPREDVDYHLYP 20

RESULT 99
US-11-054-515-2131
; Sequence 2131, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
```

```

; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2131
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-2131

```

```

Query Match      26.9%; Score 21; DB 7; Length 20;
Best Local Similarity 60.0%; Pred. No. 5e+02;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY      6 HANDYS 10
      |||
      8 HNKYA 12
DB

```

```

RESULT 100
US-11-078-469-55
; Sequence 55, Application US/11078469
; Publication No. US20050282755A1
; GENERAL INFORMATION:
; APPLICANT: HART, SCOTT A.
; APPLICANT: ZEH, KARIN
; APPLICANT: MACHEIDT, THOMAS
; APPLICANT: STOLW, DAVID
; APPLICANT: CONGER, DEB
; TITLE OF INVENTION: COMPOSITIONS HAVING ANTIMICROBIAL ACTIVITY AND USES
; FILE REFERENCE: ANS-2001-UT
; CURRENT APPLICATION NUMBER: US/11/078,469
; CURRENT FILING DATE: 2005-03-11
; PRIOR APPLICATION NUMBER: 60/554,526
; PRIOR FILING DATE: 2004-03-18
; PRIOR APPLICATION NUMBER: 60/618,948
; PRIOR FILING DATE: 2004-10-15
; NUMBER OF SEQ ID NOS: 294
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 55
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide moiety
; FEATURE:
; OTHER INFORMATION: This sequence is composed of all D-isomers
; NAME/KEY: MOD_RES
; LOCATION: (1)

```

```

; OTHER INFORMATION: Ac-Thr
US-11-078-469-55
Query Match      26.9%; Score 21; DB 7; Length 20;
Best Local Similarity 57.1%; Pred. No. 5e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY      8 DYSGNPM 14
      |||
      13 DMSRNTM 19
DB

```

Search completed: January 20, 2006, 19:46:27  
 Job time : 6.65385 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 20, 2006, 18:55:50 : Search time 7.94231 Seconds  
(without alignments)  
169.602 Million cell updates/sec

Title: US-09-662-293-1

Perfect score: 78

Sequence: 1 SIKRDNDYSKNPM 14

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 3886

Minimum DB seq length: 0  
Maximum DB seq length: 20

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

PIR 80:\*  
1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	25.5	32.7	20	2	665605
2	25	32.1	20	2	S56005
3	24.5	31.4	19	2	S63476
4	24	30.8	15	2	S27248
5	23	29.5	11	2	S65395
6	23	29.5	18	2	PH1629
7	22	28.2	17	2	S32587
8	22	28.2	20	2	A53875
9	21	26.9	11	2	PC2330
10	21	26.9	11	2	A26930
11	21	26.9	14	2	PS0252
12	21	26.9	14	2	A41589
13	21	26.9	15	2	I67525
14	21	26.9	17	2	PH0769
15	21	26.9	18	2	H64711
16	21	26.9	18	2	B41589
17	21	26.9	19	2	PT0244
18	20	25.6	9	2	S66608
19	20	25.6	9	2	PT0272
20	20	25.6	10	2	S62208
21	20	25.6	11	2	S65377
22	20	25.6	14	1	NYPE14
23	20	25.6	16	2	PH1778
24	20	25.6	16	2	S09084
25	20	25.6	17	2	B42965
26	20	25.6	20	2	E61497
27	20	25.6	20	2	S77992
28	19	24.4	9	2	PT0299
29	19	24.4	10	2	A13687

30	19	24.4	10	2	S74176
31	19	24.4	10	2	S23370
32	19	24.4	11	2	S23926
33	19	24.4	12	2	S65730
34	19	24.4	15	2	PH1342
35	19	24.4	15	2	PL0143
36	19	24.4	15	2	A35417
37	19	24.4	16	2	PH0791
38	19	24.4	16	2	S22040
39	19	24.4	18	2	C56211
40	19	24.4	19	2	I45957
41	19	24.4	19	2	S59485
42	19	24.4	19	2	PH1360
43	19	24.4	19	2	A61377
44	19	24.4	20	2	PH1338
45	19	24.4	20	2	T48881
46	19	24.4	20	2	A61506
47	19	24.4	20	2	B56894
48	18	23.1	7	2	A28709
49	18	23.1	11	2	A38841
50	18	23.1	11	2	S00616
51	18	23.1	13	2	S47365
52	18	23.1	14	2	PH1471
53	18	23.1	14	2	PA0007
54	18	23.1	15	1	SPRT
55	18	23.1	15	2	PA0090
56	18	23.1	15	2	G35141
57	18	23.1	15	2	C44101
58	18	23.1	15	2	S62641
59	18	23.1	15	2	S77987
60	18	23.1	16	1	MTDPBS
61	18	23.1	16	1	D58501
62	18	23.1	16	2	S11760
63	18	23.1	16	2	B44820
64	18	23.1	16	2	B28027
65	18	23.1	17	2	A61117
66	18	23.1	17	2	S57991
67	18	23.1	17	2	B28027
68	18	23.1	17	2	B61491
69	18	23.1	18	2	PH1815
70	18	23.1	18	2	T08159
71	18	23.1	18	2	A59137
72	18	23.1	19	2	S43657
73	18	23.1	19	2	S31613
74	18	23.1	20	2	S50741
75	18	23.1	20	2	S71017
76	18	23.1	20	2	A44773
77	18	23.1	20	2	I54283
78	18	23.1	20	2	H49164
79	17.5	22.4	13	2	A26999
80	17	21.8	7	2	S17976
81	17	21.8	8	2	B54823
82	17	21.8	9	2	S30494
83	17	21.8	9	2	B24362
84	17	21.8	11	2	S18385
85	17	21.8	12	2	B47171
86	17	21.8	12	2	PH1605
87	17	21.8	12	2	T46794
88	17	21.8	13	2	PT0331
89	17	21.8	13	4	I70075
90	17	21.8	14	2	PT0029
91	17	21.8	15	2	A58945
92	17	21.8	15	2	PH1631
93	17	21.8	15	2	B26501
94	17	21.8	15	2	PA0059
95	17	21.8	16	2	C45133
96	17	21.8	16	2	PT0224
97	17	21.8	17	2	S48635
98	17	21.8	17	2	B44923
99	17	21.8	17	2	A46592
100	17	21.8	18	2	S24780

glucocortikase (EC  
T-cell receptor al  
major glycoprotein  
hemoglobin, extrac  
Ig heavy chain DJ  
carbon-monoxide de  
28K serine protein  
T-cell receptor al  
cob protein - comm  
progesterone recep  
protein kinase (EC  
hydroxyproline-rich  
Ig heavy chain DJ  
endometrial secret  
Ig heavy chain DJ  
leader peptide [Im  
alpha-1-antitrypsin  
intracystalline c  
phosphonocetaldh  
rhodopsin homolog  
parastatal crystal  
T-cell antigen rec  
T-cell receptor be  
lectin B1 - Peop  
scotophobin - rat  
protein QP100022 -  
T-cell receptor de  
calmodulin, vasoac  
porphobilinogen sy  
cytochrome-c oxida  
melanotropin beta  
26K kidney and gal  
f1g1 protein - Cau  
7K protein - Esche  
protein P8 - curle  
homoostatin precu  
hydroxyproline-ric  
protein P4 - curle  
seed protein ws-2  
T cell receptor al  
S locus-linked pro  
protein p11 - gold  
hep90 protein homo  
beta-1,3-glucanase  
probable trypsin I  
hypothetical prote  
pollen allergen I  
arylsulfatase A -  
chromogranin-B - r  
carboxylesterase (  
glucose isomerase  
olfactory receptor  
cat gene leader pe  
chloramphenicol O-  
NMP-cytochrome P4  
chondroitin sulfat  
Ig H chain V-D-J r  
hypothetical prote  
Ig heavy chain CDR  
glycophorin B (m  
karatsain - Karata  
anti-neoplastic ur  
Ig H chain V-D-J r  
lipoprotein lipase  
protein QP200021 -  
casein kinase II (  
Ig heavy chain CDR  
glutathione dehydr  
carboxypeptidase 3  
lactase-phlorizin  
protein-tyrosine k

## ALIGNMENTS

RESULT 1  
S65605  
dimeric protein (BDP) - barley (fragment)  
C/Species: Hordeum vulgare (barley)  
C/Date: 19-Mar-1997 #sequence\_revision 25-Apr-1997 #text\_change 09-Jul-2004  
C/Accession: S65605  
R/Garcia-Casado, G.; Armentia, A.; Sanchez-Monge, R.; Sanchez, I.M.; Lopez-Otin, C.; Sal  
PEBS Lett. 364, 36-40, 1995  
A/Title: A major baker's asthma allergen from rye flour is considerably more active than  
A/Reference number: S65604; MUID:95268763; PMID:7750539  
A/Accession: S65605  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-20 <GAR>  
A/Cross-references: UNIPROT:Q9S8H1; UNIPARC:UPI00009D53B

Query Match 32.7%; Score 25.5; DB 2; Length 20;  
Best Local Similarity 26.3%; Pred. No. 4.7e+02;  
Matches 5; Conservative 5; Mismatches 2; Indels 7; Gaps 1;

Oy 3 KRDNHYSK-----NPM 14  
|||:|:|:|:|:|:  
Db 1 ERDGYGVCRVKSIPNPL 19

RESULT 2  
S56005  
lysosomal protein 22K - rat (fragment)  
C/Species: Rattus norvegicus (Norway rat)  
C/Date: 10-Oct-1995 #sequence\_revision 03-Nov-1995 #text\_change 07-May-1999  
C/Accession: S56005  
R/Kuwana, T.; Mullock, B.M.; Luzzio, J.P.  
Biochem. J. 308, 937-946, 1995  
A/Title: Identification of a lysosomal protein causing lipid transfer, using a fluoresce  
A/Reference number: S56005; MUID:97104296; PMID:8948454  
A/Accession: S56005  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-20 <KUM>  
A/Cross-references: UNIPARC:UPI0000E7C21

Query Match 32.1%; Score 25; DB 2; Length 20;  
Best Local Similarity 44.4%; Pred. No. 5.7e+02;  
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Oy 5 DHNDYKNP 13  
||:|:|:|:|:  
Db 4 DNDDEGKDP 12

RESULT 3  
S63476  
dihydrolipoamide dehydrogenase (EC 1.8.1.4) beta chain E1 - Pseudomonas putida (fragment)  
N/Alternate names: branched-chain oxoacid dehydrogenase chain E1  
C/Species: Pseudomonas putida  
C/Date: 28-Oct-1996 #sequence\_revision 13-Mar-1997 #text\_change 09-Jul-2004  
C/Accession: S63476; S63477  
R/Hester, K.; Luo, J.; Burns, G.; Braswell, E.H.; Sokatch, J.R.  
Eur. J. Biochem. 233, 828-836, 1995  
A/Title: Purification of active E1-alpha(2)-beta(2) of Pseudomonas putida branched-chain  
A/Reference number: S63475; MUID:96085147; PMID:8521848  
A/Accession: S63476  
A/Molecule type: protein  
A/Residues: 1-19 <HES>  
A/Cross-references: UNIPROT:Q7MOQ1; UNIPARC:UPI000017A9F

A/Accession: S63477  
A/Molecule type: protein  
A/Residues: 15-19 <HEW>  
A/Cross-references: UNIPARC:UPI000017A990  
C/Comment: Dihydrolipoamide dehydrogenase beta chain E1 exists in two forms (37K and 39K

C/Genetics:  
A/Gene: bhdA2  
C/Keywords: alternative initiators; PAD; flavoprotein; lipoamide; NAD; oxidoreductase  
F/1-19/Product: dihydrolipoamide dehydrogenase beta chain E1, 39K (fragment) #status ex  
F/15-19/Product: dihydrolipoamide dehydrogenase beta chain E1, 37K (fragment) #status e

Query Match 31.4%; Score 24.5; DB 2; Length 19;  
Best Local Similarity 66.7%; Pred. No. 6.6e+02;  
Matches 6; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

Oy 5 DHNDYKNP 13  
|||:|:|:|:|:  
Db 3 DHNN-SINP 10

RESULT 4  
S27248  
pseudogerm - wheat  
C/Species: Triticum aestivum (common wheat)  
C/Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 29-Aug-1997  
C/Accession: S27248  
R/Lane, B.G.; Cuming, A.C.; Fregeau, J.; Carpica, N.C.; Hurkman, W.J.; Bernier, F.; Dra  
Eur. J. Biochem. 209, 961-969, 1992  
A/Title: Germ in isoforms are discrete temporal markers of wheat development. Pseudogerm  
ated embryos, it is incorporated into cell walls.  
A/Reference number: S27247; MUID:93049354; PMID:1425703  
A/Accession: S27248  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-15 <LAN>  
A/Cross-references: UNIPARC:UPI000017B14D

Query Match 30.8%; Score 24; DB 2; Length 15;  
Best Local Similarity 66.7%; Pred. No. 6.6e+02;  
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 8 DYSKNP 13  
|||:|:|:|:|:  
Db 3 DYKPNP 8

RESULT 5  
S65395  
chemical-sense-related lipophilic-ligand-binding protein - fruit fly (Drosophila melano  
C/Species: Drosophila melanogaster  
C/Date: 28-Oct-1996 #sequence\_revision 13-Mar-1997 #text\_change 09-Jul-2004  
C/Accession: S65395  
R/Ozaki, M.; Morisaki, K.; Idei, W.; Ozaki, K.; Tokunaga, F.  
Eur. J. Biochem. 230, 298-308, 1995  
A/Title: A putative lipophilic stimulant carrier protein commonly found in the taste an  
A/Reference number: S65394; MUID:95324537; PMID:7601113  
A/Accession: S65395  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-11 <OZA>  
A/Cross-references: UNIPROT:Q8MYT1; UNIPROT:Q9VR97; UNIPARC:UPI000017BB82

Query Match 29.5%; Score 23; DB 2; Length 11;  
Best Local Similarity 80.0%; Pred. No. 6.8e+02;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 2 IKRDH 6  
|||:|:|:|:|:  
Db 4 INRDH 8

RESULT 6  
P1629  
19 H chain V-D-J region (clone B-1e8 155) - mouse (fragment)  
C/Species: Mus musculus (house mouse)  
C/Date: 02-Jun-1994 #sequence\_revision 02-Jun-1994 #text\_change 17-Mar-1999  
C/Accession: P1629  
R/Levinson, D.A.; Campos-Torres, J.; Leder, P.

J. Exp. Med. 178, 317-329, 1993  
 A>Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice  
 A'Reference number: PH1580; MUID:93301609; PMID:8315387  
 A'Accession: PH1629  
 A'Molecule type: DNA  
 A'Residuals: 1-18 <LEV>  
 A'Cross-references: UNIPARC:UPI000017C695  
 A'Experimental source: bone marrow pre-B lymphocyte  
 C'Keywords: immunoglobulin

Query Match 29.5%; Score 23; DB 2; Length 18;  
 Best Local Similarity 44.4%; Pred. No. 1.1e+03;  
 Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 IRDNDYS 10  
 |||:  
 Db 2 VARDYDGS 10

## RESULT 7

S32587  
 L-ascorbate peroxidase (EC 1.11.1.11) isozyme II - spinach (fragment)  
 C'Species: Spinacia oleracea (spinach)  
 C'Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 30-Sep-1993  
 C'Accession: S32587; S15878  
 R'Kudo, A.; Saji, H.; Tanaka, K.; Kondo, N.  
 Plant Mol. Biol. 18, 691-701, 1992

A>Title: Cloning and sequencing of a cDNA encoding ascorbate peroxidase from Arabidopsis  
 A'Reference number: S20866; MUID:92216045; PMID:1558944  
 A'Accession: S32587  
 A'Molecule type: protein

A'Residuals: 1-17 <KUB>  
 A'Cross-references: UNIPARC:UPI000017A924

A'Note: This is a revision to the sequence from reference S15878  
 R'Tanaka, K.; Takeuchi, E.; Kudo, A.; Sakaki, T.; Harauchi, K.; Kawamura, Y.  
 Arch. Biochem. Biophys. 286, 371-375, 1991

A>Title: Two immunologically different isozymes of ascorbate peroxidase from spinach leaf  
 A'Reference number: S15878; MUID:91378325; PMID:1897862  
 A'Accession: S15878

A'Molecule type: Protein  
 A'Residuals: 1,3-17 <TAN>

A'Cross-references: UNIPARC:UPI000017A925

A'Note: This sequence has been revised in reference S20866  
 C'Keywords: chloroplast; oxidoreductase

Query Match 28.2%; Score 22; DB 2; Length 17;  
 Best Local Similarity 42.9%; Pred. No. 1.6e+03;  
 Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 6 HNDYSKN 12  
 |||:  
 Db 8 HENYKKS 14

## RESULT 8

A53875  
 creatine kinase (EC 2.7.3.2) CK-MM - coho salmon (fragment)  
 C'Species: Oncorhynchus kisutch (coho salmon)  
 C'Date: 26-Sep-1994 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004

C'Accession: A53875  
 R'White, K.C.; Babbitt, P.C.; Buechter, D.D.; Kenyon, G.L.  
 J. Protein Chem. 11, 489-494, 1992

A>Title: The principal islet of the coho salmon (*Oncorhynchus kisutch*) contains the BB is  
 A'Reference number: A53875; MUID:93080727; PMID:1445958

A'Accession: A53875  
 A'Status: preliminary; not compared with conceptual translation  
 A'Molecule type: nucleic acid

A'Residuals: 1-20 <WHI>  
 A'Cross-references: UNIPROT:Q9PS15; UNIPARC:UPI00000PB530

A'Experimental source: Brockmann body, principal islet  
 A'Note: sequence extracted from NCBI backbone (NCBIP:120599)

C'Superfamily: creatine kinase; creatine kinase repeat homology  
 C'Keywords: phosphotransferase

Query Match 28.2%; Score 22; DB 2; Length 20;  
 Best Local Similarity 42.9%; Pred. No. 1.9e+03;  
 Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 6 HNDYSKN 12  
 |||:  
 Db 6 HNNPKLN 12

## RESULT 9

PC2330  
 cyclooligoglucosaccharide fructanotransferase (EC 2.4.-.-) - Bacillus circulans (MCI-2

C'Species: Bacillus circulans  
 C'Date: 21-Mar-1995 #sequence\_revision 26-May-1995 #text\_change 09-Jul-2004  
 C'Accession: PC2330

R'Kushibe, S.; Mitsu, K.; Yamagishi, M.; Yamada, K.; Morimoto, Y.  
 Biosci. Biotechnol. Biochem. 59, 31-34, 1995

A>Title: Purification and characterization of cyclooligoglucosaccharide fructanotransf  
 A'Reference number: PC2330; MUID:95201377; PMID:7765973

A'Accession: PC2330  
 A'Molecule type: protein

A'Cross-references: UNIPROT:Q7M0L3; UNIPARC:UPI000017AC93  
 C'Comment: This enzyme hydrolyzes beta-(2-1) glycosidic linkages and acts in intermole  
 C'Keywords: glycosyltransferase; hexosyltransferase

Query Match 26.9%; Score 21; DB 2; Length 11;  
 Best Local Similarity 50.0%; Pred. No. 1.5e+03;  
 Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 6 HNDYSKNP 13  
 |||:  
 Db 2 HLPYQNP 9

## RESULT 10

A26930  
 ermG leader peptide 1 - Bacillus sphaericus

C'Species: Bacillus sphaericus  
 C'Date: 08-Mar-1989 #sequence\_revision 08-Mar-1989 #text\_change 05-Oct-2004

C'Accession: A26930  
 R'Monod, M.; Mohan, S.; Dubnau, D.

J. Bacteriol. 169, 340-350, 1987  
 A>Title: Cloning and analysis of ermG, a new macrolide-lincosamide-streptogramin B res

A'Reference number: A91840; MUID:87083389; PMID:3025178  
 A'Accession: A26930

A'Molecule type: DNA  
 A'Residuals: 1-11 <MON>

A'Cross-references: UNIPROT:P26840; UNIPARC:UPI000016B856; GB:M15332; NID:G142881; PIDT

Query Match 26.9%; Score 21; DB 2; Length 11;  
 Best Local Similarity 80.0%; Pred. No. 1.5e+03;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 NDYSK 11  
 |||:  
 Db 2 NKYSK 6

## RESULT 11

PS0252  
 16k protein 5404 - rice (strain Nihonbare) (fragment)

C'Species: Oryza sativa (rice)  
 C'Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 05-Apr-1995

C'Accession: PS0252  
 R'Tsugita, A.  
 Submitted to JIPID, April 1993

A'Reference number: PS0206  
 A'Accession: PS0252

A'Molecule type: protein  
 A'Residuals: 1-14 <TSU>

A'Cross-references: UNIPARC:UPI000017B0EF

A:Experimental source: strain Nihonbare  
C:Comment: Molecular weight 16k, pI 4.9.

Query Match 26.9%; Score 21; DB 2; Length 14;  
Best Local Similarity 37.5%; Pred. No. 2e+03;  
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 IKRDHNY 9  
:|:|:  
Db 3 LEADDDY 10

RESULT 12  
A41589  
25k elastin-binding protein - Staphylococcus aureus (fragment)  
C:Species: Staphylococcus aureus  
C>Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 09-Jul-2004  
C:Accession: A41589  
R:Park, P.W.; Roberts, D.D.; Grosbo, L.E.; Parks, W.C.; Rosenbloom, J.; Abrams, W.R.; Mc  
J. Biol. Chem. 266: 23399-23406, 1991  
A:Title: Binding of elastin to Staphylococcus aureus.  
A:Reference number: A41589; MUID:92078218; PMID:11744133  
A:Accession: A41589  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-14 <PAR>  
A:Cross-references: UNIPROT:Q9RSR5; UNIPARC:UPI00000BC64C

Query Match 26.9%; Score 21; DB 2; Length 14;  
Best Local Similarity 50.0%; Pred. No. 2e+03;  
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 7 NDYSKN 12  
:|:|:  
Db 6 DDFEKN 11

RESULT 13  
167525  
CD3 antigen homolog - mouse (fragment)  
C:Species: Mus sp. (mouse)  
C>Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 09-Jul-2004  
C:Accession: 167525  
R:Chies, J.A.; Lembezat, M.P.; Freltas, A.A.  
Eur. J. Immunol. 24, 1657-1664, 1994  
A:Title: Entry of B lymphocytes into the persistent cell pool in non-immunized mice is r  
A:Reference number: 153392; MUID:94298870; PMID:8026526  
A:Accession: 167525  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-15 <RES>  
A:Cross-references: UNIPROT:Q7M0G8; UNIPARC:UPI000017C992; GB:S71349; NID:9550037  
A:Gene: Ig VH7183

Query Match 26.9%; Score 21; DB 2; Length 15;  
Best Local Similarity 75.0%; Pred. No. 2.1e+03;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 KRDH 6  
:|:|:  
Db 4 RRDH 7

RESULT 14  
PH0769  
T-cell receptor beta chain (J2) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C>Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 05-Nov-1999  
C:Accession: PH0769  
R:Caenova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.  
J. Exp. Med. 174, 1371-1383, 1991  
A:Title: T cell receptor genes in a series of class I major histocompatibility complex-r

allelic exclusion and antigen-specific repertoire.  
A:Reference number: PH0746; MUID:92078846; PMID:1836010  
A:Accession: PH0769  
A:Molecule type: mRNA  
A:Residues: 1-17 <CAS>  
A:Cross-references: UNIPARC:UPI000015FBC; EMBL:X60863; NID:952743; PIDN:CAA43253.1; PI  
A:Experimental source: T lymphocyte  
C:Keywords: T-cell receptor

Query Match 26.9%; Score 21; DB 2; Length 17;  
Best Local Similarity 37.5%; Pred. No. 2.4e+03;  
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 4 RDNDYSK 11  
:|:|:  
Db 6 RDRGNVAF 13

RESULT 15  
H64711  
hypothetical protein HP1536 - Helicobacter pylori (strain 26695)  
C:Species: Helicobacter pylori  
C>Date: 09-Aug-1997 #sequence\_revision 09-Aug-1997 #text\_change 09-Jul-2004  
C:Accession: H64711  
R:Tomb, J.F.; White, O.; Kervavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.I  
Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKen  
son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Wathey, I  
Nature 388, 539-547, 1997  
A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C  
A:Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.  
A:Reference number: A64520; MUID:97394467; PMID:9252185  
A:Accession: H64711  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-18 <TOM>  
A:Cross-references: UNIPROT:O26062; UNIPARC:UPI00000C07C3; GB:AE00651; GB:AE00511; NI

Query Match 26.9%; Score 21; DB 2; Length 18;  
Best Local Similarity 57.1%; Pred. No. 2.6e+03;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 7 NDYSKNP 13  
:|:|:  
Db 9 NHPSRNP 15

RESULT 16  
B41589  
40k elastin-binding protein - Staphylococcus aureus (fragment)  
C:Species: Staphylococcus aureus  
C>Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 09-Jul-2004  
C:Accession: B41589  
R:Park, P.W.; Roberts, D.D.; Grosbo, L.E.; Parks, W.C.; Rosenbloom, J.; Abrams, W.R.; M  
J. Biol. Chem. 266, 23399-23406, 1991  
A:Title: Binding of elastin to Staphylococcus aureus.  
A:Reference number: A41589; MUID:92078218; PMID:11744133  
A:Accession: B41589  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-18 <PAR>  
A:Cross-references: UNIPROT:Q9RSR6; UNIPARC:UPI00000B32A9

Query Match 26.9%; Score 21; DB 2; Length 18;  
Best Local Similarity 50.0%; Pred. No. 2.6e+03;  
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 7 NDYSKN 12  
:|:|:  
Db 6 DDFEKN 11

RESULT 17  
PT0244



Ig heavy chain CDR3 region (clone 2-103B) - human (fragment)  
CISpecies: Homo sapiens (man)  
CjDate: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 06-Jun-1997  
CjAccession: P10244  
R.Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.  
J. Exp. Med. 173, 395-407, 1991  
A>Title: Preferential utilization of specific immunoglobulin heavy chain diversity and J  
A.Reference number: P10222; MUID:91108337; PMID:1899102  
AjAccession: P10244  
AjMolecule type: DNA  
AjResidues: 1-19 <YAM>  
AjCross-references: UNIPARC:UPI000017693B  
AjExperimental source: B lymphocyte  
CjSuperfamily: immunoglobulin V region, immunoglobulin homology  
CjKeywords: heterotrimer; immunoglobulin

Query Match 26.9%; Score 21; DB 2; Length 19;  
Best Local Similarity 60.0%; Pred. No. 2.7e+03;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 DHNDY 9  
|||  
Db 6 DYGDY 10

RESULT 18  
566608  
quinoline 2-oxidoreductase gamma chain - Comamonas testosteroni (fragment)  
CISpecies: Comamonas testosteroni  
CjDate: 15-Feb-1997 #sequence\_revision 13-Mar-1997 #text\_change 17-Mar-1999  
CjAccession: S66608  
R.Schach, S.; Ishisaka, B.; Petzner, S.; Lingens, F.  
Eur. J. Biochem. 232, 536-544, 1995  
A>Title: Quinoline 2-oxidoreductase and 2-oxo-1,2-dihydroquinoline 5,6-dioxygenase from  
A.Reference number: S66606; MUID:96035889; PMID:7556104  
AjAccession: S66608  
AjMolecule type: protein  
AjResidues: 1-9 <SCH>  
AjCross-references: UNIPARC:UPI000017A956  
AjExperimental source: strain 63

Query Match 25.6%; Score 20; DB 2; Length 9;  
Best Local Similarity 75.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 11 KNPM 14  
|||  
Db 6 KNPL 9

RESULT 19  
P10272  
Ig heavy chain CDR3 region (clone 3-103B) - human (fragment)  
CISpecies: Homo sapiens (man)  
CjDate: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996  
CjAccession: P10272  
R.Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.  
J. Exp. Med. 173, 395-407, 1991  
A>Title: Preferential utilization of specific immunoglobulin heavy chain diversity and J  
A.Reference number: P10222; MUID:91108337; PMID:1899102  
AjAccession: P10272  
AjMolecule type: DNA  
AjResidues: 1-9 <YAM>  
AjCross-references: UNIPARC:UPI000017C1F4  
AjExperimental source: B lymphocyte  
CjKeywords: heterotrimer; immunoglobulin

Query Match 25.6%; Score 20; DB 2; Length 9;  
Best Local Similarity 66.7%; Pred. No. 2.8e+05;  
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 NDYSKN 12  
|||

Db 4 NDEKKN 9

RESULT 20  
S62208  
polyferredoxin - Methanococcus barkeri (fragment)  
CISpecies: Methanococcus barkeri  
CjDate: 28-Oct-1996 #sequence\_revision 13-Mar-1997 #text\_change 31-Mar-1997  
CjAccession: S62208  
R.Vorholt, J.A.; Vaupel, M.; Thauer, R.K.  
Eur. J. Biochem. 236, 309-317, 1996  
A>Title: A polyferredoxin with eight (4Fe-4S) clusters as a subunit of molybdenum formy  
A.Reference number: S62194; MUID:96184912; PMID:8617280  
AjAccession: S62208  
AjStatus: preliminary  
AjMolecule type: protein  
AjResidues: 1-10 <VOR>  
AjCross-references: UNIPARC:UPI000017AB9C

Query Match 25.6%; Score 20; DB 2; Length 10;  
Best Local Similarity 42.9%; Pred. No. 2.1e+03;  
Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 HNDYSKN 12  
|||  
Db 2 NTDYDNN 8

RESULT 21  
S65377  
cytochrome-c oxidase (EC 1.9.3.1) chain VIA-H, cardiac - rat (fragment)  
CISpecies: Rattus norvegicus (Norway rat)  
CjDate: 28-Oct-1996 #sequence\_revision 13-Mar-1997 #text\_change 09-Jul-2004  
CjAccession: S65377  
R.Schaeffer, H.; Noack, H.; Halanek, W.; Brandt, U.; von Jagow, G.  
Eur. J. Biochem. 230, 235-241, 1995  
A>Title: Cytochrome-c oxidase in developing rat heart. Enzymic properties and amino-ter  
A.Reference number: S65372; MUID:95324529; PMID:7601105  
AjAccession: S65377  
AjStatus: preliminary  
AjMolecule type: protein  
AjResidues: 1-11 <SCH>  
AjCross-references: UNIPROT:Q7MOD4; UNIPARC:UPI000017C8FD  
CjKeywords: cardiac muscle; heart; oxidoreductase

Query Match 25.6%; Score 20; DB 2; Length 11;  
Best Local Similarity 66.7%; Pred. No. 2.3e+03;  
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 SIKRDH 6  
|||  
Db 2 SAKGDH 7

RESULT 22  
NYPG14  
hypothalamic tetradecapeptide - pig  
CISpecies: Sus scrofa domestica (domestic pig)  
CjDate: 13-Jul-1991 #sequence\_revision 13-Jul-1981 #text\_change 09-Jul-2004  
CjAccession: A01419  
R.Schlesinger, D.H.; Niall, H.D.; Linthicum, G.L.; Dupont, A.; Schally, A.V.  
submitted to the Atlas, November 1976  
AjAccession: A01419  
AjMolecule type: protein  
AjResidues: 1-14 <SCH>  
AjCross-references: UNIPROT:P01155; UNIPARC:UPI000012CFC3  
CjSuperfamily: hypothalamic tetradecapeptide  
CjKeywords: amidated carboxyl end; hypothalamus  
P14/Modified site: amidated carboxyl end (Tyr) #status experimental

Query Match 25.6%; Score 20; DB 1; Length 14;  
Best Local Similarity 60.0%; Pred. No. 2.9e+03;

Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 9 YSKNP 13  
Db 3 YGKSP 7

## RESULT 23

PH1778

T cell receptor alpha chain V region (clone 1PBL V alpha 24-5) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 16-Jul-1999

C/Accession: PH1778

R/Portelli, S.; Yockey, C.E.; Brenner, M.B.; Balk, S.F.

J. Exp. Med. 178, 1-16, 1993

A/Title: Analysis of T cell antigen receptor (TCR) expression by human peripheral blood

A/Reference number: PH1754; PMID:93301585; PMID:8391057

A/Accession: PH1778

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-16 &lt;PQR&gt;

A/Cross-references: UNIPARC:UPI000017C36C

Query Match 25.6%; Score 20; DB 2; Length 16;  
Best Local Similarity 37.5%; Pred. No. 3.4e+03;  
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 IKRDHNTY 9  
Db 5 VRPTFNDY 12

## RESULT 24

S09084

proteasome chain 3 - rat (fragment)

N/Alternate names: multicatalytic proteinase chain 3

C/Species: Rattus norvegicus (Norway rat)

C/Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 09-Jul-2004

C/Accession: S09084

R/Lilley, K.S.; Davison, M.D.; Rivett, A.J.

FEBS Lett. 262, 337-329, 1990

A/Title: N-terminal sequence similarities between components of the multicatalytic prote

A/Reference number: S09082; PMID:90242957; PMID:2335214

A/Accession: S09084

A/Molecule type: protein

A/Residues: 1-16 &lt;LII&gt;

A/Cross-references: UNIPROT:P34067; UNIPARC:UPI000017C99E

Query Match 25.6%; Score 20; DB 2; Length 16;  
Best Local Similarity 60.0%; Pred. No. 3.4e+03;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 10 SKNPM 14  
Db 1 TQNP 5

## RESULT 25

B42965

talin (glycosylated sites) - chicken (fragment)

C/Species: Gallus gallus (chicken)

C/Date: 04-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change 28-Apr-1995

C/Accession: B42965

R/Hagmann, J.; Grob, M.; Burger, M.M.

J. Biol. Chem. 267, 14424-14428, 1992

A/Title: The cytoskeletal protein talin is O-glycosylated.

A/Reference number: A42965; PMID:92333560; PMID:1629228

A/Accession: B42965

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-17 &lt;HAG&gt;

A/Cross-references: UNIPARC:UPI000017C03A

A/Experimental source: gizzard  
A/Note: sequence extracted from NCBI backbone (NCBIP:108592)

Query Match 25.6%; Score 20; DB 2; Length 17;  
Best Local Similarity 60.0%; Pred. No. 3.6e+03;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 NDYSK 11  
Db 9 NDYQ 13

## RESULT 26

E61497

seed protein ws-20 - winged bean (fragment)

C/Species: Psophocarpus tetragonolobus (winged bean)

C/Date: 07-Oct-1994 #sequence\_revision 07-Oct-1994 #text\_change 09-Jul-2004

C/Accession: E61497

R/Hirano, H.

J. Protein Chem. 8, 115-130, 1989

A/Title: Microsequence analysis of winged bean seed proteins electrophoretically separated from two di-

A/Reference number: A61491; PMID:89351606; PMID:2765119

A/Accession: E61497

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-20 &lt;HTR&gt;

A/Cross-references: UNIPROT:Q9S8J4; UNIPARC:UPI000017B06E

C/Keywords: glycoprotein; seed

Query Match 25.6%; Score 20; DB 2; Length 20;  
Best Local Similarity 28.6%; Pred. No. 4.3e+03;  
Matches 4; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 SIKRDHNDYSKPM 14  
Db 5 SFNPDHRENSNEL 18

## RESULT 27

S77992

cytochrome-c oxidase (EC 1.9.3.1) chain VIIb - bigeye tuna (fragment)

C/Species: Thunnus obesus (bigeye tuna)

C/Date: 17-Sep-1997 #sequence\_revision 17-Sep-1997 #text\_change 09-Jul-2004

C/Accession: S77992

R/Arnold, S.; Lee, J.; Kim, M.; Song, E.; Lindner, D.; Lottspeich, F.; Kadenbach, B.

submitted to the Protein Sequence Database, June 1997

A/Reference number: S77980

A/Accession: S77992

A/Molecule type: protein

A/Residues: 1-20 &lt;ARN&gt;

A/Cross-references: UNIPROT:P80981; UNIPARC:UPI0000128164

A/Experimental source: liver

C/Genetics:

A/Genome: nuclear

C/Function:

A/Pathway: oxidative phosphorylation; respiratory chain

C/Keywords: electron transfer; membrane-associated complex; mitochondrial inner membran

Query Match 25.6%; Score 20; DB 2; Length 20;  
Best Local Similarity 44.4%; Pred. No. 4.3e+03;  
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 6 HNDYSKPM 14  
Db 9 HSPFYGTNLM 17

## RESULT 28

PT0299

Ig heavy chain CRD3 region (clone 5-103B) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996

C/Accession: PT0299

R.Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Royera, G.

J. Exp. Med. 173, 395-407, 1991

A>Title: Preferential utilization of specific immunoglobulin heavy chain diversity and J

A/Reference number: P10222; MUID:91108337; PMID:1899102

A/Accession: P10299

A/Molecule type: DNA

A/Residues: 1-9 <YAM>

A/Cross-references: UNIPARC:UPI000017C209

A/Experimental source: B lymphocyte

C/Keywords: heterocyclamer; immunoglobulin

Query Match

Best Local Similarity 24.4%; Score 19; DB 2; Length 9;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 4 RDNDYS 10

Db 1 RSMWYS 7

RESULT 29

A13687

caerulein-like peptide - African tree frog (Kassina maculata)

C/Species: Kassina maculata

C/Date: 13-Mar-1997 #sequence\_revision 13-Mar-1997 #text\_change 09-Jul-2004

C/Accession: A13687

R/Monteucci, P.; Falconieri, E.; Gasser, G.; Visser, J.

Experientia 33, 118-119, 1977

A/Title: Occurrence of Asn(2), Leu(5)-caerulein in the skin of the African frog Hyalambate

A/Reference number: A13687; MUID:77246547; PMID:891852

A/Accession: A13687

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-10 <MON>

A/Cross-references: UNIPROT:Q7LZC5; UNIPARC:UPI000017668C

C/Species: gasterin

C/Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid; skin; sulfoprotein

F.1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F.10/Modified site: sulfate (Tyr) (covalent) #status experimental

F.10/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match

Best Local Similarity 24.4%; Score 19; DB 2; Length 10;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 NDY 9

Db 2 NDY 4

RESULT 30

S74176

glucokinase (EC 2.7.1.12), thermoresistant - Escherichia coli (fragment)

C/Species: Escherichia coli

C/Date: 14-Apr-1998 #sequence\_revision 24-Apr-1998 #text\_change 07-May-1999

C/Accession: S74176

R/izu, H.; Adachi, O.; Yamada, M.

FEBS Lett. 394, 14-16, 1996

A/Title: Purification and characterization of the Escherichia coli thermoresistant gluc

A/Reference number: S74176; MUID:97074194; PMID:8925917

A/Accession: S74176

A/Molecule type: protein

A/Residues: 1-10 <IZU>

A/Cross-references: UNIPARC:UPI000017A3B

A/Experimental source: strain K-12

C/Genetics:

A/Keywords: dimer; phosphotransferase

Query Match

Best Local Similarity 24.4%; Score 19; DB 2; Length 10;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 5 DHNDY 9

Db 6 DHNTY 10

RESULT 31

S23370

T-cell receptor alpha chain J region - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 22-Nov-1993 #sequence\_revision 26-May-1995 #text\_change 17-Mar-1999

C/Accession: S23370

R/Plugsche, G.; Ricken, G.; Taube, H.; Kroninger, S.; Melchers, I.; Peter, H.H.; Eichma

Bur J. Immunol. 21, 2749-2754, 1991

A/Title: Biased T cell receptor V(alpha) region repertoire in the synovial fluid of the

A/Reference number: S23364; MUID:92037820; PMID:1657615

A/Accession: S23370

A/Status: preliminary; translation not shown

A/Molecule type: mRNA

A/Residues: 1-10 <PLU>

A/Cross-references: UNIPARC:UPI000017C391; EMBL:X58165

C/Keywords: T-cell receptor

Query Match

Best Local Similarity 24.4%; Score 19; DB 2; Length 10;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 5 DHND 8

Db 4 DHND 7

RESULT 32

S23926

major glycoprotein PAS-6 - bovine (fragment)

C/Species: Bos primigenius taurus (cattle)

C/Date: 19-Mar-1997 #sequence\_revision 01-Feb-1999 #text\_change 09-Jul-2004

C/Accession: S23926

R/Kim, D.H.; Kanno, C.; Mizokami, Y.

Biochim. Biophys. Acta 1122, 203-211, 1992

A/Title: Purification and characterization of major glycoproteins, PAS-6 and PAS-7, fro

A/Reference number: S23926; MUID:92351107; PMID:1643094

A/Accession: S23926

A/Molecule type: protein

A/Residues: 1-11 <KIM>

A/Cross-references: UNIPROT:Q7M2M1; UNIPARC:UPI000017C53F

C/Keywords: glycoprotein; milk; blocked amino end

Query Match

Best Local Similarity 24.4%; Score 19; DB 2; Length 11;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 10 SKNP 13

Db 4 KNP 7

RESULT 33

S65730

hemoglobin, extracellular, component - earthworm (Lumbricus terrestris) (fragment)

C/Species: Lumbricus terrestris (common earthworm)

C/Date: 06-Dec-1996 #sequence\_revision 13-Mar-1997 #text\_change 13-Mar-1997

C/Accession: S65730

R/Fushitani, K.; Higashiyama, K.; Asao, M.; Hosokawa, K.

Biochim. Biophys. Acta 1292, 273-280, 1996

A/Title: Characterization of the constituent polypeptides of the extracellular hemoglob

A/Reference number: S65721; MUID:96176855; PMID:8557573

A/Accession: S65730

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-12 <FUS>

A/Cross-references: UNIPARC:UPI000017BD88

Query Match

Best Local Similarity 24.4%; Score 19; DB 2; Length 12;

Best Local Similarity 100.0%; Pred. No. 3.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 RDH 6  
|||  
Db 6 RDH 8

## RESULT 34

PH1342  
Ig heavy chain DJ region (clone C507-95) - human (fragment)

C/Species: Homo sapiens (man)  
C/Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999  
C/Accession: PH1342  
R/Masseran, R.; Galli, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.  
J. Exp. Med. 176, 1577-1581, 1992  
A/Title: Predominance of fetal type DH joining in young children with B precursor lymphoma  
A/Reference number: PH1302; MUID:93094761; PMID:1460419  
A/Accession: PH1342  
A/Molecule type: DNA  
A/Residues: 1-15 <MAS>  
A/Cross-references: UNIPARC:UPI000017C240  
C/Keywords: heterotrimer; immunoglobulin

Query Match 24.4%; Score 19; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 4.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 RDH 6  
|||  
Db 13 RDH 15

## RESULT 35

PL0143

carbon-monoxide dehydrogenase (EC 1.2.99.2) medium chain - Pseudomonas carboxydohydrogen

C/Species: Pseudomonas carboxydohydrogen  
C/Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 09-Jul-2004  
C/Accession: PL0143  
R/Kraut, M.; Hugendieck, I.; Herwig, S.; Meyer, O.  
Arch. Microbiol. 152, 335-341, 1989  
A/Title: Homology and distribution of CO dehydrogenase structural genes in carboxydohydrogen  
A/Reference number: PL0138; MUID:9055678; PMID:2818128  
A/Accession: PL0143  
A/Molecule type: protein  
A/Residues: 1-15 <KRA>  
A/Cross-references: UNIPROT:P19917; UNIPARC:UPI0000128FDB  
C/Comment: Carbon-monoxide dehydrogenase consists of three polypeptide chains: large, me  
C/Keywords: oxidoreductase

Query Match 24.4%; Score 19; DB 2; Length 15;  
Best Local Similarity 50.0%; Pred. No. 4.7e+03;  
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 6 HNDYSK 11  
|||  
Db 6 HFDYHR 11

## RESULT 36

A35417

28K serine proteinase homolog - bovine (fragment)

C/Species: Bos primigenius taurus (cattle)  
C/Date: 18-Jan-1991 #sequence\_revision 18-Jan-1991 #text\_change 09-Jul-2004  
C/Accession: A35417  
R/Ho, P.L.; Carpenter, M.R.; Smillie, L.B.; Gambarini, A.G.  
Biochem. Biophys. Res. Commun. 170, 769-774, 1990  
A/Title: Co-purification of proteinases with basic fibroblast growth factor (FGF).  
A/Reference number: A35417; MUID:90343797; PMID:2200404  
A/Accession: A35417  
A/Status: Preliminary  
A/Molecule type: Protein  
A/Residues: 1-15 <HOA>

A/Cross-references: UNIPROT:Q7M3G3; UNIPARC:UPI000017C48D

Query Match 24.4%; Score 19; DB 2; Length 15;  
Best Local Similarity 57.1%; Pred. No. 4.7e+03;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 5 DHNDYSK 11  
|||  
Db 3 DSDYRK 9

## RESULT 37

PH0791

T-cell receptor alpha chain (OB7.3.2 V-alpha-8.F3.2) - mouse (fragment)

C/Species: Mus musculus (house mouse)  
C/Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
C/Accession: PH0791  
R/Cabanova, J.L.; Romero, P.; Widmann, C.; Kourilesky, P.; Maryanski, J.L.  
J. Exp. Med. 174, 1371-1383, 1991  
A/Title: T cell receptor genes in a series of class I major histocompatibility complex-  
allelic exclusion and antigen-specific repertoire.  
A/Reference number: PH0746; MUID:92078846; PMID:1836010  
A/Accession: PH0791  
A/Molecule type: mRNA  
A/Residues: 1-16 <CAS>  
A/Cross-references: UNIPARC:UPI000017C783; EMBL:X60896  
A/Experimental source: T lymphocyte  
C/Keywords: T-cell receptor

Query Match 24.4%; Score 19; DB 2; Length 16;  
Best Local Similarity 27.3%; Pred. No. 5.1e+03;  
Matches 3; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

OY 1 STRDHNDYSK 11  
::|::|  
Db 2 ALSGDSDGYNK 12

## RESULT 38

S22040

cob protein - common sunflower

C/Species: Helianthus annuus (common sunflower)  
C/Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 09-Jul-2004  
C/Accession: S22040  
R/Kochler, R.H.  
Submitted to the EMBL Data Library, October 1991  
A/Reference number: S22040  
A/Accession: S22040  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-16 <KOB>  
A/Cross-references: UNIPROT:Q34699; UNIPARC:UPI000008DA3A; EMBL:X62592; NID:q12990; PID

Query Match 24.4%; Score 19; DB 2; Length 16;  
Best Local Similarity 100.0%; Pred. No. 5.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 NDY 9  
|||  
Db 13 NDY 15

## RESULT 39

C56211

progesterone receptor-related protein p23 - rabbit (fragment)

C/Species: Oryctolagus cuniculus (domestic rabbit)  
C/Date: 19-Oct-1995 #sequence\_revision 19-Oct-1995 #text\_change 20-Jun-2000  
C/Accession: C56211  
R/Johnson, J.L.; Belto, T.G.; Krco, C.J.; Toft, D.O.  
Mol. Cell. Biol. 14, 1956-1963, 1994  
A/Title: Characterization of a novel 23-kilodalton protein of inactive progesterone rec  
A/Reference number: A56211; MUID:94158860; PMID:8114727  
A/Accession: C56211

A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-18 <YOH>  
 A:Cross-references: UNIPARC:UPI00001796B8  
 C:Superfamily: Caenorhabditis elegans hypothetical protein ZC395.10  
 C:Keywords: steroid hormone receptor

Query Match 24.4%; Score 19; DB 2; Length 18;  
 Best Local Similarity 60.0%; Pred. No. 5.8e+03;  
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 5 DNDY 9  
 DB 10 DRDY 14

RESULT 40  
 145957  
 protein kinase (EC 2.7.1.37), cAMP-dependent, type I-alpha regulatory chain - bovine (fr  
 C:Species: Bos primigenius taurus (cattle)  
 C:Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 05-Oct-2004  
 C:Accession: 145957  
 R:Lee, D.C.; Carmichael, D.F.; Krebs, B.G.; McKnight, G.S.  
 Proc. Natl. Acad. Sci. U.S.A. 80, 3608-3612, 1983  
 A:Title: Isolation of a cDNA clone for the type I regulatory subunit of bovine cAMP-depe  
 A:Reference number: 145957; MUID:83221645; PMID:6190178  
 A:Accession: 145957  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Residues: 1-19 <LEB>  
 A:Molecule type: mRNA  
 A:Cross-references: UNIPROT:P00514; UNIPARC:UPI000016C361; GB:K00833; NID:G163533; PIDN:  
 C:Superfamily: cAMP-dependent protein kinase regulatory subunit; cAMP receptor protein c  
 C:Keywords: phosphotransferase

Query Match 24.4%; Score 19; DB 2; Length 19;  
 Best Local Similarity 66.7%; Pred. No. 6.1e+03;  
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 IKRDN 7  
 DB 12 IDRSN 17

RESULT 41  
 559485  
 hydroxyproline-rich cell wall glycoprotein (42k and others) - kidney bean (fragment)  
 C:Species: Phaseolus vulgaris (kidney bean)  
 C:Date: 27-Apr-1996 #sequence\_revision 26-Jul-1996 #text\_change 09-Jul-2004  
 C:Accession: 559485; 559484; 559483  
 R:Wojtaszek, P.; Trechowicz, J.; Bolwell, G.P.  
 Plant Mol. Biol. 28, 1075-1087, 1995  
 A:Title: Specificity in the immobilisation of cell wall proteins in response to differ  
 A:Reference number: 559481; MUID:96011753; PMID:7548825  
 A:Accession: 559485  
 A:Molecule type: protein  
 A:Residues: 1-19 <WOU>  
 A:Cross-references: UNIPROT:O7M1W8; UNIPARC:UPI0000177B5D  
 A:Accession: 559484  
 A>Note: hydroxyproline-rich cell wall glycoprotein, 42k  
 A:Molecule type: protein  
 A:Residues: 1-15 <WOW>  
 A:Cross-references: UNIPARC:UPI0000177B5E  
 A>Note: hydroxyproline-rich cell wall glycoprotein, 84k  
 A:Accession: 559483  
 A:Molecule type: protein  
 A:Residues: 1-14 <WOF>  
 A:Cross-references: UNIPARC:UPI0000177B5F  
 A>Note: hydroxyproline-rich cell wall glycoprotein, 136k, minor component  
 C:Superfamily: proline-rich protein 3  
 C:Keywords: glycoprotein; hydroxyproline  
 F/6.11.16/Modified site: hydroxyproline (Pro) #status experimental

Query Match 24.4%; Score 19; DB 2; Length 19;

Best Local Similarity 42.9%; Pred. No. 6.1e+03;  
 Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 8 DYSKNPM 14  
 DB 1 NYDKRPV 7

RESULT 42  
 PH1360  
 Ig heavy chain DJ region (clone C178-122) - human (fragment)  
 C:Species: Homo sapiens (man)  
 C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999  
 C:Accession: PH1360  
 R:Masserman, R.; Gallili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.  
 J. Exp. Med. 176, 1577-1581, 1992  
 A:Title: Predominance of fetal type DJH joining in young children with B precursor lym  
 A:Reference number: PH1302; MUID:93094761; PMID:1460419  
 A:Accession: PH1360  
 A:Molecule type: DNA  
 A:Residues: 1-19 <WAS>  
 A:Cross-references: UNIPARC:UPI000017C231  
 C:Keywords: heterotetramer; immunoglobulin

Query Match 24.4%; Score 19; DB 2; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 6.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 RDH 6  
 DB 17 RDH 19

RESULT 43  
 A61377  
 endometrial secretory protein - sheep (fragment)  
 C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)  
 C:Date: 09-Sep-1994 #sequence\_revision 09-Sep-1994 #text\_change 17-Mar-1999  
 C:Accession: A61377  
 R:Vallet, J.L.; Barker, P.J.; Lamming, G.E.; Skinner, N.; Huekisson, N.S.  
 J. Endocrinol. 130, R1-R4, 1991  
 A:Title: A low molecular weight endometrial secretory protein which is increased by ovi  
 A:Reference number: A61377; MUID:92013712; PMID:1919388  
 A:Accession: A61377  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-19 <VAL>  
 A:Cross-references: UNIPARC:UPI000017C59D

Query Match 24.4%; Score 19; DB 2; Length 19;  
 Best Local Similarity 60.0%; Pred. No. 6.1e+03;  
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 9 YSKNP 13  
 DB 10 YSDP 14

RESULT 44  
 PH1338  
 Ig heavy chain DJ region (clone C372-115) - human (fragment)  
 C:Species: Homo sapiens (man)  
 C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999  
 C:Accession: PH1338  
 R:Masserman, R.; Gallili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.  
 J. Exp. Med. 176, 1577-1581, 1992  
 A:Title: Predominance of fetal type DJH joining in young children with B precursor lym  
 A:Reference number: PH1302; MUID:93094761; PMID:1460419  
 A:Accession: PH1338  
 A:Molecule type: DNA  
 A:Residues: 1-20 <MAS>  
 A:Cross-references: UNIPARC:UPI000017C23D  
 C:Keywords: heterotetramer; immunoglobulin

Query Match 24.4%; Score 19; DB 2; Length 20;  
A:Molecule type: protein  
A:Residues: 1-20 <CUS>  
A:Cross-references: UNIPROT:Q7M466; UNIPARC:UP1000017CAC  
A:Note: Sequence extracted from NCBI backbone (NCBI:114883)  
C:Keywords: chromoprotein

QY 4 RDH 6  
|||  
DB 18 RDH 20

## RESULT 45

T48881  
leader peptide [imported] - Vibrio sp.  
C:Species: Vibrio sp.  
C/Date: 02-Jun-2000 #sequence\_revision 02-Jun-2000 #text\_change 09-Jul-2004  
C/Accession: T48881

R/Xu, Y.; Zhang, Y.; Liang, Z.Y.; Van de Casteele, M.; Legrain, C.; Glansdorff, N.  
Microbiology 144, 1435-1441, 1998  
A>Title: Aspartate carboxyltransferase from a psychrophilic deep-sea bacterium, Vibrio  
A:Reference number: Z24845  
A:Accession: T48881  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-20 <XUY>  
A:Cross-references: UNIPROT:P64173; UNIPARC:UP1000003BBB; EMBL:X09786; PIRN:CA70922.1  
A:Experimental source: strain 2693

Query Match 24.4%; Score 19; DB 2; Length 20;  
Best Local Similarity 60.0%; Pred. No. 6.4e+03;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 RDHND 8  
|||  
DB 16 RPHNN 20

## RESULT 46

A61506  
alpha-1-antitrypsin - golden hamster (fragment)  
C/Species: Mesocricetus auratus (golden hamster)  
C/Date: 15-Oct-1994 #sequence\_revision 15-Oct-1994 #text\_change 09-Jul-2004  
C/Accession: A61506  
R/Amemiya, S.; Yamamoto, K.; Sinohara, H.  
Comp. Biochem. Physiol. B 100, 293-296, 1991  
A>Title: Purification, characterization, and acute phase response of plasma alpha-1-anti  
A:Reference number: A61506; MUID:92191572; PMID:1724745  
A:Accession: A61506  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-20 <AME>  
A:Cross-references: UNIPROT:Q7M0E1; UNIPARC:UP1000017C610

Query Match 24.4%; Score 19; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 6.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 RDH 6  
|||  
DB 18 RDH 20

## RESULT 47

B56894  
intracytalline chromoprotein 1 - Waltonia inconspicua (fragment)  
C/Species: Waltonia inconspicua  
C/Date: 05-Jan-1996 #sequence\_revision 05-Jan-1996 #text\_change 09-Jul-2004  
C/Accession: B56894  
R/Cusack, M.; Curry, G.; Clegg, H.; Abbott, G.  
Comp. Biochem. Physiol. B 102, 93-95, 1992  
A>Title: An intracytalline chromoprotein from red brachiopod shells: implications for  
A:Reference number: A56894; MUID:9240551; PMID:1526140  
A:Contents: Sowerby, red brachiopod shells  
A:Accession: B56894

A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-20 <CUS>  
A:Cross-references: UNIPROT:Q7M466; UNIPARC:UP1000017CAC  
A:Note: Sequence extracted from NCBI backbone (NCBI:114883)  
C:Keywords: chromoprotein

Query Match 24.4%; Score 19; DB 2; Length 20;  
Best Local Similarity 75.0%; Pred. No. 6.4e+03;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 10 SKNP 13  
|||  
DB 17 AKNP 20

## RESULT 48

A28709  
phosphonoacetaldehyde hydrolase - Bacillus cereus (fragment)  
C/Species: Bacillus cereus  
C/Date: 22-Aug-1988 #sequence\_revision 22-Aug-1988 #text\_change 30-Sep-1993  
C/Accession: A28709  
R/Olsen, D.B.; Hepburn, T.W.; Moos, M.; Mariano, P.S.; Dunaway-Mariano, D.  
Biochemistry 27, 2229-2234, 1988  
A>Title: Investigation of the Bacillus cereus phosphonoacetaldehyde hydrolase. Evidence  
A:Reference number: A28709; MUID:88241058; PMID:3132206  
A:Accession: A28709  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-7 <OLS>  
A:Cross-references: UNIPARC:UP1000017AC8C

Query Match 23.1%; Score 18; DB 2; Length 7;  
Best Local Similarity 60.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 IKRDH 6  
|||  
DB 1 LKIDH 5

## RESULT 49

A38841  
rhodopsin homolog - squid (Watasenia scintillans) (fragment)  
N/Alternate names: visual pigment protein  
C/Species: Watasenia scintillans (sparkling enope)  
C/Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 09-Jul-2004  
C/Accession: A38841  
R/Seldou, M.; Kubota, I.; Hiraki, K.; Kito, Y.  
Biochim. Biophys. Acta 957, 318-321, 1988  
A>Title: Amino acid sequence of the retinal binding site of squid visual pigment.  
A:Reference number: PT0063; MUID:89051045; PMID:3191148  
A:Accession: A38841  
A:Molecule type: protein  
A:Residues: 1-11 <SR>  
A:Cross-references: UNIPROT:Q7M3Y2; UNIPARC:UP1000017412E  
C:Superfamily: vertebrate rhodopsin  
C/Keywords: chromoprotein; retinal  
F/3/Binding site: retinal (Lys) (covalent) #status experimental

Query Match 23.1%; Score 18; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 5.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 NPM 14  
|||  
DB 9 NPM 11

## RESULT 50

S00616  
parasporal crystal protein, wax moth-specific - Bacillus thuringiensis (strain gallieria

N/Alternate names: delta-endotoxin; parasporal crystal protein positive chain  
 C/Species: *Bacillus thuringiensis*  
 C/Date: 31-Dec-1988 #sequence\_revision 31-Dec-1988 #text\_change 05-Oct-2004  
 C/Accession: S00616  
 R/Chesterkhina, G.G.; Kostina, L.I.; Zalunin, I.A.; Khodova, O.M.; Stepanov, V.M.  
 P/BS Lett. 232, 249-251, 1988  
 A/Title: *Bacillus thuringiensis* ssp. *galleriae* simultaneously produces two delta-endotox  
 A/Reference number: S00615  
 A/Accession: S00616  
 A/Molecule type: protein  
 A/Residues: 1-11 <CH>  
 A/Cross-references: UNIPROT:Q7ML54; UNIPARC:UPI00001781A1  
 C/Comment: This toxin is effective against the larvae of *Galleria mellonella* (greater wax  
 C/Keywords: delta-endotoxin

Query Match 23.1%; Score 18; DB 2; Length 11;  
 Best Local Similarity 50.0%; Pred. No. 5.1e+03;  
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 6 HNDYGR 11  
 DB 5 NNPYSQ 10

RESULT 51  
 S47365  
 T-cell antigen receptor VJ junction beta chain - human  
 C/Species: *Homo sapiens* (man)  
 C/Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 05-Nov-1999  
 C/Accession: S47365; S47375; S47379; S47397; S47398; S47355  
 R/Lehner, P.J.  
 Submitted to the EMBL Data Library, August 1994  
 A/Description: Human HLA-A0201 restricted recognition of Influenza A is dominated by T c  
 A/Reference number: S47355  
 A/Accession: S47365  
 A/Status: preliminary  
 A/Molecule type: mRNA  
 A/Residues: 1-13 <LEH>  
 A/Cross-references: UNIPARC:UPI0000116673; EMBL:Z35690; NID:G527471; PIDN:CAA84759.1; PI  
 A/Accession: S47375  
 A/Status: preliminary  
 A/Molecule type: mRNA  
 A/Residues: 1-13 <LE3>  
 A/Cross-references: UNIPARC:UPI0000116673; EMBL:Z35700; NID:G527493; PIDN:CAA84769.1; PI  
 A/Accession: S47379  
 A/Status: preliminary  
 A/Molecule type: mRNA  
 A/Residues: 1-13 <LE3>  
 A/Cross-references: UNIPARC:UPI0000116673; EMBL:Z35708; NID:G527509; PIDN:CAA84777.1; PI  
 A/Accession: S47396  
 A/Status: preliminary  
 A/Molecule type: mRNA  
 A/Residues: 1-13 <LE4>  
 A/Cross-references: UNIPARC:UPI0000116673; EMBL:Z35674; NID:G527527; PIDN:CAA84743.1; PI  
 A/Accession: S47397  
 A/Status: preliminary  
 A/Molecule type: mRNA  
 A/Residues: 1-13 <LE5>  
 A/Cross-references: UNIPARC:UPI0000116673; EMBL:Z35675; NID:G527529; PIDN:CAA84744.1; PI  
 A/Accession: S47398  
 A/Status: preliminary  
 A/Molecule type: mRNA  
 A/Residues: 1-13 <LE6>  
 A/Cross-references: UNIPARC:UPI0000116673; EMBL:Z35676; NID:G527531; PIDN:CAA84745.1; PI  
 C/Keywords: T-cell receptor

Query Match 23.1%; Score 18; DB 2; Length 13;  
 Best Local Similarity 33.3%; Pred. No. 6.1e+03;  
 Matches 3; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 SIKRDHNDY 9  
 DB 4 SIRSSEYQ 12

RESULT 52  
 PH1471  
 T-cell receptor beta chain (clone A24/PEF4) - mouse (fragment)  
 C/Species: *Mus musculus* (house mouse)  
 C/Date: 10-Mar-1994 #sequence\_revision 10-Mar-1994 #text\_change 15-Mar-2004  
 C/Accession: PH1471  
 R/Casanova, J.L.; Martison, F.; Gounrlier, H.; Barra, C.; Pannetier, C.; Regnault, A.; J.  
 J. Exp. Med. 177, 811-820, 1993  
 A/Title: T cell receptor selection by and recognition of two class I major histocompat  
 A/Reference number: PH1430; MUID:93171821; PMID:8436911  
 A/Accession: PH1471  
 A/Molecule type: mRNA  
 A/Residues: 1-14 <CAS>  
 A/Cross-references: UNIPARC:UPI000017C79B  
 A/Experimental source: cytolytic T-lymphocyte  
 C/Keywords: receptor; T-cell

Query Match 23.1%; Score 18; DB 2; Length 14;  
 Best Local Similarity 60.0%; Pred. No. 6.6e+03;  
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 RDHND 8  
 DB 5 RDNDQ 9

RESULT 53  
 PA0007  
 lectin B1 - *Psophocarpus scandens* (fragment)  
 C/Species: *Psophocarpus scandens*  
 C/Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 09-Jul-2004  
 C/Accession: PA0007  
 R/Kortt, A.A.  
 Phytochemistry 27, 2847-2855, 1988  
 A/Title: Isolation and characterization of the lectins from the seeds of *Psophocarpus*  
 A/Reference number: PA0005  
 A/Accession: PA0007  
 A/Molecule type: protein  
 A/Residues: 1-14 <KOR>  
 A/Cross-references: UNIPROT:P22584; UNIPARC:UPI000012E3DA  
 A/Experimental source: seed  
 C/Comment: The seeds of *Psophocarpus* contain two distinct groups of lectins which can b  
 C/Keywords: lectin

Query Match 23.1%; Score 18; DB 2; Length 14;  
 Best Local Similarity 25.0%; Pred. No. 6.6e+03;  
 Matches 3; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 SIKRDHNDYSKN 12  
 DB 2 TISNPNQFOON 13

RESULT 54  
 SPRT  
 scotophobin - rat  
 C/Species: *Rattus norvegicus* (Norway rat)  
 C/Date: 23-Oct-1981 #sequence\_revision 23-Oct-1981 #text\_change 09-Jul-2004  
 C/Accession: A93164; A92757; A01423  
 R/Ungar, G.; Desiderio, D.M.; Parr, W.  
 Nature 238, 198-202, 1972  
 A/Title: Isolation, identification and synthesis of a specific-behaviour-inducing brain  
 A/Reference number: A93164; MUID:72240741; PMID:4558348  
 A/Accession: A93164  
 A/Molecule type: protein  
 A/Residues: 1-15 <UNG>  
 A/Cross-references: UNIPROT:P01159; UNIPARC:UPI000013567B  
 A/Note: chemical synthesis  
 R/Desiderio, D.M.; Ungar, G.; White, P.A.  
 J. Chem. Soc. D Chem. Commun. 1971, 432-433, 1971  
 A/Title: The use of mass spectrometry in the structural elucidation of scotophobin -- a

A/Reference number: A92757  
A/Accession: A92757  
A/Molecule type: protein  
A/Residues: 1-15 <DES>  
A/Cross-references: UNIPARC:UPI0000135678  
A/Experimental source: brain  
A/Note: the sequence was determined by mass spectrometry  
R/Stewart, W.W.  
Nature 238, 202-209, 1972  
A/Title: Comments on the chemistry of scotophobin.  
A/Reference number: A93165; MUID:72240742; PMID:4558349  
A/Contents: annotation; referee's comments on first reference above  
R/Ungar, G.; Desiderio, D.M.; Parr, W.  
Nature 238, 209-210, 1972  
A/Reference number: A93166  
A/Contents: annotation  
A/Note: reply to referee's comments  
R/Wilson, D.  
Nature 320, 313-314, 1986  
A/Title: Scotophobin resurrected as a neuropeptide.  
A/Reference number: A93076; MUID:86175024; PMID:3960116  
A/Contents: annotation  
A/Note: comparison with other neuropeptides; author presents scotophobin sequence in the  
acting the amino end  
C/Superfamily: scotophobin  
C/Keywords: amidated carboxyl end  
F/15/Modified site: amidated carboxyl end (Tyr) #status experimental

Query Match 23.1%; Score 18; DB 1; Length 15;  
Best Local Similarity 37.5%; Pred. No. 7.1e+03;  
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 5 DHNDYSKN 12  
|:|:|:  
Db 2 DNNQGGKS 9

RESULT 55  
Protein QP100022 - fungus (Fusarium sporotrichioides) (fragment)  
C/Species: Fusarium sporotrichioides  
C/Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 23-Mar-2001  
C/Accession: PA0090  
R/Chow, L.P.; Fukaya, N.; Sugita, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.  
submitted to JIPID, October 1994  
A/Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrichi  
A/Reference number: PA0051  
A/Accession: PA0090  
A/Molecule type: protein  
A/Residues: 1-15 <CHO>  
A/Cross-references: UNIPARC:UPI0000178407  
C/Keywords: pyroglutamic acid  
F/11/Modified site: pyroglutamic acid (Gln) #status experimental

Query Match 23.1%; Score 18; DB 2; Length 15;  
Best Local Similarity 60.0%; Pred. No. 7.1e+03;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 10 SKNPM 14  
|:|:|:  
Db 4 SXNPL 8

RESULT 56  
T-cell receptor delta chain V region (105.7) - mouse (fragment)  
G35141  
C/Species: Mus musculus (house mouse)  
C/Date: 31-Aug-1990 #sequence\_revision 31-Aug-1990 #text\_change 30-May-1997  
C/Accession: G35141  
R/Sim, G.K.; Augustin, A.  
Cell 61, 397-405, 1990  
A/Title: Dominantly inherited expression of BID, an invariant undiversified T cell recep  
A/Reference number: A35141; MUID:90242386; PMID:2110506

A/Accession: G35141  
A/Status: preliminary; not compared with conceptual translation  
A/Molecule type: mRNA  
A/Residues: 1-15 <SIM>  
A/Cross-references: UNIPARC:UPI000017C85F  
C/Keywords: T-cell receptor

Query Match 23.1%; Score 18; DB 2; Length 15;  
Best Local Similarity 50.0%; Pred. No. 7.1e+03;  
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 KRDPND 8  
|:|:|:  
Db 8 RRDTS 13

RESULT 57  
C44101  
calmodulin, vasoactive intestinal peptide-binding protein, VIP binding protein, p18 - gr  
C/Species: Cavia porcellus (guinea pig)  
C/Date: 27-Apr-1993 #sequence\_revision 18-Nov-1994 #text\_change 07-Feb-1997  
C/Accession: C44101  
R/Stallwood, D.; Bruggier, C.H.; Baggenstoss, B.A.; Stemmer, P.M.; Shiraga, H.; Landers, J.  
J. Biol. Chem. 267, 19617-19621, 1992  
A/Title: Identity of a membrane-bound vasoactive intestinal peptide-binding protein with  
A/Reference number: A44101; MUID:92406918; PMID:1527080  
A/Accession: C44101  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-15 <STG>  
A/Cross-references: UNIPARC:UPI000017CA28  
A/Experimental source: lung membranes  
A/Note: sequence extracted from NCBI backbone (NCBIP:114109)  
C/Keywords: intestine

Query Match 23.1%; Score 18; DB 2; Length 15;  
Best Local Similarity 50.0%; Pred. No. 7.1e+03;  
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 4 RDNDY 9  
|:|:|:  
Db 4 KDGNY 9

RESULT 58  
S62641  
porphobilinogen synthase (BC 4.2.1.24) - green alga (Scenedesmus obliquus) (fragment)  
N/Alternate names: 5-aminolevulinic acid dehydratase  
C/Species: Scenedesmus obliquus  
C/Date: 14-Feb-1997 #sequence\_revision 13-Mar-1997 #text\_change 09-Jul-2004  
C/Accession: S62641  
R/Stolz, M.; Doernemann, D.  
Eur. J. Biochem. 236, 600-608, 1996  
A/Title: Purification, metal cofactor, N-terminal sequence and subunit composition of a  
A/Reference number: S62641; MUID:96195670; PMID:8612634  
A/Accession: S62641  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-15 <STO>  
A/Cross-references: UNIPROT:Q958B1; UNIPARC:UPI000009F06B  
C/Keywords: carbon-oxygen lyase; hydro-lyase

Query Match 23.1%; Score 18; DB 2; Length 15;  
Best Local Similarity 25.0%; Pred. No. 7.1e+03;  
Matches 3; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 2 IKRDNDYSKNP 13  
|:|:|:|:  
Db 3 VNQSKNDIIVSP 14

RESULT 59  
S77987



Cytochrome-c oxidase (BC 1.9.3.1) chain Vic.2 - bigeye tuna (fragments)

C/Species: Thunnus obesus (bigeye tuna)

C/Date: 17-Sep-1997 #sequence\_revision 17-Sep-1997 #text\_change 09-Jul-2004

C/Accession: S77987

R/Arnold, S.; Lee, J.; Kim, M.; Song, B.; Linder, D.; Lottepech, F.; Kadenbach, B. submitted to the Protein Sequence Database, June 1997

A/Reference number: S77980

A/Accession: S77987

A/Molecule type: protein

A/Residues: 1-819-15 <ARN>

A/Cross-references: UNIPROT:P80978; UNIPARC:UPI000017BF73; UNIPARC:UPI000017BF74

A/Experimental source: heart

C/Genetics:

A/Genome: nuclear

C/Function: oxidative phosphorylation; respiratory chain

C/Keywords: electron transfer; membrane-associated complex; mitochondrial inner membrane

Query Match 23.1%; Score 18; DB 2; Length 15;

Best Local Similarity 42.9%; Pred. No. 7.6e+03;

Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 3 KDNDY 9

Db 8 KKPMDDY 14

#### RESULT 60

melanotropin beta - spiny dogfish

C/Species: Squalus acanthias (spiny dogfish)

C/Date: 13-Jul-1981 #sequence\_revision 13-Jul-1991 #text\_change 09-Jul-2004

C/Accession: A01471

R/Bennett, H.P.; Lowry, P.J.; McMartin, C.; Scott, A.P.

Biochem. J. 141, 439-444, 1974

A/Title: Structural studies of alpha-melanocyte-stimulating hormone and a novel beta-mel

A/Reference number: A90277; MUID:75127390; PMID:437578

A/Accession: A01471

A/Molecule type: protein

A/Residues: 1-16 <BEN>

A/Cross-references: UNIPROT:P01207; UNIPARC:UPI000012FLC2

C/Superfamily: corticotropin-lipotropin

C/Keywords: hormone

Query Match 23.1%; Score 18; DB 1; Length 16;

Best Local Similarity 60.0%; Pred. No. 7.6e+03;

Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 5 DHNDY 9

Db 1 DGDY 5

#### RESULT 61

26K kidney and gallbladder stone protein - unidentified bacterium (fragment)

C/Species: unidentified bacterium

C/Date: 07-Feb-1997 #sequence\_revision 07-Feb-1997 #text\_change 09-Jul-2004

C/Accession: D58501

R/Binette, J.P.; Binette, M.B.

submitted to the Protein Sequence Database, October 1996

A/Description: The proteins of kidney and gallbladder stones.

A/Reference number: A58501

A/Accession: D58501

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-16 <BIN>

A/Cross-references: UNIPROT:Q7MD3; UNIPARC:UPI000017A8CE

A/Experimental source: human kidney and gallbladder stones

Query Match 23.1%; Score 18; DB 2; Length 16;

Best Local Similarity 50.0%; Pred. No. 7.6e+03;

Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 7 NDYSKN 12

Db 7 NEVSEN 12

#### RESULT 62

flgB protein - Caulobacter crescentus (fragment)

C/Species: Caulobacter crescentus

C/Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 09-Jul-2004

C/Accession: P00126; A25882; S11760

R/Schoenlein, P.V.; Gallman, L.S.; Winkler, M.E.; Ely, B.

Gene 93, 17-25, 1990

A/Title: Nucleotide sequence of the Caulobacter crescentus flgB and flgT genes and an

A/Reference number: J00741; MUID:91033011; PMID:1699845

A/Accession: P00126

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-16 <SCH>

A/Cross-references: UNIPROT:P18914; UNIPARC:UPI000016EAB1; GB:X15134; NID:G40418; PIDN

R/Mimlich, S.A.; Newton, A.

Proc. Natl. Acad. Sci. U.S.A. 84, 1142-1146, 1987

A/Title: Promoter mapping and cell cycle regulation of flagellin gene transcription in

A/Reference number: A25882; MUID:87147229; PMID:3465658

A/Accession: A25882

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-12, 'V', 14-16 <MIN>

A/Cross-references: UNIPARC:UPI000016EABE; GB:M15688; NID:G144267; PIDN:AAA23050.1; PTL

C/Genetics:

A/Genes: flgB

Query Match 23.1%; Score 18; DB 2; Length 16;

Best Local Similarity 42.9%; Pred. No. 7.6e+03;

Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 7 NDYSKN 13

Db 3 NSINTNP 9

#### RESULT 63

7K protein - Escherichia coli

C/Species: Escherichia coli

C/Date: 31-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004

C/Accession: B44820

R/Lopez, J.; Delgado, D.; Andree, I.; Ortiz, J.M.; Rodriguez, J.C.

J. Gen. Microbiol. 137, 1093-1099, 1991

A/Title: Isolation and evolutionary analysis of a RepFVB replicon of the plasmid pSU21

A/Reference number: A44820; MUID:91324851; PMID:1865183

A/Contents: IncFVI plasmid pSU212

A/Accession: B44820

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-16 <LOP>

A/Cross-references: UNIPROT:Q8KQF9; UNIPARC:UPI000017AA2D

A/Note: sequence extracted from NCBI backbone (NCBIN:45962, NCBI:45966)

#### RESULT 64

protein P8 - curled-leaved tobacco (fragment)

C/Species: Nicotiana glauca (curled-leaved tobacco)

Query Match 23.1%; Score 18; DB 2; Length 16;

Best Local Similarity 75.0%; Pred. No. 7.6e+03;

Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 10 SKNP 13

Db 9 SBNP 12

C/Date: 19-May-1989 #sequence\_revision 19-May-1989 #text\_change 09-Jul-2004  
C/Accession: B28027  
R/Bauw, G.; De Loose, M.; Inze, D.; Van Montagu, M.; Vandekerckhove, J.  
Proc. Natl. Acad. Sci. U.S.A. 84, 4806-4810, 1987  
A/Title: Alterations in the phenotype of plant cells studied by NH2-terminal amino acid-  
A/Reference number: A94167  
A/Accession: B28027  
A/Molecule type: protein  
A/Residues: 1-16 <BAU>  
A/Cross-references: UNIPROT:Q7M1V7; UNIPARC:UPI000017B09F  
A/Note: 10-Lys was also found

Query Match 23.1%; Score 18; DB 2; Length 16;  
Best Local Similarity 80.0%; Pred. No. 7.6e+03;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 7 NDYSK 11  
Db 10 NDGSK 14

RESULT 65  
A61117  
somatoostatin precursor processing enzyme (EC 3.4.21.-) - American goosefish (fragment)  
C/Species: Lophius americanus (American goosefish)  
C/Date: 10-Mar-1994 #sequence\_revision 10-Mar-1994 #text\_change 13-Sep-1996  
C/Accession: A61117  
R/Mackin, R.B.; Noe, B.D.; Spiess, J.  
Endocrinology 129, 2263-2265, 1991  
A/Title: Identification of a somatoostatin-14-generating propeptide converting enzyme as  
A/Reference number: A61117; MUID:92007528; PMID:1680673  
A/Accession: A61117  
A/Molecule type: protein  
A/Residues: 1-17 <MAC>  
A/Cross-references: UNIPARC:UPI0000175CD6  
A/Experimental source: pancreatic islets  
A/Superfamily: kexin; subtilisin homology  
C/Keywords: hydrolase; serine proteinase

Query Match 23.1%; Score 18; DB 2; Length 17;  
Best Local Similarity 44.4%; Pred. No. 8.1e+03;  
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 4 RDNDYSKN 12  
Db 3 RNNDIEVN 11

RESULT 66  
S57991  
hydroxyproline-rich protein - Sesbania rostrata (fragment)  
C/Species: Sesbania rostrata  
C/Date: 13-Jan-1996 #sequence\_revision 01-Mar-1996 #text\_change 09-Jul-2004  
C/Accession: S57991  
R/Gormachitg, S.; Valerio-Lepintec, M.; Szczylowski, K.; van Montagu, M.; Holsters, M.  
submitted to the EMBL Data Library, March 1995  
A/Description: Use of differential display to identify novel Sesbania rostrata genes ent  
A/Reference number: S57991  
A/Accession: S57991  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-17 <GOO>  
A/Cross-references: UNIPROT:Q41400; UNIPARC:UPI00000ACD95; EMBL:Z48673; NID:g899484; PIT  
C/Superfamily: hydroxyproline-rich glycoprotein

Query Match 23.1%; Score 18; DB 2; Length 17;  
Best Local Similarity 60.0%; Pred. No. 8.1e+03;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 9 YSKNP 13  
Db 6 YKSP 10

RESULT 67  
B28027  
protein P4 - curled-leaved tobacco (fragment)  
C/Species: Nicotiana glumabagifolia (curled-leaved tobacco)  
C/Date: 19-May-1989 #sequence\_revision 19-May-1989 #text\_change 18-Jun-1993  
C/Accession: B28027  
R/Bauw, G.; De Loose, M.; Inze, D.; Van Montagu, M.; Vandekerckhove, J.  
Proc. Natl. Acad. Sci. U.S.A. 84, 4806-4810, 1987  
A/Title: Alterations in the phenotype of plant cells studied by NH2-terminal amino acid  
A/Reference number: A94167  
A/Accession: B28027  
A/Molecule type: protein  
A/Residues: 1-17 <BAU>  
A/Cross-references: UNIPARC:UPI000017B09D

Query Match 23.1%; Score 18; DB 2; Length 17;  
Best Local Similarity 28.6%; Pred. No. 8.1e+03;  
Matches 2; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 8 DYKNPM 14  
Db 8 EYNQNAL 14

RESULT 68  
B61491  
seed protein ws-2 - winged bean (fragment)  
C/Species: Psophocarpus tetragonolobus (winged bean)  
C/Date: 07-Oct-1994 #sequence\_revision 07-Oct-1994 #text\_change 09-Jul-2004  
C/Accession: B61491  
R/Hirano, H.  
J. Protein Chem. 8, 115-130, 1989  
A/Title: Microsequence analysis of winged bean seed proteins electrophoretically  
A/Reference number: A61491; MUID:89351606; PMID:2765119  
A/Accession: B61491  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-17 <HR>  
A/Cross-references: UNIPROT:Q7M1H7; UNIPARC:UPI000017B06D  
C/Keywords: seed

Query Match 23.1%; Score 18; DB 2; Length 17;  
Best Local Similarity 25.0%; Pred. No. 8.1e+03;  
Matches 3; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

OY 1 SIKRDNDYSKN 12  
Db 2 TISFNFQPDON 13

RESULT 69  
PH1815  
T cell receptor alpha chain V region (clone 4PB1 V alpha 24-7) - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 16-Jul-1999  
C/Accession: PH1815  
R/Poccellil, S.; Jockey, C.E.; Brenner, M.B.; Balk, S.P.  
J. Exp. Med. 178, 1-16, 1993  
A/Title: Analysis of T cell antigen receptor (TCR) expression by human peripheral blood  
A/Reference number: PH1754; MUID:93301585; PMID:8391057  
A/Accession: PH1815  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-18 <POR>  
A/Cross-references: UNIPARC:UPI000017C387

Query Match 23.1%; Score 18; DB 2; Length 18;  
Best Local Similarity 66.7%; Pred. No. 8.6e+03;  
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 5 DHNDYS 10

Db 5 DLMRYs 10

## RESULT 70

T08159  
S locus-linked protein SL1a - rape  
C/Species: Brassica napus (rape)  
C/Date: 21-May-1999 #sequence\_revision 21-May-1999 #text\_change 09-Jul-2004  
C/Accession: T08159  
R/Yu, K.; Schuster, U.; Glavin, T.L.; Goring, D.R.; Nothstein, S.J.  
Plant Cell 8, 2369-2380, 1996  
A/Title: Molecular characterization of the S locus in two self-incompatible Brassica nap  
A/Reference number: 216388; MUID:97143881; PMID:8989868  
A/Accession: T08159  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: mRNA  
A/Residues: 1-18 <YUK>  
A/Cross-references: UNIPROT:Q96345; UNIPARC:UPI00000A8040; EMBL:U66192; NID:G1518109; PI

## Query Match

Best Local Similarity 23.1%; Score 18; DB 2; Length 18;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 9 YSKNP 13  
Db 10 YSDDP 14

## RESULT 71

A59137  
protein p11 - golden needle mushroom (fragment)  
C/Species: Flammulina velutipes (golden needle mushroom)  
C/Date: 12-Nov-1999 #sequence\_revision 12-Nov-1999 #text\_change 09-Jul-2004  
C/Accession: A59137  
R/Sakamoto, Y.; Ando, A.; Tamai, Y.; Miura, K.  
submitted to the Protein Sequence Database, November 1999  
A/Description: Differences of proteins expressed in the fruiting dikaryon and the non-fr  
A/Reference number: A59137  
A/Accession: A59137  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-18 <SAK>  
A/Cross-references: UNIPROT:Q7M4W6; UNIPARC:UPI000017CB27

## Query Match

Best Local Similarity 23.1%; Score 18; DB 2; Length 18;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 10 SKNP 13  
Db 12 SQNP 15

## RESULT 72

S43657  
hsp90 protein homolog - quail (fragments)  
N/Alternate names: p89 protein  
C/Species: Phasianidae gen. sp. (quail)  
C/Date: 19-Mar-1997 #sequence\_revision 01-Feb-1999 #text\_change 01-Feb-1999  
C/Accession: S43657  
R/Lovric, J.; Bischof, O.; Moelling, K.  
FEBS Lett. 343, 15-21, 1994  
A/Title: Cell cycle-dependent association of Gag-M1 and hsp90.  
A/Reference number: S43657; MUID:94215698; PMID:8163010  
A/Accession: S43657  
A/Molecule type: protein  
A/Residues: 1-19 <LOV>  
A/Cross-references: UNIPARC:UPI0000177D66  
A/Experimental source: embryo fibroblasts  
C/Superfamily: heat shock protein 90  
C/Keywords: heat shock

Query Match 23.1%; Score 18; DB 2; Length 19;  
Best Local Similarity 33.3%; Pred. No. 9.1e+03;  
Matches 3; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 3 KRDNHYSK 11  
Db 11 KKFYEQFSK 19

## RESULT 73

S31613  
beta-1,3-glucanase homolog (clone A28) - rape (fragment)  
C/Species: Brassica napus (rape)  
C/Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 09-Jul-2004  
C/Accession: S31613  
R/Hird, D.; Worral, D.; Hodge, R.; Paul, W.; Smart, S.; Draper, J.; Scott, R.  
submitted to the EMBL Data Library, December 1992  
A/Description: The anther-specific protein encoded by the Brassica napus and Arabidops  
A/Reference number: S31612  
A/Accession: S31613  
A/Molecule type: mRNA  
A/Residues: 1-19 <HIR>  
A/Cross-references: UNIPROT:Q06914; UNIPARC:UPI000009F3B; EMBL:X69890; NID:G17735; PI  
A/Experimental source: clone A28  
C/Superfamily: beta-1,3-glucanase

Query Match 23.1%; Score 18; DB 2; Length 19;  
Best Local Similarity 57.1%; Pred. No. 9.1e+03;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 7 NDYSKNP 13  
Db 9 NDRCKFP 15

## RESULT 74

S50741  
probable trypsin inhibitor - potato (fragment)  
N/Alternate names: PKPI major protein  
C/Species: Solanum tuberosum (potato)  
C/Date: 14-Jul-1995 #sequence\_revision 12-Apr-1996 #text\_change 09-Jul-2004  
C/Accession: S50741  
R/Mitsunori, C.; Yamagishi, K.; Fujino, K.; Kikuta, Y.  
Plant Mol. Biol. 26, 961-969, 1994  
A/Title: Detection of immunologically related Kunitz and Bowman-Birk proteinase inhibit  
A/Reference number: S50741; MUID:95093035; PMID:8000008  
A/Accession: S50741  
A/Molecule type: protein  
A/Residues: 1-20 <MIT>  
A/Cross-references: UNIPROT:Q9S8K2; UNIPARC:UPI00000A9BHF  
C/Superfamily: cathepsin D inhibitor

Query Match 23.1%; Score 18; DB 2; Length 20;  
Best Local Similarity 42.9%; Pred. No. 9.6e+03;  
Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 8 DYSKNPM 14  
Db 8 DQDNPL 14

## RESULT 75

S71017  
hypothetical protein - Streptococcus pneumoniae (fragment)  
C/Species: Streptococcus pneumoniae  
C/Date: 15-Feb-1997 #sequence\_revision 13-Mar-1997 #text\_change 31-Dec-2004  
C/Accession: S71017  
R/Martin, B.; Sharples, G.J.; Humbert, O.; Lloyd, R.G.; Claverys, J.P.  
Mol. Microbiol. 19, 1035-1045, 1996  
A/Title: The mmsA locus of Streptococcus pneumoniae encodes a RecG-like protein involve  
A/Reference number: S71015; MUID:96249697; PMID:8830261  
A/Accession: S71017  
A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA  
A:Residues: 1-20 <MAR>  
A:Cross-references: UNIPROT:Q97PE0, UNIPROT:Q8DNUL, UNIPARC:UPI000017AC6F, EMBL:Z49988  
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1995  
C:Superfamily: cephalosporin-C deacetylase

Query Match 23.1%; Score 18; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 9.6e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 KNP 13  
DB 2 KNP 4

RESULT 76  
A44773  
pollen allergen I - Japanese cedar (fragment)  
C:Species: Cryptomeria japonica (Japanese cedar)  
C:Date: 03-Mar-1993 #sequence\_revision 03-Mar-1993 #text\_change 09-Jul-2004  
C:Accession: A44773  
R:Matita, M.; Ando, S.; Usui, M.; Kurimoto, M.; Sakaguchi, M.; Inouye, S.; Matsushi, T.  
FEBS Lett. 239, 329-332, 1988  
A:Title: N-terminal amino acid sequence of a major allergen of Japanese cedar pollen (Cr  
A:Reference number: A44773; MUID:89031257; PMID:3181436  
A:Accession: A44773  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-20 <TAN>  
A:Cross-references: UNIPROT:P18632, UNIPARC:UPI0000157693  
C:Superfamily: pectate lyase LAM59  
C:Keywords: pollen

Query Match 23.1%; Score 18; DB 2; Length 20;  
Best Local Similarity 27.3%; Pred. No. 9.6e+03;  
Matches 3; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 4 RDHNDYSKNPM 14  
DB 9 RGSNNWQNRM 19

RESULT 77  
I54283  
arylsulfatase A - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 21-Jul-2000  
C:Accession: I54283  
R:Regis, S.; Carozzo, R.; Filocamo, M.; Serra, G.; Mastropalo, C.; Gatti, R.  
Hum. Genet. 96, 233-235, 1995  
A:Title: An AT-deletion causing a frameshift in the arylsulfatase A gene of a late infan  
A:Reference number: I54283; MUID:95362256; PMID:7635478  
A:Accession: I54283  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-20 <RES>  
A:Cross-references: UNIPARC:UPI00001177BE, GB:S78735; NID:G1037139; PIDN:AAB35013.1; PIT

Query Match 23.1%; Score 18; DB 2; Length 20;  
Best Local Similarity 33.3%; Pred. No. 9.6e+03;  
Matches 2; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 6 HNDYSK 11  
DB 3 HSDHCR 8

RESULT 78  
H49164  
chromogranin-B - rat (fragment)  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 19-Dec-1993 #sequence\_revision 18-Nov-1994 #text\_change 04-Dec-1994  
C:Accession: H49164

R:Nielsen, B.; Wellinder, B.S.; Madsen, O.D.  
Endocrinology 129, 3147-3156, 1991  
A:Title: Chromogranin-B, a putative precursor of eight novel rat glucagonoma peptides t  
A:Reference number: A49164; MUID:92063871; PMID:1954895  
A:Accession: H49164  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-20 <NIE>  
A:Cross-references: UNIPARC:UPI0000086626  
A:Note: sequence extracted from NCBI backbone (NCBIP:66364)

Query Match 23.1%; Score 18; DB 2; Length 20;  
Best Local Similarity 60.0%; Pred. No. 9.6e+03;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 RDHND 8  
DB 6 RDXNME 10

RESULT 79  
A26999  
carboxylesterase (EC 3.1.1.1), intestinal - Caenorhabditis elegans (fragment)  
C:Species: Caenorhabditis elegans  
C:Date: 16-Aug-1988 #sequence\_revision 16-Aug-1988 #text\_change 09-Jul-2004  
C:Accession: A26999  
R:McGhee, J.D.  
Biochemistry 26, 4101-4107, 1987  
A:Title: Purification and characterization of a carboxylesterase from the intestine of  
A:Reference number: A26999; MUID:88000636; PMID:3651439  
A:Accession: A26999  
A:Molecule type: protein  
A:Residues: 1-13 <MCS>  
A:Cross-references: UNIPROT:Q7M3Q8, UNIPARC:UPI000017B6B3  
C:Keywords: carboxylic ester hydrolase; intestine

Query Match 22.4%; Score 17.5; DB 2; Length 13;  
Best Local Similarity 57.1%; Pred. No. 7.4e+03;  
Matches 4; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 5 DHNDYSK 11  
DB 5 EHN-YGK 10

RESULT 80  
S17976  
glucose isomerase - Thermoaerobacterium saccharolyticum (fragment)  
C:Species: Thermoaerobacterium saccharolyticum  
C:Date: 12-Feb-1998 #sequence\_revision 12-Feb-1998 #text\_change 09-Jul-2004  
C:Accession: S17976  
R:Lee, C.; Zeikus, J.G.  
Biochem. J. 273, 565-571, 1991  
A:Title: Purification and characterization of thermostable glucose isomerase from Clost  
A:Reference number: S15119; MUID:91144536; PMID:1996956  
A:Accession: S17976  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-7 <LBS>  
A:Cross-references: UNIPROT:P30435, UNIPARC:UPI0000173053  
A:Note: the sequence from page 568 is inconsistent with that from page 565 in having 6-

Query Match 21.8%; Score 17; DB 2; Length 7;  
Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 7 NDYSKN 12  
DB 2 NKYPEN 7

RESULT 81

B54823  
 olfactory receptor 17 - western wild mouse (fragment)  
 C/Species: Mus spretus (western wild mouse)  
 C/Date: 28-Apr-1995 #sequence\_revision 28-Apr-1995 #text\_change 17-Mar-1999  
 C/Accession: B54823  
 R/Cheser, A.; Simon, I.; Cedar, H.; Axel, R.  
 Cell 78, 823-834, 1994  
 A/Title: Allelic inactivation regulates olfactory receptor gene expression.  
 A/Reference number: A54823; PMID:94373818; PMID:8087849  
 A/Accession: B54823  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-8 <CH2>  
 A/Cross-references: UNIPARC:UPI000017C89B

Query Match 21.8%; Score 17; DB 2; Length 8;  
 Best Local Similarity 40.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 KRDN 7  
 DB 3 RNNHS 7

RESULT 82  
 S30494  
 cat gene leader peptide - Streptococcus agalactiae plasmid pIP501  
 C/Species: Streptococcus agalactiae  
 C/Date: 12-Feb-1998 #sequence\_revision 20-Feb-1998 #text\_change 16-Aug-2004  
 C/Accession: S30494  
 R/Trieu-Quoc, P.; de Cespedes, G.; Horvud, T.  
 Plasmid 28, 272-276, 1992  
 A/Title: Nucleotide sequence of the chloramphenicol resistance determinant of the Strept  
 A/Reference number: J01950; PMID:93096867; PMID:1461942  
 A/Accession: S30494  
 A/Molecule type: DNA  
 A/Residues: 1-9 <TRI>  
 A/Cross-references: UNIPROT:P36884; UNIPARC:UPI00000004AB; EMBL:X65462; NID:949071; PIDN  
 A/Genome: plasmid pIP501

Query Match 21.8%; Score 17; DB 2; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 DYS 10  
 DB 6 DYS 8

RESULT 83  
 B24362  
 chloramphenicol O-acetyltransferase leader peptide - Staphylococcus aureus plasmid pUB11  
 C/Species: Staphylococcus aureus  
 C/Date: 07-Apr-1994 #sequence\_revision 07-Apr-1994 #text\_change 05-Oct-2004  
 C/Accession: B24362  
 R/Bruckner, R.; Matczura, H.  
 EMBO J. 4, 2295-2300, 1985  
 A/Title: Regulation of the inducible chloramphenicol acetyltransferase gene of the Staph  
 A/Reference number: A24362; PMID:86081739; PMID:13865770  
 A/Accession: B24362  
 A/Molecule type: DNA  
 A/Residues: 1-9 <BNV>  
 A/Cross-references: UNIPROT:P36884; UNIPARC:UPI00000004AB; GB:X02872; NID:946536; PIDN:  
 A/Comment: Ribosomes stalling in the translation of this leader peptide, caused by the ef  
 A/Title: chloramphenicol O-acetyltransferase from a ribosome binding site located  
 A/Genome: plasmid

Query Match 21.8%; Score 17; DB 2; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 DYS 10  
 DB 6 DYS 8

RESULT 84  
 S18385  
 NADP-cytochrome P450 reductase-related protein - rat (fragment)  
 C/Species: Rattus norvegicus (Norway rat)  
 C/Date: 22-Nov-1993 #sequence\_revision 12-Apr-1996 #text\_change 07-Feb-1997  
 C/Accession: S18385  
 R/Nadler, S.G.; Strobel, H.W.  
 Arch. Biochem. Biophys. 290, 277-284, 1991  
 A/Title: Identification and characterization of an NADPH-cytochrome P450 reductase der  
 A/Reference number: S18385; PMID:92027739; PMID:1929397  
 A/Accession: S18385  
 A/Molecule type: protein  
 A/Residues: 1-11 <NAD>  
 A/Cross-references: UNIPARC:UPI000017C961  
 C/Keywords: NADP

Query Match 21.8%; Score 17; DB 2; Length 11;  
 Best Local Similarity 60.0%; Pred. No. 7.6e+03;  
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 DHNDY 9  
 DB 5 DPEDY 9

RESULT 85  
 B47171  
 chondroitin sulfate proteoglycan PG-M core protein, splice form VI - chicken (fragment)  
 N/Alternate names: versican-like chondroitin sulfate proteoglycan  
 C/Species: Gallus gallus (chicken)  
 C/Date: 21-Sep-1993 #sequence\_revision 18-Nov-1994 #text\_change 28-Feb-1997  
 C/Accession: B47171  
 R/Shinomura, T.; Nishida, Y.; Ito, K.; Kimata, K.  
 J. Biol. Chem. 268, 14461-14469, 1993  
 A/Title: cDNA cloning of PG-M, a large chondroitin sulfate proteoglycan expressed durin

A/Reference number: A47171; PMID:93300846; PMID:8314802  
 A/Accession: B47171  
 A/Status: preliminary  
 A/Molecule type: nucleic acid  
 A/Residues: 1-12 <SHI>  
 A/Cross-references: UNIPARC:UPI000017BPF2  
 A/Experimental source: CER, embryo fibroblasts  
 A/Note: sequence extracted from NCBI backbone (NCBIN:134459, NCBI:134462)

Query Match 21.8%; Score 17; DB 2; Length 12;  
 Best Local Similarity 50.0%; Pred. No. 8.4e+03;  
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 SIKRDH 6  
 DB 3 SEBDH 8

RESULT 86  
 PH1605  
 Ig H chain V-D-J region (wild-type clone 328) - mouse (fragment)  
 C/Species: Mus musculus (house mouse)  
 C/Date: 02-Jun-1994 #sequence\_revision 02-Jun-1994 #text\_change 17-Mar-1999  
 C/Accession: PH1605  
 R/Levinson, D.A.; Campos-Torres, J.; Leder, P.  
 J. Exp. Med. 178, 317-329, 1993  
 A/Title: Molecular characterization of transgene-induced immunodeficiency in B-less mic  
 A/Reference number: PH1605; PMID:93301609; PMID:8315387  
 A/Accession: PH1605  
 A/Molecule type: DNA  
 A/Residues: 1-12 <LRV>  
 A/Cross-references: UNIPARC:UPI000017C6C1

A;Experimental source: bone marrow pre-B lymphocyte  
A;Keywords: immunoglobulin

Query Match 21.8%; Score 17; DB 2; Length 12;  
Best Local Similarity 42.9%; Pred. No. 8.4e+03;  
Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 KRDNNDY 9  
| | |  
Db 6 REDAMDY 12

## RESULT 87

146794  
hypothetical protein [imported] - Haloarcula marismortui (fragment)

C;Species: Haloarcula marismortui  
C;Date: 17-Mar-2000 #sequence\_revision 17-Mar-2000 #text\_change 09-Jul-2004  
C;Accession: 146794  
R;Arndt, E.

PEBS Lett. 267, 193-198, 1990  
A;Title: Nucleotide sequence of four genes encoding ribosomal proteins from the 'S10 and  
A;Reference number: S10731; MUID:90336772; PMID:2143141

A;Accession: 146794  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-12 <ARN>  
A;Cross-references: UNIPROT:P10971, UNIPARC:UPI0000167C4; EMBL:X5511; NID:643610; PIDD

Query Match 21.8%; Score 17; DB 2; Length 12;  
Best Local Similarity 27.3%; Pred. No. 8.4e+03;  
Matches 3; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 2 IKRDNDYSKN 12  
| | | | |  
Db 1 IQGREGDLOEN 11

## RESULT 88

PT0331

Ig heavy chain CRD3 region (clone J2-121) - human (fragment)

C;Species: Homo sapiens (man)  
C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996  
C;Accession: PT0331  
R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.

J. Exp. Med. 173, 395-407, 1991  
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and  
A;Reference number: PT0222; MUID:91108337; PMID:1899102

A;Accession: PT0331  
A;Molecule type: DNA  
A;Residues: 1-13 <YAM>  
A;Cross-references: UNIPARC:UPI000017C219  
A;Experimental source: B lymphocyte  
A;Keywords: heterotetramer; immunoglobulin

Query Match 21.8%; Score 17; DB 2; Length 13;  
Best Local Similarity 30.0%; Pred. No. 9.1e+03;  
Matches 3; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 4 RDNDYKNP 13  
| | | | |  
Db 2 RGRDGNMPP 11

## RESULT 89

170075

glycophorin B (mistranslated) - human (fragment)

C;Species: Homo sapiens (man)  
C;Date: 21-Feb-1997 #sequence\_revision 14-Aug-1997 #text\_change 09-Jul-2004  
C;Accession: 170075  
R;Rearden, A.; Phan, H.; Dubnicoff, T.; Kudo, S.; Fukuda, M.

J. Biol. Chem. 265, 9259-9263, 1990  
A;Title: Identification of the crossing-over point of a hybrid gene encoding human glyco  
A;Reference number: I55334; MUID:90264417; PMID:1971625

A;Accession: 170075  
A;Status: translated from GB/EMBL/DBJ

A;Molecule type: DNA  
A;Residues: 1-13 <REA>  
A;Cross-references: UNIPROT:Q14461, UNIPARC:UPI00000730D2; GB:M33505; GB:J05465; NID:91  
A;Note: this sequence was not determined in this report; the translation is from an inc  
C;Genetics:  
A;Gene: GDB:GYPB  
A;Cross-references: GDB:118891  
A;Map position: 4q28-4q31

Query Match 21.8%; Score 17; DB 4; Length 13;  
Best Local Similarity 75.0%; Pred. No. 9.1e+03;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 KRDN 6  
| | |  
Db 2 KRDN 5

## RESULT 90

PT0029

karataasin - karatas (fragment)

C;Species: Bromelia plumieri (karatas)  
C;Date: 31-Dec-1990 #sequence\_revision 31-Dec-1990 #text\_change 09-Jul-2004  
C;Accession: PT0029  
R;Montes, C.; Amador, M.; Cuevas, D.; Cordoba, F.

Agric. Biol. Chem. 54, 17-24, 1990  
A;Title: Subunit structure of karataasin, the proteinase isolated from Bromelia plumieri  
A;Reference number: PT0029; MUID:90344224; PMID:1368518  
A;Accession: PT0029  
A;Molecule type: protein  
A;Residues: 1-14 <MON>

A;Cross-references: UNIPROT:P22442; UNIPARC:UPI000012DC38  
A;Note: the amino terminal sequence shows similarity with papain and stem bromelain  
C;Comment: This enzyme is composed of two small subunits linked by disulfide bonds.

Query Match 21.8%; Score 17; DB 2; Length 14;  
Best Local Similarity 60.0%; Pred. No. 9.8e+03;  
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 DNDY 9  
| | | | |  
Db 6 DXXDY 10

## RESULT 91

A58945

anti-neoplastic urinary protein - human (fragment)

N;Alternate names: ANUP  
C;Species: Homo sapiens (man)  
C;Date: 09-Apr-1999 #sequence\_revision 09-Apr-1999 #text\_change 09-Apr-1999  
C;Accession: A58945  
R;Ridge, R.J.; Sloane, N.H.

Cytokine 8, 1-5, 1996  
A;Title: Partial N-terminal amino acid sequence of the anti-neoplastic urinary protein  
A;Reference number: A58945; MUID:96351837; PMID:8742060  
A;Accession: A58945  
A;Molecule type: protein  
A;Residues: 1-15 <RID>

A;Cross-references: UNIPARC:UPI000017C089  
A;Note: 13-Thr was also seen; residues 4 and 7 are assumed to be Cys; the authors report  
the terminal is blocked  
C;Keywords: cytokine; pyroglutamic acid  
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status predicted

Query Match 21.8%; Score 17; DB 2; Length 15;  
Best Local Similarity 75.0%; Pred. No. 1.1e+04;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 KNPM 14  
| | | | |

Db 8 KEPM 11

## RESULT 92

Pht631

Ig H chain V-D-J region (clone B-lees 202) - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 02-Jun-1994 #sequence\_revision 02-Jun-1994 #text\_change 17-Mar-1999

C/Accession: Pht631

R/Levinson, D.A.; Campos-Torres, J.; Leder, P.

J. Exp. Med. 178, 317-329, 1993

A/Title: Molecular characterization of transgene-induced immunodeficiency in B-lees mice

A/Reference number: Pht580; MUID:93301609; PMID:8315387

A/Accession: Pht631

A/Molecule type: DNA

A/Residues: 1-15 &lt;LEV&gt;

A/Cross-references: UNIPARC:UPI000017C699

A/Experimental source: bone marrow pre-B lymphocyte

C/Keywords: immunoglobulin

Query Match 21.8%; Score 17; DB 2; Length 15;

Best Local Similarity 75.0%; Pred. No. 1.1e+04;

Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 KNPM 14

Db 2 KTFM 5

## RESULT 93

B26501

Lipoprotein lipase (BC 3.1.1.34) - guinea pig (fragment)

C/Species: Cavia porcellus (guinea pig)

C/Date: 21-May-1988 #sequence\_revision 21-May-1988 #text\_change 28-Apr-1993

C/Accession: B26501

R/Bergstrom-Olivera, G.; Oliveira, T.; Jornvall, H.

Eur. J. Biochem. 161, 281-288, 1986

A/Title: Lipoprotein lipases from cow, guinea-pig and man. Structural characterization &amp;

A/Reference number: A3178; MUID:87054027; PMID:3536511

A/Accession: B26501

A/Molecule type: protein

A/Residues: 1-15 &lt;BEN&gt;

A/Cross-references: UNIPARC:UPI000017CA2B

C/Keywords: carboxylic ester hydrolase

Query Match 21.8%; Score 17; DB 2; Length 15;

Best Local Similarity 40.0%; Pred. No. 1.1e+04;

Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 4 RDND 8

Db 5 KDYD 9

## RESULT 94

PA0059

Protein QP200021 - fungus (Fusarium sporotrichioides) (fragment)

C/Species: Fusarium sporotrichioides

C/Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 09-Jul-2004

C/Accession: PA0059

R/Chow, L.P.; Fukaya, N.; Sugita, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.

Submitted to JFIP, October 1994

A/Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrichi

A/Reference number: PA0059

A/Accession: PA0059

A/Molecule type: protein

A/Residues: 1-15 &lt;CHO&gt;

A/Cross-references: UNIPROT:Q7M4Y3; UNIPARC:UPI000017B410

Query Match

Best Local Similarity 21.8%; Score 17; DB 2; Length 15;

Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 IKRDH 6  
Db 4 LEBDH 8

## RESULT 95

C45133

casein kinase II (BC 2.7.1.1-) alpha chain - dog (fragment)

C/Species: Canis lupus familiaris (dog)

C/Date: 30-Apr-1993 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004

C/Accession: C45133

R/Ou, W.J.; Thomas, D.Y.; Bell, A.W.; Bergeron, J.J.

J. Biol. Chem. 267, 23789-23796, 1992

A/Title: Casein kinase II phosphorylation of signal sequence receptor alpha and the ass

A/Reference number: A45133; MUID:93054738; PMID:1331100

A/Accession: C45133

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-16 &lt;OU&gt;

A/Cross-references: UNIPROT:Q9TRK9; UNIPARC:UPI0000088890

A/Experimental source: endoplasmic reticulum, pancreas

A/Note: sequence extracted from NCBI backbone (NCBI:P:118799)

C/Suprafamily: kinase-related transforming protein; protein kinase homology

C/Keywords: ATP; heterotrimer; phosphotransferase; serine/threonine-specific protein

Query Match 21.8%; Score 17; DB 2; Length 16;

Best Local Similarity 50.0%; Pred. No. 1.1e+04;

Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 6 HNDY 9

Db 12 HDNY 15

## RESULT 96

PT0224

Ig heavy chain CDR3 region (clone 1-91) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996

C/Accession: PT0224

R/Yanada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Catton, A.J.; Rovera, G.

J. Exp. Med. 173, 395-407, 1991

A/Title: Preferential utilization of specific immunoglobulin heavy chain diversity and

A/Reference number: PT0222; MUID:91108337; PMID:1899102

A/Accession: PT0224

A/Molecule type: DNA

A/Residues: 1-16 &lt;YAM&gt;

A/Cross-references: UNIPARC:UPI0000017C1D6

A/Experimental source: B lymphocyte

A/Note: the authors translated the stop codon for residue 9 as X

C/Keywords: heterotrimer; immunoglobulin

Query Match 21.8%; Score 17; DB 2; Length 16;

Best Local Similarity 100.0%; Pred. No. 1.1e+04;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 DYS 10

Db 4 DYS 6

## RESULT 97

S48655

glutathione dehydrogenase (ascorbate) (BC 1.8.5.1) - spinach (fragment)

N/Alternate names: dehydroascorbate reductase; DHA reductase; tryptan inhibitor (Kunitz

C/Species: Spinacia oleracea (spinach)

C/Date: 15-Jul-1995 #sequence\_revision 12-Apr-1996 #text\_change 09-Jul-2004

C/Accession: S48655

R/Trempier, S.; Folmann, H.; Haeblerlein, I.

FEBS Lett. 352, 159-162, 1994

A/Title: A novel dehydroascorbate reductase from spinach chloroplasts homologous to pla

A/Reference number: S48655; MUID:95010699; PMID:7925967

A/Accession: S48655

A:Molecule type: protein  
 A:Residues: 1-17 <TRU>  
 A:Cross-references: UNIPROT:Q9T2H6, UNIPARC:UPI000093AAAF  
 C:Superfamily: plant kunitz-type proteinase inhibitor  
 C:Keywords: chloroplast; oxidoreductase

Query Match 21.8%; Score 17; DB 2; Length 17;  
 Best Local Similarity 42.9%; Pred. No. 1.2e+04;  
 Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 8 DYSKNPM 14  
 | | |  
 | | |  
 Db 5 DNEGNPL 11

## RESULT 98

B44923  
 carboxypeptidase 3 - Rhizomucor circinelloides f. lusitanicus (fragment)  
 C:Species: Rhizomucor circinelloides f. lusitanicus  
 C>Date: 01-Apr-1993 #sequence\_revision 18-Nov-1994 #text\_change 04-Dec-1994  
 C:Accession: B44923  
 R:DiSanto, M.E.; Li, Q.H.; Logan, D.A.  
 J. Bacteriol. 174, 447-455, 1992

A:Title: Purification and characterization of a developmentally regulated carboxypeptidase  
 A:Reference number: A44923; MUID:92105011; PMID:1729237

A:Accession: B44923  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-17 <Dis>  
 A:Cross-references: UNIPARC:UPI000017B1C0  
 A:Note: sequence extracted from NCBI backbone (NCBIP:75616)

Query Match 21.8%; Score 17; DB 2; Length 17;  
 Best Local Similarity 40.0%; Pred. No. 1.2e+04;  
 Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 6 HNDYS 10  
 | : |  
 | : |  
 Db 11 HERS 15

## RESULT 99

A46592  
 lactase-phlorizin hydrolase, 200K isoform - rat (fragment)

C:Species: Rattus norvegicus (Norway rat)

C>Date: 16-Feb-1994 #sequence\_revision 18-Nov-1994 #text\_change 01-Nov-1996

C:Accession: A46592

R:Dudley, M.A.; Hachey, D.L.; Quaroni, A.; Hutches, T.W.; Nichols, B.L.; Rosenberger, J.

J. Biol. Chem. 268, 13609-13616, 1993

A:Title: In vivo sucrase-isomaltase and lactase-phlorizin hydrolase turnover in the fed

A:Reference number: A46592; MUID:92293888; PMID:8514793

A:Accession: A46592

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-17 <DUD>

A:Cross-references: UNIPARC:UPI0000067CC  
 A:Note: sequence extracted from NCBI backbone (NCBIP:134559)

C:Keywords: carbohydrate digestion; intestine  
 Query Match 21.8%; Score 17; DB 2; Length 17;  
 Best Local Similarity 30.0%; Pred. No. 1.2e+04;  
 Matches 3; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 5 DHNDYSKNPM 14  
 | | | | |  
 | | | | |  
 Db 4 DRNPIAAGPL 13

## RESULT 100

S24780

protein-tyrosine kinase (EC 2.7.1.112) lck - rat (fragment)

C:Species: Rattus norvegicus (Norway rat)

C>Date: 19-Feb-1994 #sequence\_revision 26-Jul-1996 #text\_change 05-Oct-2004

C:Accession: I58370; S24780

R:Shin, S.; Steffen, D.L.

Oncogene 8, 141-149, 1993

A:Title: Frequent activation of the lck gene by promoter insertion and aberrant splicing

A:Reference number: I58370; MUID:93141260; PMID:8423992

A:Accession: I58370

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-18 <RES>

A:Cross-references: UNIPROT:Q01621; UNIPARC:UPI00001709FB; EMBL:Z15029; NID:956567; PDB:

C:Genetics:

A:Gene: lck

C:Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homolog

C:Keywords: ATP; blocked amino end; lipoprotein; myristylation; phosphoryltransferase; thl

P;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted

F;3/Binding site: palmitate (Cys) (covalent) #status predicted

QY 10 SKNP 13  
 | | |  
 | | |

Db 6 SSNP 9

Search completed: January 20, 2006, 19:12:09  
 Job time : 8.94231 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 20, 2006, 18:54:54 ; Search time 46.5769 Seconds  
(without alignments)  
212.066 Million cell updates/sec

Title: US-09-662-293-1  
Perfect score: 78  
Sequence: 1 SIKRDHNDYSKNPM 14

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues  
Total number of hits satisfying chosen parameters: 14590

Minimum DB seq length: 0  
Maximum DB seq length: 20

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : UniProt\_05.80:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	35	44.9	20 2	Q9PRS5 ONCMY
2	28	35.9	15 1	AVP2 CAVPO
3	28	35.9	20 2	Q711V5 9RHIZ
4	27	34.6	13 2	Q53KLI ORYSA
5	27	34.6	14 2	Q8W1T7 BOSCA
6	26	33.3	11 2	Q9UNL8 HUMAN
7	26	33.3	20 2	Q9UCB5 HUMAN
8	25	32.7	20 2	Q9S8H1 HORVU
9	25	32.1	19 2	Q4X3T4 PLACH
10	25	32.1	20 1	SPAZ_ARTOL
11	25	32.1	20 2	Q9QUW2 9MURI
12	24.5	31.4	17 2	Q4XBK6 PLACH
13	24.5	31.4	19 2	Q7M0Q1 PSBPU
14	24	30.8	19 2	Q9S8G9 PSOTR
15	24	30.8	19 2	Q90510 9HIVI
16	24	30.8	20 2	Q9S8H0 PSOTR
17	23.5	30.1	13 2	Q4YHVI PLABE
18	23	29.5	13 2	Q83171 9VIRU
19	23	29.5	15 1	TK2B_BUNCA
20	23	29.5	18 2	Q711V7 9RHIZ
21	23	29.5	18 2	Q90W82 RAT
22	23	29.5	19 2	Q90514 9HIVI
23	23	29.5	20 2	Q4XKID PLACH
24	23	29.5	20 2	Q6V0Z6 MDSPP
25	22.5	28.8	18 2	Q7YX44 CABEL
26	22.5	28.8	19 2	Q905G4 9HIVI
27	22.5	28.8	19 2	Q90RGS 9HIVI
28	22	28.2	14 2	Q9UNM9 HUMAN
29	22	28.2	16 2	Q9R4Z5 STRSU
30	22	28.2	16 2	Q5DJ22 SOLSO
31	22	28.2	17 1	BMTID_BOOMI

32	22	28.2	17 2	Q34216 9SEPN	Q34216 sphingomona
33	22	28.2	18 2	Q4XK28 PLACH	Q4XK28 plasmidium
34	22	28.2	18 2	Q64134 9MURI	Q64134 ractus sp.
35	22	28.2	18 2	Q6DUU4 RAT	Q6DUU4 ractus norv
36	22	28.2	19 2	Q4XGA8 PLACH	Q4XGA8 plasmidium
37	22	28.2	20 2	Q7JNH9 DROME	Q7JNH9 drosophila
38	22	28.2	20 2	Q4Y3Y1 PLACH	Q4Y3Y1 plasmidium
39	22	28.2	20 2	Q9PS15 ONCKI	Q9PS15 oncorhynch
40	21.5	27.6	19 2	Q4NSW7 THEPA	Q4NSW7 theileria p
41	21.5	27.6	19 2	Q905G8 9HIVI	Q905G8 human immun
42	21.5	27.6	19 2	Q905J6 9HIVI	Q905J6 human immun
43	21	26.9	11 2	Q7M0L3 BACCI	Q7M0L3 bacillus ci
44	21	26.9	12 2	Q4XW72 PLACH	Q4XW72 plasmidium
45	21	26.9	12 2	Q4YET5 PLABE	Q4YET5 plasmidium
46	21	26.9	13 2	Q9QCK3 BVV	Q9QCK3 borna disea
47	21	26.9	13 2	Q9QCK6 BVV	Q9QCK6 borna disea
48	21	26.9	13 2	Q9QCK9 BVV	Q9QCK9 borna disea
49	21	26.9	13 2	Q9QCL2 BVV	Q9QCL2 borna disea
50	21	26.9	13 2	Q9QCL5 BVV	Q9QCL5 borna disea
51	21	26.9	13 2	Q9QCL8 BVV	Q9QCL8 borna disea
52	21	26.9	13 2	Q9QCM1 BVV	Q9QCM1 borna disea
53	21	26.9	13 2	Q9QCM4 BVV	Q9QCM4 borna disea
54	21	26.9	14 2	Q69Z00 HUMAN	Q69Z00 homo sapien
55	21	26.9	14 2	Q9TWX8 MANSE	Q9TWX8 manduca sex
56	21	26.9	14 2	Q54394 STRLI	Q54394 streptomyce
57	21	26.9	14 2	Q9RSR5 STRAU	Q9RSR5 straphylococ
58	21	26.9	15 1	MK1_PALPR	MK1_PALPR
59	21	26.9	15 1	MK2A_PALPR	MK2A_PALPR
60	21	26.9	15 1	TX12B_BUNCA	TX12B_BUNCA
61	21	26.9	15 1	UP02_METAN	UP02_METAN
62	21	26.9	15 2	Q9UC17 HUMAN	Q9UC17 homo sapien
63	21	26.9	15 2	Q7M0C8 9MURI	Q7M0C8 9MURI
64	21	26.9	15 2	Q9PXC5 TEV	Q9PXC5 tobacco etc
65	21	26.9	16 1	MK2B_PALPR	MK2B_PALPR
66	21	26.9	16 1	Q61EJ3 MOUSE	Q61EJ3 palomona pr
67	21	26.9	16 2	Q9RSR6 STRAU	Q9RSR6 mus musculu
68	21	26.9	18 2	Q260E2 HELPY	Q260E2 helicobacte
69	21	26.9	18 2	Q4X617 PLACH	Q4X617 plasmidium
70	21	26.9	19 2	Q9QW83 RAT	Q9QW83 ractus norv
71	21	26.9	19 2	Q905F6 9HIVI	Q905F6 human immun
72	21	26.9	20 1	MEFP_MYTEID	MEFP_MYTEID
73	21	26.9	20 2	Q9UCF0 HUMAN	Q9UCF0 homo sapien
74	21	26.9	20 2	Q9TPW8 NABGR	Q9TPW8 naegleria g
75	21	26.9	20 2	Q4YQV7 PLABE	Q4YQV7 plasmidium
76	21	26.9	20 2	Q9RSB1 ABRHY	Q9RSB1 aeromonas h
77	21	26.9	20 2	Q9QVC1 9MURI	Q9QVC1 ractus sp.
78	21	26.9	20 2	Q34694 HOMAN	Q34694 homarut ame
79	20.5	26.3	8 2	Q15893 HUMAN	Q15893 homo sapien
80	20	25.6	8 2	Q9UDZ4 HUMAN	Q9UDZ4 homo sapien
81	20	25.6	8 2	Q5RLS1 PIG	Q5RLS1 sus scrofa
82	20	25.6	8 2	Q93SR0 STABP	Q93SR0 straphylococ
83	20	25.6	10 2	P82136 SPIOL	P82136 spindacia ol
84	20	25.6	10 2	Q9QVW7 9MURI	Q9QVW7 mus sp. mep
85	20	25.6	11 2	P96319 DBSDS	P96319 deasilfovir
86	20	25.6	11 2	Q6LBU0 MOUSR	Q6LBU0 mus musculu
87	20	25.6	11 2	Q7MOD4 RAT	Q7MOD4 ractus norv
88	20	25.6	13 2	Q6LDS1 BPT3	Q6LDS1 bacterioph
89	20	25.6	13 2	Q51605 9ZZZZ	Q51605 plasmid col
90	20	25.6	14 1	HY14_PIG	HY14 sus scrofa
91	20	25.6	14 2	Q5XVW6 9MOU	Q5XVW6 candidatus
92	20	25.6	14 2	Q6XWV1 9MOU	Q6XWV1 chrysaanthem
93	20	25.6	14 2	Q6XWV4 9MOU	Q6XWV4 hydrangea p
94	20	25.6	14 2	Q6XWV7 9MOU	Q6XWV7 plantago vi
95	20	25.6	14 2	Q6XWXX 9MOU	Q6XWXX apicoc ast
96	20	25.6	14 2	Q6XWXX3 9MOU	Q6XWXX3 leatfopper-
97	20	25.6	14 2	Q6XWXX6 9MOU	Q6XWXX6 grey dogwo
98	20	25.6	14 2	Q6XWXX9 9MOU	Q6XWXX9 blueberry s
99	20	25.6	14 2	Q6XWXX8 9MOU	Q6XWXX8 clover phyl
100	20	25.6	14 2	Q6XWXX8 9MOU	Q6XWXX8 clover phyl

## ALIGNMENTS



RA Buell C., Yuan Q., Ouyang S., Liu J., Wang A., Maiti R., Lin H.,  
 RA Zhu W., Hamilton J., Jones K., Tallon L., Feldblyum T., Taittin T.,  
 RA Bera J., Kim M., Jin S., Fedrosh D., Vuong H., Overton II L.,  
 RA Readon M., Weaver B., John S., Lewis M., Ulteback T., Van Aken S.,  
 RA Wortman J., Haas B., Koo H., Zismann V., Hsiao J., Iobst S.,  
 RA de Vazaliles A., White O., Salzberg S., Fraser C.,  
 RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AC146328; AAX95034.1; -; Genomic DNA.  
 DR EMBL; AC135794; AAX96196.1; -; Genomic DNA.  
 KW Hypothetical protein.  
 SQ SEQUENCE 13 AA; 1520 MW; 9F1D63397ED5B5A CRC64;

Query Match 34.6%; Score 27; DB 2; Length 13;  
 Best Local Similarity 71.4%; Pred. No. 1e+03;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 DHNDYSK 11  
 DB 6 DYNDSK 12

RESULT 5  
 Q8W17\_BOSCA PRELIMINARY; PRT; 14 AA.  
 ID Q8W17\_BOSCA PRELIMINARY; PRT; 14 AA.  
 AC Q8W17;  
 DT 01-MAR-2002 (TREMBLrel. 20, Created)  
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)  
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)  
 DE Ribulose-1,5-bisphosphate large subunit (Fragment).  
 GN Name=rdcl;  
 OS Bosneria callictera.  
 OC Chloroplast.  
 OC Eukaryota; Rhodophyta; Florideophyceae; Ceramiales; Rhodomeleaceae;  
 OC Bosneria.  
 OX NCBI\_TaxID=161377;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.

RA Zuccarello G.C., West J.A.;  
 RT "Phylogeography of the Bosneria callictera/B. pinna complex  
 (Rhodomeleaceae, Rhodophyta) and divergence rates based on nuclear,  
 RT mitochondrial and plastid DNA markers."  
 RL Phycologia 41:49-60(2002).  
 DR EMBL; AF382909; AAL67239.1; -; Genomic DNA.  
 DR GO; GO:0009507; C:chloroplast; IEA.  
 KM Chloroplast.  
 FT NON\_TER  
 SQ SEQUENCE 14 AA; 1484 MW; 93ED4984B765AF05 CRC64;

Query Match 34.6%; Score 27; DB 2; Length 14;  
 Best Local Similarity 55.6%; Pred. No. 1.1e+03;  
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 5 DHNDYSK 13  
 DB 2 DTADYSRP 10

RESULT 6  
 Q9UNL8\_HUMAN PRELIMINARY; PRT; 11 AA.  
 ID Q9UNL8\_HUMAN PRELIMINARY; PRT; 11 AA.  
 AC Q9UNL8;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)  
 DE APC2 protein (Fragment).  
 GN Name=APC2;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Euteraia; Euarchontoglires; Primates; Catarrhini; Homnidae;  
 OC Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.

RA Carr I.M., Markham A.F., Colleta P.L., Wei L., Ashkan J., Morrison E.,  
 RA Meredith D.M.,  
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF10338; AAD29275.1; -; Genomic DNA.  
 FT NON\_TER  
 FT NON\_TER  
 SQ SEQUENCE 11 AA; 1326 MW; 75881D7B441EAB4 CRC64;

Query Match 33.3%; Score 26; DB 2; Length 11;  
 Best Local Similarity 66.7%; Pred. No. 1.3e+03;  
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 IKRDHN 7  
 DB 2 VLKRDHN 7

RESULT 7  
 Q9UCB5\_HUMAN PRELIMINARY; PRT; 20 AA.  
 ID Q9UCB5\_HUMAN PRELIMINARY; PRT; 20 AA.  
 AC Q9UCB5;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
 DE Ribonuclease HB-1 (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Euteraia; Euarchontoglires; Primates; Catarrhini; Homnidae;  
 OC Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP PROTEIN SEQUENCE.

RA MEDLINE=94107224; PubMed=8280059;  
 RA Yasuda T., Nadano D., Takeshita H., Kishi K.;  
 RT "Two distinct secretory ribonucleases from human cerebrum:  
 RT purification, characterization and relationships to other  
 RT ribonucleases."  
 RL Biochem. J. 296:617-625(1993).  
 DR PIR; S45003; NRH01.  
 DR GO; GO:0004519; F:endonuclease activity; IEA.  
 DR GO; GO:0016787; F:hydrolyase activity; IEA.  
 DR GO; GO:0003676; F:nucleic acid binding; IEA.  
 DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.  
 DR InterPro; IPR001427; RNaseA.  
 DR Pfam; PF00074; RNaseA; 1.  
 SQ SEQUENCE 20 AA; 2352 MW; D85B5BA27234551 CRC64;

Query Match 33.3%; Score 26; DB 2; Length 20;  
 Best Local Similarity 36.4%; Pred. No. 2.5e+03;  
 Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 3 KRDNDYSK 13  
 DB 9 BRHMDSDSP 19

RESULT 8  
 Q9S8H1\_HORVU PRELIMINARY; PRT; 20 AA.  
 ID Q9S8H1\_HORVU PRELIMINARY; PRT; 20 AA.  
 AC Q9S8H1;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)  
 DE BAKER'S ASTHMA allergen BDP (Fragment).  
 OS Hordeum vulgare (Barley).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;  
 OC Triticeae; Hordeum.  
 OX NCBI\_TaxID=4513;  
 RN [1]  
 RP PROTEIN SEQUENCE.  
 RX MEDLINE=95269763; PubMed=7750539; DOI=10.1016/0014-5793(95)00355-D;  
 RA Garcia-Casado G., Armentia A., Sanchez-Monge R., Sanchez L.M.,

RA Lopez-Otin C., Salcedo G.;  
 RT "A major baker's asthma allergen from rye flour is considerably more  
 active than its barley counterpart.";  
 RL FEBS Lett. 364:36-40(1995).

DR PIR; S65605; S65605.  
 SQ SEQUENCE 20 AA; 2307 MW; 28DDC7C002364803 CRC64;

Query Match 33.7%; Score 25.5; DB 2; Length 20;  
 Best Local Similarity 26.3%; Pred. No. 3e+03;  
 Matches 5; Conservative 5; Mismatches 2; Indels 7; Gaps 1;

QY 3 KRHDYSK-----NPM 14  
 Db 1 ERDYGECRGVSKSIPNPL 19

RESULT 9  
 Q4X374 PLACH  
 ID Q4X374 PLACH PRELIMINARY; PRT; 19 AA.

AC Q4X374;  
 DT 13-SEP-2005 (TRENBLREL. 31, Created)  
 DT 13-SEP-2005 (TRENBLREL. 31, Last sequence update)  
 DE Hypothetical protein (Fragment).  
 GN ORFNames=PC404988.00.0;  
 OS Plasmodium chabaudi;  
 CC Eukaryota; Alveolata; Apicomplexa; Haemosporidia; Plasmodium.

NCBI\_TaxID=5825;  
 RN NUCLEOTIDE SEQUENCE.

RA Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,  
 RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,  
 RA James K., Rutherford K., Harris B., Harris D., Churcher C.,  
 RA Quail M.A., Ormond D., Duggett J., Truman H.E., Mendoza J.,  
 RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,  
 RA Jance C.J., Barrett B., Turner C.M.R., Waters A.P., Sinden R.S.;  
 RT "A comprehensive survey of the Plasmodium life cycle by genomic,  
 RT transcriptomic, and proteomic analyses.";  
 RL Science 307:82-86(2005).

CC -!- CAUTION: The sequence shown here is derived from an  
 CC EMBL/Genbank/DBJ whole genome shotgun (WGS) entry which is  
 CC preliminary data.

DR EMBL; CAJ01010317; CAH88659.1; -; Genomic\_DNA.  
 KM Hypothetical protein.1  
 FT NON TER 1

SQ SEQUENCE 19 AA; 2089 MW; F6F5B66FD7348F CRC64;  
 Query Match 32.1%; Score 25; DB 2; Length 19;  
 Best Local Similarity 62.5%; Pred. No. 3.5e+03;  
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 SIKRDAND 8  
 Db 10 SIKRVHNV 17

RESULT 10  
 SPAZ ARTOL  
 ID SPAZ ARTOL STANDARD; PRT; 20 AA.

AC P83290;  
 DT 25-OCT-2004 (Rel. 45, Created)  
 DT 25-OCT-2004 (Rel. 45, Last sequence update)  
 DE Serine protease (EC 3.4.21.-) (Aoz) (Fragment).  
 OS Archaeobolys oligospora (Nematode-trapping fungus).  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Orbiliomycetes;  
 OC Orbiliales; Orbiliaceae; Orbilia.  
 CX NCBI\_TaxID=13349;

RN [1]  
 RP PROTEIN SEQUENCE AND FUNCTION.  
 RC STRAIN=807;  
 RA Zhao M., Zhang K.;  
 RL Submitted (FEB-2002) to Swiss-Prot.

CC -!- FUNCTION: Degrades native collagen. Immobilizes P.redivivus. Seems  
 CC to have a role in the infection of nematode cuticle.

CC -!- SIMILARITY: Belongs to the peptidase S8 family.

CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.

CC Interpro: IPR000209; Pept\_S8\_S53.

DR PROSITE; PS00137; SUBTILASE ASP; PARTIAL.

DR PROSITE; PS00138; SUBTILASE SER; PARTIAL.

KW Collagen degradation, direct protein sequencing, Hydrolase, Protease;

KW Serine protease.

FT NON TER 20  
 SQ SEQUENCE 20 AA; 2281 MW; 1AA7A11CC4EAB73B CRC64;

Query Match 32.1%; Score 25; DB 1; Length 20;  
 Best Local Similarity 80.0%; Pred. No. 3.7e+03;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 HNDYS 10  
 Db 15 HEDYS 19

RESULT 11  
 Q9QUW2 9MURI  
 ID Q9QUW2 9MURI PRELIMINARY; PRT; 20 AA.

AC Q9QUW2;  
 DT 01-MAY-2000 (TRENBLREL. 13, Created)  
 DT 01-MAY-2000 (TRENBLREL. 13, Last sequence update)  
 DT 01-DEC-2001 (TRENBLREL. 19, Last annotation update)  
 DE 22 kDa INTRALYSOSOMAL lipid-transfer protein (Fragment).

OS Rattus sp.

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

CC Mammalia; Eutheria; Barchontoglires; Glires; Rodentia; Sciurognathi;

CC Muridae; Murinae; Rattus.

NCBI\_TaxID=10118;

RN [1]

RP PROTEIN SEQUENCE.

RX MEDLINE=97104296; PubMed=8948454;

RA Kuwana T., Mullock B.M., Luzzio J.P.;

RT "Identification of a lysosomal protein causing lipid transfer, using a  
 RT fluorescence assay designed to monitor membrane fusion between rat  
 RT liver endosomes and lysosomes.";

RL Biochem. J. 308:937-946(1995).

DR HSSP; P17900; 1G13.

SQ SEQUENCE 20 AA; 2211 MW; 3A160591EA5542C5 CRC64;

Query Match 32.1%; Score 25; DB 2; Length 20;  
 Best Local Similarity 44.4%; Pred. No. 3.7e+03;  
 Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 5 DHNDYSNP 13  
 Db 4 DNDDEKDP 12

RESULT 12  
 Q4XB8 PLACH  
 ID Q4XB8 PLACH PRELIMINARY; PRT; 17 AA.

AC Q4XB8;  
 DT 13-SEP-2005 (TRENBLREL. 31, Created)  
 DT 13-SEP-2005 (TRENBLREL. 31, Last sequence update)  
 DE Hypothetical protein (Fragment).

GN ORFNames=PC403652.00.0;

OS Plasmodium chabaudi.

CC Eukaryota; Alveolata; Apicomplexa; Haemosporidia; Plasmodium.  
 CX NCBI\_TaxID=5825;

[1]  
 RN NUCLEOTIDE SEQUENCE.  
 RA Hall N., Karras M., Raine J.D., Carlton J.M., Kool J.T.W.A.,  
 RA Bertalan M., Florens L., Janssen C.S., Pain A., Christophides G.K.,  
 RA James K., Rutherford K., Harris B., Harris D., Churcher C.,  
 RA Quail M.A., Ormond D., Doggett J., Trueman H.B., Mendoza J.,  
 RA Biddlewell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,  
 RA Jane C.J., Barrett B., Turner C.M.R., Waters A.P., Sinden R.S.,  
 RT "A comprehensive survey of the *Plasmodium* life cycle by genomic,  
 RT transcriptomic, and proteomic analyses."  
 RL Science 307:82-86 (2005).  
 CC -1- CAUTION: The sequence shown here is derived from an  
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
 CC preliminary data.  
 DR EMBL, CAAT01007779; CAH85594.1; -? Genomic\_DNA.  
 KM Hypothetical protein.  
 FT NON\_TER  
 SQ SEQUENCE 17 AA; 2058 MW; 90C8A5A88D2E2082 CRC64;  
 Query Match 31.4%; Score 24.5; DB 2; Length 17;  
 Best Local Similarity 50.0%; Pred. No. 3.8e+03;  
 Matches 5; Conservative 3; Mismatches 1; Indels 1; Gaps 1;  
 Oy 1 SIKRDNDND 10  
 Db 5 SVRR-HQRY 13  
 RESULT 13  
 Q7M001\_PSEPU PRELIMINARY; PRT; 19 AA.  
 ID Q7M001\_PSEPU PRELIMINARY; PRT; 19 AA.  
 AC Q7M001\_PSEPU PRELIMINARY; PRT; 19 AA.  
 DT 01-MAR-2004 (TREMBlrel. 26, Created)  
 DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)  
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)  
 DE Dihydrodipicolinate dehydrogenase (EC 1.8.1.4) beta chain B1  
 (Fragment).  
 OS *Pseudomonas putida*.  
 CC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
 CC Pseudomonadaceae; Pseudomonas.  
 OX NCBI\_TaxID=303;  
 RN [1]  
 RP PROTEIN SEQUENCE.  
 RX PubMed=8521848;  
 RA Hester K., Luo J., Burns G., Braewell E.H., Sokatch J.R.,  
 RT "Purification of active E1 alpha 2 of *Pseudomonas putida*  
 RT branched-chain-oxoacid dehydrogenase.";  
 RL Eur. J. Biochem. 233:828-836(1995).  
 DR PIR: S63476; S63476.  
 DR GO: GO:0004148; P.dihydrodipicolyl dehydrogenase activity; IEA.  
 FT NON\_TER  
 FT NON\_TER  
 SQ SEQUENCE 19 AA; 2075 MW; A1989ED78655376C CRC64;  
 Query Match 31.4%; Score 24.5; DB 2; Length 19;  
 Best Local Similarity 66.7%; Pred. No. 4.3e+03;  
 Matches 6; Conservative 1; Mismatches 1; Indels 1; Gaps 1;  
 Oy 5 DHNDYKNP 13  
 Db 3 DHNN-SINP 10  
 RESULT 14  
 Q9S8G9\_PSOTE PRELIMINARY; PRT; 19 AA.  
 ID Q9S8G9\_PSOTE PRELIMINARY; PRT; 19 AA.  
 AC Q9S8G9\_PSOTE PRELIMINARY; PRT; 19 AA.  
 DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)  
 DE Proline-rich protein (Fragment).  
 OS *Psophocarpus tetragonolobus* (Goa bean) (*Asparagus bean*).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eustroids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;  
 OC Psophocarpus.  
 OX NCBI\_TaxID=3891;  
 RN [1]  
 RP PROTEIN SEQUENCE.  
 RX MEDLINE=95277008; PubMed=7757337;  
 RA Baaka M., Hayakawa H.,  
 RT "Specific secretion of proline-rich proteins by salt-adapted winged  
 RT bean cells."  
 RL Plant Cell Physiol. 36:441-446(1995).  
 SQ SEQUENCE 19 AA; 2118 MW; 59ED45C4F0E8779A CRC64;  
 Query Match 30.8%; Score 24; DB 2; Length 19;  
 Best Local Similarity 57.1%; Pred. No. 5.3e+03;  
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 Oy 8 DYSKNPM 14  
 Db 1 DYKRPV 7  
 RESULT 15  
 Q90510\_9HIV1 PRELIMINARY; PRT; 19 AA.  
 ID Q90510\_9HIV1 PRELIMINARY; PRT; 19 AA.  
 AC Q90510\_9HIV1 PRELIMINARY; PRT; 19 AA.  
 DT 01-DEC-2001 (TREMBlrel. 19, Created)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)  
 DE Tat protein (Fragment).  
 OS Human immunodeficiency virus 1.  
 CC Viruses; Retroviruses; Retroviridae; Lentivirus;  
 CC Primate lentivirus group.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=21663216; PubMed=11804559; DOI=10.1089/088922202753394745;  
 RA Taniuchi Y., Takehisa J., Bikardou B., Moudjeka I.,  
 RA N'Doundou-N'Kodia M.-Y., Obengui, M'Pandi M., M'Pele P., Harada Y.,  
 RA Ido E., Hayami M., Ichimura H., Parra H.Joseph.  
 RT "Genetic subtypes of HIV type 1 based on the *gag* sequences in the  
 RT Republic of Congo."  
 RL AIDS Res. Hum. Retroviruses 18:79-83(2002).  
 DR EMBL, AF410444; AAU10242.1; -? Genomic\_DNA.  
 FT NON\_TER  
 FT NON\_TER  
 SQ SEQUENCE 19 AA; 2353 MW; 366929ED4BE69237 CRC64;  
 Query Match 30.8%; Score 24; DB 2; Length 19;  
 Best Local Similarity 50.0%; Pred. No. 5.3e+03;  
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 Oy 4 RDNDY 9  
 Db 11 QDHQDF 16  
 RESULT 16  
 Q9S8H0\_PSOTE PRELIMINARY; PRT; 20 AA.  
 ID Q9S8H0\_PSOTE PRELIMINARY; PRT; 20 AA.  
 AC Q9S8H0\_PSOTE PRELIMINARY; PRT; 20 AA.  
 DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)  
 DE Proline-rich protein (Fragment).  
 OS *Psophocarpus tetragonolobus* (Goa bean) (*Asparagus bean*).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eustroids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;  
 OC Psophocarpus.  
 OX NCBI\_TaxID=3891;  
 RN [1]  
 RP PROTEIN SEQUENCE.

```

RX MEDLINE=95277008; PubMed=7757337;
RA Easaka M., Hayakawa H.;
RT "Specific secretion of proline-rich proteins by salt-adapted winged
RT bean cells."
RL Plant Cell Physiol. 36:441-446(1995).
SQ SEQUENCE 20 AA; 2246 MW; AEE9BD45CAF0F877 CRC64;

Query Match 30.8%; Score 24; DB 2; Length 20;
Best Local Similarity 57.1%; Pred. No. 5.6e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 8 DYKDKPM 14
   |||
Db 1 DYKDKPV 7

RESULT 17
O4YHV1_PLABE PRELIMINARY; PRT; 13 AA.
AC O4YHV1
DT 13-SEP-2005 (TREMBlrel. 31, Created)
DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)
DE Hypoetical protein (Fragment).
GN ORFNames=PB402765.00.0;
OS Plasmodium berghei.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporidia; Plasmodium.
OC NCBI_TaxID=5821;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Hall N., Karras M., Raine J.D., Carlton J.M., Kool J.T.W.A.,
RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
RA Quail M.A., Ormond D., Duggett J., Trueman H.E., Mendoza J.,
RA Blwell S.L., Rastandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
RA Jase C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.;
RT "A comprehensive survey of the Plasmodium life cycle by genomic,
RT transcriptomic, and proteomic analyses."
RL Science 307:82-86(2005).
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/Genbank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAI01004957; CAI02415.1; -; Genomic_DNA.
KW Hypoetical protein.
FT NON_TER 1
FT TER 13
SQ SEQUENCE 13 AA; 1539 MW; 1589FC880F5FA444 CRC64;

Query Match 30.1%; Score 23.5; DB 2; Length 13;
Best Local Similarity 50.0%; Pred. No. 4.3e+03;
Matches 5; Conservative 4; Mismatches 0; Indels 1; Gaps 1;

QY 1 SIKRDNDYS 10
   :|||
Db 2 TLKR-NNDYN 10

RESULT 18
Q83171_9VIRU PRELIMINARY; PRT; 13 AA.
AC Q83171
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Hypoetical protein (Fragment).
OS Cauliflower mosaic virus.
OC Viruses; Retroviruses; Caulimoviridae; Caulimovirus.
OC NCBI_TaxID=10641;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Penwick J., Hubler R., Hohn T.;
RT "A viable mutation in cauliflower mosaic virus, a retroviruslike plant

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RT virus, separates its capsid protein and polymerase genes."
RL J. Virol. 62:1460-1463(1988).
DR EMBL; M19741; AAA66605.1; -; Genomic_DNA.
KW Hypoetical protein.
FT NON_TER 1
FT TER 1
SQ SEQUENCE 13 AA; 1600 MW; 5DD9E7FDC4A5CB13 CRC64;

Query Match 29.5%; Score 23; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 5.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 KNPM 14
   |||
Db 2 KNPM 5

RESULT 19
TX2B_BUNCA STANDARD; PRT; 15 AA.
AC P84470;
DT 10-MAY-2005 (Rel. 47, Created)
DT 10-MAY-2005 (Rel. 47, Last sequence update)
DE Neurotoxin T2 B chain (Fragment).
OS Bungarus candidus (Malayan krait).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosaurs; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Elapidae; Bungarinae; Bungarus.
OC NCBI_TaxID=92438;
RN [1]
RP PROTEIN SEQUENCE, FUNCTION, SUBUNIT, SUBCELLULAR LOCATION, TISSUE
RP SPECIFICITY, AND LETHAL DOSE.
RC TISSUE=Venom;
RX PubMed=14765867; DOI=10.1093/jb/mwq187;
RA Know O., Chanhome L., Omori-Sato T., Ogawa Y., Yanoshita R.,
RA Samejima Y., Kuch U., Mebs D., Stiprila V.;
RT "Isolation, toxicity, and amino terminal sequences of three major
RT neurotoxins in the venom of Malayan krait (Bungarus candidus) from
RT Thailand."
RL J. Biochem. 134:799-804(2003).
CC -1- FUNCTION: Neurotoxin T2 is a presynaptic neurotoxin of the venom
CC that exhibits indirect hemolytic activity against human
CC erythrocytes. The B chain is homologous to venom basic protease
CC inhibitors but has no protease inhibitor activity and is non-
CC toxic.
CC -1- SUBUNIT: Heterodimer; disulfide-linked. The A chains have
CC phospholipase A2 activity and the B chains show homology with the
CC basic protease inhibitors.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the venom gland.
CC -1- TOXIC DOSE: LD50 is 0.22 mg/kg by intravenous injection in mice.
CC -1- SIMILARITY: Contains 1 BPT1/Kunitz inhibitor domain.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR InterPro; IPR002223; Prot inh Kunz-m.
DR PROSITE; PS00280; BPT1_KUNITZ_1; PARTIAL.
DR PROSITE; PSS0279; BPT1_KUNITZ_2; PARTIAL.
KW Direct protein sequencing; Neurotoxin; Presynaptic neurotoxin; Toxin.
FT NON_TER 15
FT TER 15
SQ SEQUENCE 15 AA; 1866 MW; 828AB0FB98A971A0 CRC64;

Query Match 29.5%; Score 23; DB 1; Length 15;
Best Local Similarity 36.4%; Pred. No. 6.1e+03;
Matches 4; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 3 KRDNDSKNP 13
   :|||
Db 1 KRHRDCKRP 11

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RESULT 20
ID Q711V7_9RHIZ PRELIMINARY; PRT; 18 AA.
AC Q711V7;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE NodB protein (Fragment).
GN Name=nodB;
OS Rhizobium sp. STM251.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium.
OC NCBI_TaxID=142631;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=STM251;
RA Moulin L.;
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL, AJ300259; CAC82892.1; -, Genomic_DNA.
FT NON_TER 18
SQ SEQUENCE 18 AA; 2055 MW; 1BB4F819521E2F9F CRC64;

Query Match 29.5%; Score 23; DB 2; Length 18;
Best Local Similarity 30.0%; Pred. No. 7.5e+03;
Matches 3; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 SIKRDNDYS 10
DB 9 AVRNVYGDVS 18

RESULT 21
ID Q9QW82_RAT PRELIMINARY; PRT; 18 AA.
AC Q9QW82;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE PHOSPHOPHORYN-PEPTIDE Fragment 12-45 (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Rattus.
OC NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC MEDLINE=91291127; PubMed=2064607;
RA Sabsey B., Stecler-Stevenson W.G., Lechner J.H., Vels A.;
RT "Domain structure and sequence distribution in dentin phosphophoryn.";
RL Biochem. J. 276:699-707(1991).
FT NON_TER 18
SQ SEQUENCE 18 AA; 1993 MW; 8861C9A93B5A5BA CRC64;

Query Match 29.5%; Score 23; DB 2; Length 18;
Best Local Similarity 66.7%; Pred. No. 7.5e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 DHNDYS 10
DB 3 DDDYS 8

RESULT 22
ID Q90514_9HIV1 PRELIMINARY; PRT; 19 AA.
AC Q90514;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Tat protein (Fragment).

```

```

OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus;
OC Primate lentivirus group.
OC NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21663216; PubMed=11804559; DOI=10.1089/088922202753394745;
RA Taniiguchi Y., Takehisa J., Bikanoud B., Mboudjeka I.,
RA N'Doundou-N'Kodia M.-Y., Obengui, W'Pandi M., W'Pele P., Harada Y.,
RA Ido E., Hayami M., Ichimura H., Parra H. Joseph.;
RT "Genetic subtypes of HIV type 1 based on the vpu/env sequences in the
RT Republic of Congo.";
RL AIDS Res. Hum. Retroviruses 18:79-83(2002).
DR EMBL, AF410443; AAL10238.1; -, Genomic_DNA.
FT NON_TER 19
SQ SEQUENCE 19 AA; 2151 MW; 2A91C2A4D1167636 CRC64;

Query Match 29.5%; Score 23; DB 2; Length 19;
Best Local Similarity 45.5%; Pred. No. 8e+03;
Matches 5; Conservative 2; Mismatches 0; Indels 4; Gaps 1;

QY 4 RDNDYSKNPM 14
DB 11 KDH----KNPV 17

RESULT 23
ID Q4XKU0_PLACH PRELIMINARY; PRT; 20 AA.
AC Q4XKU0;
DT 13-SEP-2005 (TREMBLrel. 31, Created)
DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TREMBLrel. 31, Last annotation update)
DE Hypothetical protein (Fragment).
GN ORFNames=PC400052.00.0;
OS Plasmodium chabaudi.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporidia; Plasmodium.
OC NCBI_TaxID=5825;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Hall N., Karra M., Raine J.D., Carlton J.M., Kool J.T.W.A.,
RA Berriman M., Plorens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
RA Quail M.A., Ormond D., Duggelt J., Trueman H.E., Mendoza J.,
RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
RA Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.;
RT "A comprehensive survey of the Plasmodium life cycle by genomic,
RT transcriptomic, and proteomic analyses.";
RL Science 307:82-86(2005).
CC -1- CAVITON: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL, CAJ01005037; CAH82472.1; -, Genomic_DNA.
KW Hypothetical protein.
FT NON_TER 20
SQ SEQUENCE 20 AA; 2393 MW; 122DCDCB7D1F44AB CRC64;

Query Match 29.5%; Score 23; DB 2; Length 20;
Best Local Similarity 40.0%; Pred. No. 8.4e+03;
Matches 6; Conservative 4; Mismatches 3; Indels 2; Gaps 1;

QY 2 IKRDHN--DYSKNPM 14
DB 5 IKKNMISKYTYNKM 19

RESULT 24
ID Q6V0Z6_MUSSP PRELIMINARY; PRT; 20 AA.
AC Q6V0Z6;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)

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DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)  
 DE Glutathione S-transferase omega 1 (Fragment).  
 GN Name=Gstol;  
 OS Mus spretus (Western wild mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Murinae; Mus.  
 NCBI\_TaxID=10096;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Liver;  
 RA Abail N., Ruiz-Laguna J., Pueyo C.;  
 RA Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AY355156; AA055841.1; -; mRNA.  
 DR GO: GO:0016740; P:transferase activity; IEA.  
 KW Transferase.  
 FT NON\_TER 1  
 FT NON\_TER 20  
 SQ SEQUENCE 20 AA; 2415 MW; E950E936504895E0 CRC64;

Query Match 29.5%; Score 23; DB 2; Length 20;  
 Best Local Similarity 50.0%; Pred. No. 8.4e+03;  
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

CY 9 YSKNPM 14  
 : |||:  
 Db 13 PEKNPL 18

RESULT 25  
 Q7YXH4 CAEEL PRELIMINARY; PRT; 18 AA.  
 ID Q7YXH4 CAEEL PRELIMINARY; PRT; 18 AA.  
 AC Q7YXH4;  
 DT 01-OCT-2003 (TREMBlrel. 25, Created)  
 DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)  
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)  
 DE Neuropeptide-like protein 16, Isoform b.  
 GN Name=nlp-16; ORFNames=T13A10.5;  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditodea;  
 OC Rhabditidae; Peioderinae; Caenorhabditis.  
 NCBI\_TaxID=6239;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 RC STRAIN=Bristol N2;  
 RX MEDLINE=99063613; PubMed=9851916;  
 RG The C. elegans sequencing consortium;  
 RT "Genome sequence of the nematode C. elegans: a platform for  
 investigating biology."  
 RL Science 282:2012-2018(1998).  
 DR EMBL: U56963; AA001524.1; -; Genomic DNA.  
 DR EMBL: T13A10.5; Caenorhabditis elegans.  
 DR WormBase; WBGene0003754; T13A10.5.  
 DR WormPeP; T13A10.5b; CE35009.  
 DR GO: GO:0007218; P:neuropeptide signaling pathway; IEA.  
 KW Complete proteome; Neuropeptide.  
 SQ SEQUENCE 18 AA; 2047 MW; A1176979A6CF773 CRC64;

Query Match 28.8%; Score 22.5; DB 2; Length 18;  
 Best Local Similarity 35.7%; Pred. No. 9.2e+03;  
 Matches 5; Conservative 4; Mismatches 4; Indels 1; Gaps 1;

CY 1 SIKRDH-NDYSKNP 13  
 : |||:  
 Db 3 SPEDHDSHSNSP 16

RESULT 26  
 Q905G4 9HIV1 PRELIMINARY; PRT; 19 AA.  
 ID Q905G4 9HIV1 PRELIMINARY; PRT; 19 AA.  
 AC Q905G4;  
 DT 01-DEC-2001 (TREMBlrel. 19, Created)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)

DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)  
 DE Tat protein (Fragment).  
 OS Human immunodeficiency virus 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus;  
 OC Primate lentivirus group.  
 NCBI\_TaxID=11676;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=21663216; PubMed=11804559; DOI=10.1089/08892202753394745;  
 RA Taniguchi Y., Takehisa J., Bikandou B., Mboudjeka I.,  
 RA N'Doundou-N'Kodia M.-Y., Obengul, M'Pandi M., M'Pele P., Harada Y.,  
 RA Ido E., Hayami M., Ichimura H., Parra H.Joseph.;  
 RT "Genetic subtypes of HIV type 1 based on the vpu/env sequences in the  
 RT Republic of Congo."  
 RL AIDS Res. Hum. Retroviruses 18:79-83(2002).  
 DR EMBL: AF410448; AA110258.1; -; Genomic DNA.  
 FT NON\_TER 1  
 FT NON\_TER 19  
 SQ SEQUENCE 19 AA; 2263 MW; 3E5E64FD66039636 CRC64;

Query Match 28.8%; Score 22.5; DB 2; Length 19;  
 Best Local Similarity 36.4%; Pred. No. 9.8e+03;  
 Matches 4; Conservative 4; Mismatches 2; Indels 1; Gaps 1;

CY 4 RDHNDYSKNPM 14  
 : |||:  
 Db 8 KSHQDH-QNPV 17

RESULT 27  
 Q90RG9 9HIV1 PRELIMINARY; PRT; 19 AA.  
 ID Q90RG9 9HIV1 PRELIMINARY; PRT; 19 AA.  
 AC Q90RG9;  
 DT 01-DEC-2001 (TREMBlrel. 19, Created)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)  
 DE Tat protein (Fragment).  
 GN Name=tat;  
 OS Human immunodeficiency virus 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus;  
 OC Primate lentivirus group.  
 NCBI\_TaxID=11676;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=96C921;  
 RX MEDLINE=21663216; PubMed=11804559; DOI=10.1089/08892202753394745;  
 RA Taniguchi Y., Takehisa J., Bikandou B., Mboudjeka I.,  
 RA N'Doundou-N'Kodia M.-Y., Obengul, M'Pandi M., M'Pele P., Harada Y.,  
 RA Ido E., Hayami M., Ichimura H., Parra H.Joseph.;  
 RT "Genetic subtypes of HIV type 1 based on the vpu/env sequences in the  
 RT Republic of Congo."  
 RL AIDS Res. Hum. Retroviruses 18:79-83(2002).  
 DR EMBL: AF127547; AA84904.1; -; Genomic DNA.  
 DR FT NON\_TER 1  
 DR FT NON\_TER 19  
 SQ SEQUENCE 19 AA; 2281 MW; 367E766D66068236 CRC64;

Query Match 28.8%; Score 22.5; DB 2; Length 19;  
 Best Local Similarity 36.4%; Pred. No. 9.8e+03;  
 Matches 4; Conservative 4; Mismatches 2; Indels 1; Gaps 1;

CY 4 RDHNDYSKNPM 14  
 : |||:  
 Db 8 KSHQDH-QNPV 17

RESULT 28  
 Q90NM9 HUMAN PRELIMINARY; PRT; 14 AA.  
 ID Q90NM9 HUMAN PRELIMINARY; PRT; 14 AA.  
 AC Q90NM9;  
 DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)



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DE RING3 protein (Fragment).
GN Name=RING3;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Keddache M, Zhang F, Greenberg D.A.;
RL Submitted (Apr-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Keddache M.;
RL Submitted (Nov-1998) to the EMBL/GenBank/DBJ databases.
FT EMBL; AF107699; AAD24963.1; -; Genomic_DNA.
FT NON_TER
SQ SEQUENCE 14 AA; 1677 MW; 5CDP036680AE22D3 CRC64;

Query Match 28.2%; Score 22; DB 2; Length 14;
Best Local Similarity 40.0%; Pred. No. 8.5e+03;
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 5 DHNDYKQPM 14
DB 1 DYHKKIKQPM 10

RESULT 29
O9R4Z5_STRSU PRELIMINARY; PRT; 16 AA.
AC O9R4Z5;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE SULIYSIN (Fragment).
OS Streptococcus suis.
OC Streptococcus; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1307;
RN [1]
RP PROTEIN SEQUENCE.
RA Jacoby A.A., Loeffen P.U., van den Berg A.J., Storm P.K.;
RT "Identification, purification, and characterization of a chlo-
  l-activated hemolysin (suliysin) of Streptococcus suis.";
RL Infect. Immun. 62:1742-1748(1994).
SO SEQUENCE 16 AA; 1979 MW; 73C2EDB25AB3850 CRC64;

Query Match 28.2%; Score 22; DB 2; Length 16;
Best Local Similarity 57.1%; Pred. No. 9.9e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 3 KRDNNDY 9
DB 3 KODINQY 9

RESULT 30
OSD322_SOLS0 PRELIMINARY; PRT; 16 AA.
ID OSD322;
AC OSD322;
DT 10-MAY-2005 (TREMBLrel. 30, Created)
DT 10-MAY-2005 (TREMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TREMBLrel. 30, Last annotation update)
DE Amylase 2B1 (Amylase 2B2) (Fragment).
GN Name=amy2B1; Synonym=amy2B2;
OS Soles solea (Common sole).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
OC Soleidae; Soleidae; Soles.

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OX NCBI_TaxID=90069;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Rolland J.-L., Bonhomme F.;
RT "Novel polymorphic exon-primed intron-crossing markers from common
  sole (Solea solea)";
RL Submitted (Sep-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY748905; AAXI4322.1; -; Genomic DNA.
DR EMBL; AY748907; AAXI4324.1; -; Genomic DNA.
DR EMBL; AY748908; AAXI4325.1; -; Genomic DNA.
DR EMBL; AY748909; AAXI4326.1; -; Genomic DNA.
DR EMBL; AY748910; AAXI4327.1; -; Genomic DNA.
DR EMBL; AY748904; AAXI4321.1; -; Genomic DNA.
FT NON_TER
FT NON_TER
SQ SEQUENCE 16 AA; 1947 MW; F3E137AED5E71C16 CRC64;

Query Match 28.2%; Score 22; DB 2; Length 16;
Best Local Similarity 50.0%; Pred. No. 9.9e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 4 RDNDY 9
DB 9 KDQNDW 14

RESULT 31
BMTID_BOOMI STANDARD; PRT; 17 AA.
ID BMTID_BOOMI;
AC P83607;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Kunitz-type serine protease inhibitor Bmti-D (Fragment).
OS Boophilus microplus (Cattle tick).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
OC Parasitiformes; Ixodida; Ixodidae; Ixodidae; Boophilus.
OX NCBI_TaxID=69411;
RN [1]
RP PROTEIN SEQUENCE, AND FUNCTION.
RC TISSUE=Larva;
RX PubMed=15556274; DOI=10.1016/j.biochi.2004.09.010;
RA Sasaki S.D., Azcolini S.S., Hirata I.Y., Andreotti R., Tanaka A.S.;
RT "Boophilus microplus tick larvae, a rich source of kunitz type serine
  protease inhibitors.";
RL Biochimie 86:643-649(2004).
CC -!- FUNCTION: Inhibits bovine trypsin and human plasma kallikrein, but
  not human neutrophil elastase.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
  between the Swiss Institute of Bioinformatics and the EMBL outstation -
  the European Bioinformatics Institute. There are no restrictions on its
  use as long as its content is in no way modified and this statement is not
  removed.
CC -----
DR InterPro; IPR02223; Prot_inh_Kunz-m.
DR PROSITE; PS00280; BPTI_KUNITZ_1; PARTIAL.
DR PROSITE; PS50279; BPTI_KUNITZ_2; PARTIAL.
KM Direct protein sequencing; Protease inhibitor;
KW Serine protease inhibitor.
FT SITE 16
FT SITE 17
FT NON_TER 17
SQ SEQUENCE 17 AA; 1649 MW; 7A151C7189F448BB CRC64;

Query Match 28.2%; Score 22; DB 1; Length 17;
Best Local Similarity 66.7%; Pred. No. 1.1e+04;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 8 DYSNKP 13
DB 3 DFKVP 8

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RESULT 32  
ID O34216\_98PHN PRELIMINARY; PRT; 17 AA.  
AC O34216;  
DT 01-JAN-1998 (TReMBLrel. 05, Created)  
DT 01-JAN-1998 (TReMBLrel. 05, Last sequence update)  
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)  
DE 2-hydroxymuconic semialdehyde dehydrogenase (Fragment).  
GN Name=phn;  
OS Sphingomonas chungbuckensis.  
OC Bacteria; Proteobacteria; Alphaproteobacteria; Sphingomonadales;  
OC Sphingomonadaceae; Sphingomonas.  
OX NCBI\_TaxID=561993;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=DU77;  
RX MEDLINE=97445124; PubMed=9299451; DOI=10.1006/brc.1997.6959;  
RA Kim S., Kwon O.K., Kim Y., Kim C.K., Lee K.S., Kim Y.C.;  
RT "Localization and sequence analysis of the phnH gene encoding 2-  
hydroxy-pent-2,4-dienoate hydratase in Pseudomonas sp. strain DU77.";  
RL Biochem. Biophys. Res. Commun. 238:56-60(1997).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=DU77;  
RA Kim Y.-C.;  
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.  
DR EMBL; U97697; AAB71650.1; -; Genomic\_DNA.  
DR GO; GO:0019866; C:inner membrane; IEA.  
DR GO; GO:0005355; F:glucose transporter activity; IEA.  
DR GO; GO:0006810; P:transport; IEA.  
DR InterPro; IPRO00803; Gluc transporter.  
DR PRINTS; PR00172; GLUCTRNSPORT.  
FT NON\_TER 1  
SQ SEQUENCE 17 AA; 2203 MW; 4B913BE1212214B CRC64;  
Query Match 28.2%; Score 22; DB 2; Length 17;  
Best Local Similarity 40.0%; Pred. No. 1.1e+04;  
Matches 4; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 2 IKRDHNDYK 11  
Db 4 LHRDHQHLRK 13

RESULT 33  
ID O4XK28\_PLACH PRELIMINARY; PRT; 18 AA.  
AC O4XK28;  
DT 13-SEP-2005 (TReMBLrel. 31, Created)  
DT 13-SEP-2005 (TReMBLrel. 31, Last sequence update)  
DT 13-SEP-2005 (TReMBLrel. 31, Last annotation update)  
DE Hypothetical protein (Fragment).  
GN ORFNames=PC400359.00.0;  
OS Plasmodium chabaudi.  
OC Eukaryota; Alveolata; Apicomplexa; Haemosporidia; Plasmodium.  
OX NCBI\_TaxID=5825;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Hall N., Karras M., Raine J.D., Carlton J.M., Kool J.T.W.A.,  
RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,  
RA James K., Rutherford K., Harris B., Harris D., Churcher C.,  
RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,  
RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Katatos F.C.,  
RA Janse C.J., Barrett B., Turner C.M.R., Waters A.P., Sinden R.S.;  
RT "A comprehensive survey of the Plasmodium life cycle by genomic,  
transcriptomic, and proteomic analyses.";  
RL Science 307:82-86(2005).  
CC -!- CAUTION: The sequence shown here is derived from an  
preliminary data.  
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
EMBL; CAJ01005284; CAH82734.1; -; Genomic\_DNA.

KM Hypothetical protein.  
FT NON\_TER 1  
SQ SEQUENCE 18 AA; 2322 MW; DC5241E9253A3411 CRC64;  
Query Match 28.2%; Score 22; DB 2; Length 18;  
Best Local Similarity 44.4%; Pred. No. 1.1e+04;  
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 KRDHNDYK 11  
Db 3 KROYSPFSK 11

RESULT 34  
ID O64134\_9MURI PRELIMINARY; PRT; 18 AA.  
AC O64134;  
DT 01-NOV-1996 (TReMBLrel. 01, Created)  
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)  
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)  
DE Cyclic adenosine 3',5'-monophosphate response element-binding protein  
DB CREB (Fragment).  
GN Name=CREB;  
OS Rattus sp.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10118;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=9210991; PubMed=1723142;  
RA Weber G., Meyer T.E., Lesieur M., Hermann H.L., Gerard N.,  
RA Habener J.F.;  
RT "Developmental stage-specific expression of cyclic adenosine 3',5'-  
monophosphate response element-binding protein CREB during  
spermatogenesis involves alternative exon splicing.";  
RL Mol. Endocrinol. 5:1418-1430(1991).  
DR EMBL; S78641; AAB21253.2; -; Genomic\_DNA.  
FT NON\_TER 1  
SQ SEQUENCE 18 AA; 2058 MW; 00840D65B42ECD6F CRC64;  
Query Match 28.2%; Score 22; DB 2; Length 18;  
Best Local Similarity 37.5%; Pred. No. 1.1e+04;  
Matches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 2 IKRDHNDY 9  
Db 5 VKQDVSDP 12

RESULT 35  
ID O6DU04\_RAT PRELIMINARY; PRT; 18 AA.  
AC O6DU04;  
DT 25-OCT-2004 (TReMBLrel. 28, Created)  
DT 25-OCT-2004 (TReMBLrel. 28, Last sequence update)  
DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)  
DE Glial glutamate transporter GLT1/V4 (Fragment).  
GN Name=SLC1A2;  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=Sprague-Dawley;  
RA Rozyczka J., Engle J.;  
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY643517; AAT66430.1; -; mRNA.  
FT NON\_TER 18  
SQ SEQUENCE 18 AA; 2153 MW; CADCA20790427F3 CRC64;

Query Match 28.2%; Score 22; DB 2; Length 18;  
 Best Local Similarity 45.5%; Pred. No. 1.1e+04;  
 Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 SIKDDHNDYSK 11  
 ||:|:  
 8 SIORSANNMPK 18

# RESULT 36

Q4XGA8\_PLACH  
 ID Q4XGA8\_PLACH PRELIMINARY; PRT; 19 AA.

DT 13-SEP-2005 (TREMBlrel. 31, Created)  
 DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)  
 DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)  
 DE Hypothetical protein (Fragment).  
 GN ORFNames=PC401844.00.0;  
 OS Plasmodium chabaudi.  
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporidia; Plasmodium.  
 NX NCBI\_TaxID=5825;

# NCBI\_TaxID=5825;

RA Hall N., Karras M., Raine J.D., Carlton J.M., Kool J.T.W.A.,  
 RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,  
 RA James K., Rutherford K., Harris B., Harris D., Churcher C.,  
 RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,  
 RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,  
 RA Jase C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.,  
 RA "A comprehensive survey of the Plasmodium life cycle by genomic,  
 RT transcriptomic, and proteomic analyses.";  
 RL Science 307:82-86(2005).

CC -1- CAUTION: The sequence shown here is derived from an  
 CC EMBL/Genbank/DBJ whole genome shotgun (WGS) entry which is  
 CC preliminary data.

DR EMBL; CAJ01006479; CAH84060.1; -; Genomic\_DNA.

KM Hypothetical protein.

FT NON TER 1

SO SEQUENCE 19 AA; 2381 MW; 63D14AB1EC9293B7 CRC64;

Query Match 28.2%; Score 22; DB 2; Length 19;  
 Best Local Similarity 75.0%; Pred. No. 1.2e+04;  
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 HNDY 9  
 ||:|:  
 11 HNNY 14

# RESULT 37

Q7JNH9\_DROME  
 ID Q7JNH9\_DROME PRELIMINARY; PRT; 20 AA.

DT 05-JUL-2004 (TREMBlrel. 27, Created)

DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)

DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)

DE Peptide1glycine-alpha-hydroxylating monooxygenase (Fragment).

GN Name=dPM;

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.

NX NCBI\_TaxID=7227;

RA Elpiper B.A., Tagher P.H.,

RA "Neuropeptide amidation in Drosophila: separate genes encode the two

RT enzymes catalyzing amidation.";

RL J. Neurosci. 17:1363-1376(1997).

DR EMBL; U77431; AAB52571.1; -; Genomic DNA.

GO; GO:0004497; P:monooxygenase activity; IEA.

KW Monooxygenase.  
 FT NON TER 1  
 FT NON TER 20  
 SO SEQUENCE 20 AA; 2257 MW; 9D1796B8C7E2C68A CRC64;

Query Match 28.2%; Score 22; DB 2; Length 20;  
 Best Local Similarity 50.0%; Pred. No. 1.3e+04;  
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 8 DYSDNP 13  
 ||:|:  
 11 DYTEEP 16

# RESULT 38

Q4Y3Y1\_PLACH  
 ID Q4Y3Y1\_PLACH PRELIMINARY; PRT; 20 AA.

DT 13-SEP-2005 (TREMBlrel. 31, Created)

DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)

DE Hypothetical protein (Fragment).

GN ORFNames=PC102140.00.0;

OS Plasmodium chabaudi.

OC Eukaryota; Alveolata; Apicomplexa; Haemosporidia; Plasmodium.

NX NCBI\_TaxID=5825;

RA Hall N., Karras M., Raine J.D., Carlton J.M., Kool J.T.W.A.,

RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,

RA James K., Rutherford K., Harris B., Harris D., Churcher C.,

RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,

RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,

RA Jase C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.,

RA "A comprehensive survey of the Plasmodium life cycle by genomic,

RT transcriptomic, and proteomic analyses.";

RL Science 307:82-86(2005).

CC -1- CAUTION: The sequence shown here is derived from an

CC EMBL/Genbank/DBJ whole genome shotgun (WGS) entry which is

CC preliminary data.

DR EMBL; CAJ01001233; CAH76129.1; -; Genomic\_DNA.

KM Hypothetical protein.

FT NON TER 1

SO SEQUENCE 20 AA; 2391 MW; 22256D25639FBD57 CRC64;

Query Match 28.2%; Score 22; DB 2; Length 20;  
 Best Local Similarity 75.0%; Pred. No. 1.3e+04;  
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 HNDY 9  
 ||:|:  
 2 HNNY 5

RESULT 39  
 Q9PS15\_ONCKI  
 ID Q9PS15\_ONCKI PRELIMINARY; PRT; 20 AA.

DT 01-MAY-2000 (TREMBlrel. 13, Created)

DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)

DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)

DE Creatine kinase (EC 2.7.3.2) (Fragment).

OS Oncorhynchus kisutch (Coho salmon).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;

OC Proteanopterygii; Salmoniformes; Salmonidae; Oncorhynchus.

NX NCBI\_TaxID=8013;

RA Elpiper B.A., Tagher P.H.,

RA "The principal islet of the Coho salmon (Oncorhynchus kisutch) contains

RT the BB isoenzyme of creatine kinase.";

RL J. Protein Chem. 11:489-494(1992).  
 DR PIR; A53875; A53875.  
 DR GO; GO:0004111; F:creatine kinase activity; IRA.  
 SQ SEQUENCE 20 AA; 2425 MW; BFB71D6D2A86E11 CRC64;

Query Match 28.2%; Score 22; DB 2; Length 20;  
 Best Local Similarity 42.9%; Pred. No. 1.3e+04;  
 Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 6 HNDYSKN 12  
 DB 6 HNNFKLN 12

RESULT 40  
 QANSW7 THEPA PRELIMINARY; PRT; 19 AA.

DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
 DE Hypothetical protein.  
 GN ORFNames=IP02\_0175;  
 OS Theileria parva.  
 OC Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Theileridae;  
 OC Theileria.  
 OX NCBI\_TaxID=5875;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=Muguga;  
 RA Gardner M.J., Bishop R., Shah T., de Villiers E.P., Carlton J.M.,  
 Hall N., Ren Q., Paulsen I.T., Pain A., Berriman M., Wilson R.J.M.,  
 Sato S., Ralph S.A., Mann D.J., Xiong Z., Shallom S.J., Weidman J.,  
 Jiang L., Lynn J., Weaver B., Shoatdi A., Wasawo D., Crabtree J.,  
 Wortman J.R., Haas B., Angiuoli S.V., Creasy T.H., Lu C., Suh B.,  
 Silva J.C., Utecherback T.R., Feldblyum T.V., Pereira M., Allen J.,  
 RA Tarcha E.L.N., Salzberg S.L., White O.R., Fitzhugh H.A., Morzaria S.,  
 RA Venter J.C., Fraser C.M., Nene V.;  
 RT "Genome sequence of Theileria parva, a bovine pathogen that transforms  
 lymphocytes.";  
 RL Science 309:134-137(2005).  
 RU [2]  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.

RC STRAIN=Muguga;  
 RA Gardner M., Bishop R., Shah T., de Villiers E., Carlton J.M., Hall N.,  
 Ren Q., Paulsen I.T., Pain A., Berriman M., Wilson R.J.M., Sato S.,  
 Ralph S.A., Mann D.J., Xiong Z., Shallom S.J., Weidman J., Jiang L.,  
 Lynn J., Weaver B., Shoatdi A., Wasawo D., Crabtree J., Wortman J.R.,  
 Haas B., Angiuoli S., Creasy T.H., Lu C., Suh B., Silva J.C.,  
 Utecherback T., Feldblyum T., Pereira M., Allen J., Tarcha E.L.,  
 RA Salzberg S.L., White O., Fitzhugh H.A., Morzaria S., Venter J.C.,  
 RA Fraser C.M., Nene V.;  
 RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.  
 CC -!- CAUTION: The sequence shown here is derived from an  
 EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
 CC preliminary data.  
 DR EMBL; AAGK0100002; EMBL32456.1; -; Genomic\_DNA.  
 KM Hypothetical protein.  
 SQ SEQUENCE 19 AA; 2310 MW; F72C5732A54B8EFC CRC64;

Query Match 27.6%; Score 21.5; DB 2; Length 19;  
 Best Local Similarity 33.3%; Pred. No. 1.5e+04;  
 Matches 5; Conservative 3; Mismatches 4; Indels 3; Gaps 1;

QY 3 KRDH---NDYSKNPM 14  
 DB 5 RRRHYKSTKYSDDPV 19

RESULT 41  
 Q905G8 9HIV1 PRELIMINARY; PRT; 19 AA.  
 ID Q905G8 9HIV1 PRELIMINARY;  
 AC Q905G8;

DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE Tat protein (Fragment).  
 OS Human immunodeficiency virus 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus;  
 OC Primate lentivirus group.  
 OX NCBI\_TaxID=11676;  
 RN [1]

QY 4 RDHNDYSKNPM 14  
 DB 8 QSHQDH-QNPV 17

RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=21663216; PubMed=11804559; DOI=10.1089/0892220275394745;  
 RA Taniguchi Y., Takehisa J., Bikandou B., Mboudjeka I.,  
 RA N'Doundou-N'Kodia M.-Y., Obengui, M'Pandi M., M'Pele P., Harada Y.,  
 RA Ido B., Hayami M., Ichimura H., Parra H.Joseph.;  
 RT "Genetic subtypes of HIV type 1 based on the vpu/env sequences in the  
 RT Republic of Congo.";  
 RL AIDS Res. Hum. Retroviruses 18:79-83(2002).  
 DR EMBL; AF410447; AAL10254.1; -; Genomic\_DNA.  
 FT NON TER 1  
 FT NON TER 1  
 SQ SEQUENCE 19 AA; 2366 MW; 367E64E194069237 CRC64;

Query Match 27.6%; Score 21.5; DB 2; Length 19;  
 Best Local Similarity 36.4%; Pred. No. 1.5e+04;  
 Matches 4; Conservative 4; Mismatches 2; Indels 1; Gaps 1;

QY 4 RDHNDYSKNPM 14  
 DB 8 QSHQDH-QNPV 17

RESULT 42  
 Q905J6 9HIV1 PRELIMINARY; PRT; 19 AA.

DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE Tat protein (Fragment).  
 OS Human immunodeficiency virus 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus;  
 OC Primate lentivirus group.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=21663216; PubMed=11804559; DOI=10.1089/0892220275394745;  
 RA Taniguchi Y., Takehisa J., Bikandou B., Mboudjeka I.,  
 RA N'Doundou-N'Kodia M.-Y., Obengui, M'Pandi M., M'Pele P., Harada Y.,  
 RA Ido B., Hayami M., Ichimura H., Parra H.Joseph.;  
 RT "Genetic subtypes of HIV type 1 based on the vpu/env sequences in the  
 RT Republic of Congo.";  
 RL AIDS Res. Hum. Retroviruses 18:79-83(2002).  
 DR EMBL; AF410440; AAL10226.1; -; Genomic\_DNA.  
 FT NON TER 1  
 FT NON TER 1  
 SQ SEQUENCE 19 AA; 2391 MW; 3B5E7ED9D0038637 CRC64;

Query Match 27.6%; Score 21.5; DB 2; Length 19;  
 Best Local Similarity 40.0%; Pred. No. 1.5e+04;  
 Matches 4; Conservative 4; Mismatches 1; Indels 1; Gaps 1;

QY 5 DHNDYSKNPM 14  
 DB 9 NHQDH-QNPV 17

RESULT 43  
 Q7M0L3 BACCI PRELIMINARY; PRT; 11 AA.  
 ID Q7M0L3 BACCI PRELIMINARY;  
 AC Q7M0L3;  
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE Cyclooligomannosyltransferase (EC 2.4.-.-)  
 (Fragment).  
 OS Bacillus circulans.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 OX NCBI\_TaxID=1397;  
 RN [1]  
 RP PROTEIN SEQUENCE.  
 RX MEDLINE=95201377; PubMed=7765973;  
 RA Kuehle S., Mitoul K., Yamagishi M., Yamada K., Morimoto Y.;  
 RT "Purification and characterization of cyclooligomannosyltransferase  
 fructotransferase (CPTase) from *Bacillus circulans* MCI-2554.";  
 RL Biosci. Biotechnol. Biochem. 59:31-34(1995).  
 DR PIR; PC2330; PC2330.  
 FT NON\_TER 1 1  
 PT NON\_TER 1 1  
 SQ SEQUENCE 11 AA; 1398 MW; D841E119466CB59 CRC64;  
 Query Match 26.9%; Score 21; DB 2; Length 11;  
 Best Local Similarity 50.0%; Pred. No. 9.8e+03;  
 Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 Oy 6 HNDYSKNP 13  
 Db 2 HLPYQNP 9

RESULT 44  
 Q4XW72\_PLACH PRELIMINARY; PRT; 12 AA.  
 AC Q4XW72;  
 DT 13-SEP-2005 (TREMBlrel. 31, Created)  
 DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)  
 DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)  
 DE Hypothetical protein (Fragment).  
 GN ORName=PC105378.00.0;  
 OS Plasmodium chabaudi.  
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporidia; Plasmodium.  
 OX NCBI\_TaxID=5625;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Hall N., Karrae M., Raine J.D., Carlton J.M., Kooij T.W.A.,  
 RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,  
 RA James K., Rutherford K., Harris B., Harris D., Churcher C.,  
 RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,  
 RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,  
 RA Jans C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.;  
 RT "A comprehensive survey of the Plasmodium life cycle by genomic,  
 RT transcriptomic, and proteomic analyses.";  
 RL Science 307:82-86(2005).  
 CC -1- CAUTION: The sequence shown here is derived from an  
 CC EMBL/Genbank/DBJ whole genome shotgun (WGS) entry which is  
 CC preliminary data.  
 DR EMBL; CAJ01002684; CAH78839.1; -; Genomic\_DNA.  
 KM Hypothetical protein.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 12 AA; 1376 MW; 5099241BBB0441E3 CRC64;  
 Query Match 26.9%; Score 21; DB 2; Length 12;  
 Best Local Similarity 57.1%; Pred. No. 1.1e+04;  
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 Oy 1 SIKRDHN 7  
 Db 1 SASRKN 7

RESULT 45  
 Q4YET5\_PLABE PRELIMINARY; PRT; 12 AA.  
 AC Q4YET5;  
 DT 13-SEP-2005 (TREMBlrel. 31, Created)  
 DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)  
 DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)

DE Hypothetical protein (Fragment).  
 GN ORName=PB405057.00.0;  
 OS Plasmodium berghei.  
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporidia; Plasmodium.  
 OX NCBI\_TaxID=5821;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Hall N., Karrae M., Raine J.D., Carlton J.M., Kooij T.W.A.,  
 RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,  
 RA James K., Rutherford K., Harris B., Harris D., Churcher C.,  
 RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,  
 RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,  
 RA Jans C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.;  
 RT "A comprehensive survey of the Plasmodium life cycle by genomic,  
 RT transcriptomic, and proteomic analyses.";  
 RL Science 307:82-86(2005).  
 CC -1- CAUTION: The sequence shown here is derived from an  
 CC EMBL/Genbank/DBJ whole genome shotgun (WGS) entry which is  
 CC preliminary data.  
 DR EMBL; CAJ01005850; CAI03484.1; -; Genomic\_DNA.  
 KM Hypothetical protein.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 12 AA; 1468 MW; 9A7C7B45DB5B0B5A CRC64;  
 Query Match 26.9%; Score 21; DB 2; Length 12;  
 Best Local Similarity 75.0%; Pred. No. 1.1e+04;  
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Oy 6 HNDY 9  
 Db 3 YNDY 6

RESULT 46  
 Q9QCK3\_BDV PRELIMINARY; PRT; 13 AA.  
 AC Q9QCK3;  
 DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-MAY-2001 (TREMBlrel. 16, Last annotation update)  
 DE P40 ORF (Fragment).  
 OS Borna disease virus (BDV).  
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales; Bornaviridae;  
 OC Bornavirus.  
 OX NCBI\_TaxID=12455;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=99445641; PubMed=10515835; DOI=10.1096/315068;  
 RA Cryan M., Hallensleben W., Hofer M., Pollak S., Sauder C., Bilzer T.,  
 RA Blumcke I., Riederer P., Bogerts B., Falkai P., Schwarz M.J.,  
 RA Maillath B., Staeheli P., Hufert F.T., Lieb K.;  
 RT "Borna disease virus in human brains with a rare form of hippocampal  
 RT degeneration but not in brains of patients with common  
 RT neuropsychiatric disorders.";  
 RL J. Infect. Dis. 180:1695-1699(1999).  
 DR EMBL; AJ246865; CAB52108.1; -; Genomic\_RNA.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 13 AA; 1620 MW; 8F80680E4021A40A CRC64;  
 Query Match 26.9%; Score 21; DB 2; Length 13;  
 Best Local Similarity 44.4%; Pred. No. 1.2e+04;  
 Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
 Oy 3 KRHDNYSK 11  
 Db 4 ENDRCDSK 12

RESULT 47  
 Q9QCK6\_BDV PRELIMINARY; PRT; 13 AA.  
 AC Q9QCK6;  
 DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2001 (TREMBlrel. 16, Last annotation update)

DT 01-MAY-2000 (Tremblrel. 13, Created)  
DT 01-MAY-2000 (Tremblrel. 13, last sequence update)  
DT 01-MAR-2001 (Tremblrel. 16, last annotation update)  
DE P40 ORF (Fragment).  
OS Borna disease virus (BDV).  
OC Viruses; ssRNA negative-strand viruses; Mononegavirales; Bornaviridae;  
OC Bornavirus.  
OX NCBI\_TaxID=12455;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=99445641; PubMed=10515835; DOI=10.1086/315068;  
RA Cygan M., Hallensleben W., Hofer M., Pollak S., Sauder C., Bilzer T.,  
RA Blumcke I., Riederer P., Bogerts B., Falkai P., Schwarz M.J.,  
RA Meillich E., Staeheli P., Hufert F.T., Lieb K.;  
RT "Borna disease virus in human brains with a rare form of hippocampal  
degeneration but not in brains of patients with common  
neuropsychiatric disorders.";  
RT J. Infect. Dis. 180:1695-1699(1999).  
DR EMBL; AJ246864; CAB52105.1; -; Genomic\_RNA.  
FT NON\_TER 1  
FT NON\_TER 13  
SQ SEQUENCE 13 AA; 1620 MW; 8F80680B4021A40A CRC64;  
  
Query Match 26.9%; Score 21; DB 2; Length 13;  
Best Local Similarity 44.4%; Pred. No. 1.2e+04;  
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
  
Qy 3 KRPHNDYSK 11  
Db 4 ENDRCDWSK 12

RESULT 48  
Q9QCK9\_BDV PRELIMINARY; PRT; 13 AA.  
ID Q9QCK9\_BDV  
AC Q9QCK9;  
DT 01-MAY-2000 (Tremblrel. 13, Created)  
DT 01-MAY-2000 (Tremblrel. 13, last sequence update)  
DT 01-MAR-2001 (Tremblrel. 16, last annotation update)  
DE P40 ORF (Fragment).  
OS Borna disease virus (BDV).  
OC Viruses; ssRNA negative-strand viruses; Mononegavirales; Bornaviridae;  
OC Bornavirus.  
OX NCBI\_TaxID=12455;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=99445641; PubMed=10515835; DOI=10.1086/315068;  
RA Cygan M., Hallensleben W., Hofer M., Pollak S., Sauder C., Bilzer T.,  
RA Blumcke I., Riederer P., Bogerts B., Falkai P., Schwarz M.J.,  
RA Meillich E., Staeheli P., Hufert F.T., Lieb K.;  
RT "Borna disease virus in human brains with a rare form of hippocampal  
degeneration but not in brains of patients with common  
neuropsychiatric disorders.";  
RT J. Infect. Dis. 180:1695-1699(1999).  
DR EMBL; AJ246863; CAB52102.1; -; Genomic\_RNA.  
FT NON\_TER 1  
FT NON\_TER 13  
SQ SEQUENCE 13 AA; 1620 MW; 8F80680B4021A40A CRC64;  
  
Query Match 26.9%; Score 21; DB 2; Length 13;  
Best Local Similarity 44.4%; Pred. No. 1.2e+04;  
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
  
Qy 3 KRPHNDYSK 11  
Db 4 ENDRCDWSK 12

RESULT 49  
Q9QCL2\_BDV PRELIMINARY; PRT; 13 AA.  
ID Q9QCL2\_BDV  
AC Q9QCL2;  
DT 01-MAY-2000 (Tremblrel. 13, Created)

DT 01-MAY-2000 (Tremblrel. 13, last sequence update)  
DT 01-MAR-2001 (Tremblrel. 16, last annotation update)  
DE P40 ORF (Fragment).  
OS Borna disease virus (BDV).  
OC Viruses; ssRNA negative-strand viruses; Mononegavirales; Bornaviridae;  
OC Bornavirus.  
OX NCBI\_TaxID=12455;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=99445641; PubMed=10515835; DOI=10.1086/315068;  
RA Cygan M., Hallensleben W., Hofer M., Pollak S., Sauder C., Bilzer T.,  
RA Blumcke I., Riederer P., Bogerts B., Falkai P., Schwarz M.J.,  
RA Meillich E., Staeheli P., Hufert F.T., Lieb K.;  
RT "Borna disease virus in human brains with a rare form of hippocampal  
degeneration but not in brains of patients with common  
neuropsychiatric disorders.";  
RT J. Infect. Dis. 180:1695-1699(1999).  
DR EMBL; AJ246862; CAB52099.1; -; Genomic\_RNA.  
FT NON\_TER 1  
FT NON\_TER 13  
SQ SEQUENCE 13 AA; 1620 MW; 8F80680B4021A40A CRC64;  
  
Query Match 26.9%; Score 21; DB 2; Length 13;  
Best Local Similarity 44.4%; Pred. No. 1.2e+04;  
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
  
Qy 3 KRPHNDYSK 11  
Db 4 ENDRCDWSK 12

RESULT 50  
Q9QCL5\_BDV PRELIMINARY; PRT; 13 AA.  
ID Q9QCL5\_BDV  
AC Q9QCL5;  
DT 01-MAY-2000 (Tremblrel. 13, Created)  
DT 01-MAY-2000 (Tremblrel. 13, last sequence update)  
DT 01-MAR-2001 (Tremblrel. 16, last annotation update)  
DE P40 ORF (Fragment).  
OS Borna disease virus (BDV).  
OC Viruses; ssRNA negative-strand viruses; Mononegavirales; Bornaviridae;  
OC Bornavirus.  
OX NCBI\_TaxID=12455;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=99445641; PubMed=10515835; DOI=10.1086/315068;  
RA Cygan M., Hallensleben W., Hofer M., Pollak S., Sauder C., Bilzer T.,  
RA Blumcke I., Riederer P., Bogerts B., Falkai P., Schwarz M.J.,  
RA Meillich E., Staeheli P., Hufert F.T., Lieb K.;  
RT "Borna disease virus in human brains with a rare form of hippocampal  
degeneration but not in brains of patients with common  
neuropsychiatric disorders.";  
RT J. Infect. Dis. 180:1695-1699(1999).  
DR EMBL; AJ246861; CAB52096.1; -; Genomic\_RNA.  
FT NON\_TER 1  
FT NON\_TER 13  
SQ SEQUENCE 13 AA; 1620 MW; 8F80680B4021A40A CRC64;  
  
Query Match 26.9%; Score 21; DB 2; Length 13;  
Best Local Similarity 44.4%; Pred. No. 1.2e+04;  
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
  
Qy 3 KRPHNDYSK 11  
Db 4 ENDRCDWSK 12

RESULT 51  
Q9QCL8\_BDV PRELIMINARY; PRT; 13 AA.  
ID Q9QCL8\_BDV  
AC Q9QCL8;  
DT 01-MAY-2000 (Tremblrel. 13, last sequence update)  
DT 01-MAY-2000 (Tremblrel. 13, last sequence update)

DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)  
 DE P40 ORF (Fragment).  
 OS Borna disease virus (BDV).  
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales; Bornaviridae;  
 OC Bornavirus.  
 CX NCBI\_TaxID=12455;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=99445641; PubMed=10515835; DOI=10.1086/315068;  
 RA Czygan M., Hallensleben W., Hofer M., Pollak S., Sauder C., Bilzer T.,  
 RA Blumcke I., Riederer P., Bogerts B., Falkai P., Schwarz M.J.,  
 RA Maillan E., Staeheli P., Hufert F.T., Lieb K.;  
 RT "Borna disease virus in human brains with a rare form of hippocampal  
 RT degeneration but not in brains of patients with common  
 RT neuropsychiatric disorders."  
 RL J. Infect. Dis. 180:1695-1699(1999).  
 DR EMBL; AJ246860; CAB52093.1; -; Genomic\_RNA.  
 FT NON\_TER 1 13  
 FT NON\_TER 1 13  
 SQ SEQUENCE 13 AA; 1673 MW; 8F80680B534A40A CRC64;  
 Query Match 26.9%; Score 21; DB 2; Length 13;  
 Best Local Similarity 44.4%; Pred. No. 1.2e+04;  
 Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

## RESULT 52

ID 090CM1\_BDV PRELIMINARY; PRT; 13 AA.  
 AC 090CM1;  
 DT 01-MAY-2000 (Tremblrel. 13, Created)  
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)  
 DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)  
 DE P40 ORF (Fragment).  
 OS Borna disease virus (BDV).  
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales; Bornaviridae;  
 OC Bornavirus.  
 CX NCBI\_TaxID=12455;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=99445641; PubMed=10515835; DOI=10.1086/315068;  
 RA Czygan M., Hallensleben W., Hofer M., Pollak S., Sauder C., Bilzer T.,  
 RA Blumcke I., Riederer P., Bogerts B., Falkai P., Schwarz M.J.,  
 RA Maillan E., Staeheli P., Hufert F.T., Lieb K.;  
 RT "Borna disease virus in human brains with a rare form of hippocampal  
 RT degeneration but not in brains of patients with common  
 RT neuropsychiatric disorders."  
 RL J. Infect. Dis. 180:1695-1699(1999).  
 DR EMBL; AJ246859; CAB52090.1; -; Genomic\_RNA.  
 FT NON\_TER 1 13  
 FT NON\_TER 1 13  
 SQ SEQUENCE 13 AA; 1620 MW; 8F80680B4021A40A CRC64;  
 Query Match 26.9%; Score 21; DB 2; Length 13;  
 Best Local Similarity 44.4%; Pred. No. 1.2e+04;  
 Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

## RESULT 53

ID 090CM4\_BDV PRELIMINARY; PRT; 13 AA.  
 AC 090CM4;  
 DT 01-MAY-2000 (Tremblrel. 13, Created)  
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)  
 DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)

DE P40 ORF (Fragment).  
 OS Borna disease virus (BDV).  
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales; Bornaviridae;  
 OC Bornavirus.  
 CX NCBI\_TaxID=12455;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=99445641; PubMed=10515835; DOI=10.1086/315068;  
 RA Czygan M., Hallensleben W., Hofer M., Pollak S., Sauder C., Bilzer T.,  
 RA Blumcke I., Riederer P., Bogerts B., Falkai P., Schwarz M.J.,  
 RA Maillan E., Staeheli P., Hufert F.T., Lieb K.;  
 RT "Borna disease virus in human brains with a rare form of hippocampal  
 RT degeneration but not in brains of patients with common  
 RT neuropsychiatric disorders."  
 RL J. Infect. Dis. 180:1695-1699(1999).  
 DR EMBL; AJ246858; CAB52087.1; -; Genomic\_RNA.  
 FT NON\_TER 1 13  
 FT NON\_TER 1 13  
 SQ SEQUENCE 13 AA; 1620 MW; 8F80680B4021A40A CRC64;  
 Query Match 26.9%; Score 21; DB 2; Length 13;  
 Best Local Similarity 44.4%; Pred. No. 1.2e+04;  
 Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

## RESULT 54

ID 069200\_HUMAN PRELIMINARY; PRT; 14 AA.  
 AC 069200;  
 DT 25-OCT-2004 (Tremblrel. 28, Created)  
 DT 25-OCT-2004 (Tremblrel. 28, Last sequence update)  
 DT 25-OCT-2004 (Tremblrel. 28, Last annotation update)  
 DE Hypothetical protein DKFZP564G2272 (Fragment).  
 GN Name=DKFZP564G2272;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae;  
 OC Homo.  
 CX NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RG TISSUE=Brain;  
 RC The German cDNA Consortium;  
 RA Blum H., Bauersachs S., Mewes H.W., Weill B., Amid C., Oanger A.,  
 RA Fodor G., Han M., Wiemann S.;  
 RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AL080100; CAH10728.1; -; mRNA.  
 KW Hypothetical protein.  
 FT NON\_TER 1 1  
 FT NON\_TER 1 1  
 SQ SEQUENCE 14 AA; 1596 MW; 737A4A679F6E1B CRC64;  
 Query Match 26.9%; Score 21; DB 2; Length 14;  
 Best Local Similarity 40.0%; Pred. No. 1.3e+04;  
 Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

## RESULT 55

ID 09TWX8\_MANSE PRELIMINARY; PRT; 14 AA.  
 AC 09TWX8;  
 DT 01-MAY-2000 (Tremblrel. 13, Created)  
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)  
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)  
 DE Juvenile hormone binding protein, JHBP=5.3 kDa Lys-C peptide  
 (Fragment).

OS Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Sphingoidea;  
 OC Sphingidae; Sphinginae; Manduca.  
 ON NCBI\_TaxID=7130;  
 RX MEDLINE=92134256; PubMed=1734862;  
 RA Tsuchida K., Prestwich G.D.;  
 RT "Binding site mapping of a photoaffinity-labeled juvenile hormone  
 binding protein.";  
 RL Biochem. Biophys. Res. Commun. 182:466-473(1992).  
 FT NON\_TER 1  
 FT NON\_TER 1  
 SQ SEQUENCE 14 AA; 1710 MW; CF018C469B291372 CRC64;  
 Query Match 26.9%; Score 21; DB 2; Length 14;  
 Best Local Similarity 42.9%; Pred. No. 1.3e+04;  
 Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 8 DYSKNPM 14  
 DB 1 DYENHPV 7

RESULT 56  
 ID 054394\_STRLI PRELIMINARY; PRT; 14 AA.  
 AC 054394;  
 DT 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
 DE S-adenosyl-L-homocysteine hydrolase (Fragment).  
 OS Streptomyces lividans  
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 OC Streptomycetaceae; Streptomycetaceae; Streptomyces.  
 ON NCBI\_TaxID=1916;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=TK21;  
 RA Romero N.M., Mellado R.P.;  
 RT "Activation of the actinophodol biosynthetic pathway in Streptomyces  
 lividans.";  
 RL FEMS Microbiol. Lett. 1217:79-84(1995).  
 DR EMBL: X79814; GSA56211.1; -: Genomic DNA.  
 DR GO: GO:0004013; F:adenosylhomocysteinease activity; IEA.  
 DR GO: GO:0016787; F:hydrolase activity; IEA.  
 DR GO: GO:0006730; P:one-carbon compound metabolism; IEA.  
 DR InterPro: IPR000043; Ad\_hcy\_hydrolase.  
 DR Pfam: PF05221; AdhCysase; 1.  
 KM Hydrolase.  
 FT NON\_TER 1  
 FT NON\_TER 1  
 SQ SEQUENCE 14 AA; 1725 MW; 1303D5023C485D2B CRC64;

Query Match 26.9%; Score 21; DB 2; Length 14;  
 Best Local Similarity 57.1%; Pred. No. 1.3e+04;  
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 3 KRDHNDY 9  
 DB 8 KADHYRY 14

RESULT 57  
 ID 09R5R5\_STAUP PRELIMINARY; PRT; 14 AA.  
 AC 09R5R5;  
 DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)  
 DE 25-kDa elastin-binding protein (Fragment).  
 OS Staphylococcus aureus.  
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.

OX NCBI\_TaxID=1280;  
 RN [1]  
 RP PROTEIN SEQUENCE.  
 RX MEDLINE=92078218; PubMed=1744133;  
 RA Park P.W., Roberts D.D., Groso L.E., Parks W.C., Rosenbloom J.,  
 RA Abrams W.R., Mecham R.P.;  
 RT "Binding of elastin to Staphylococcus aureus.";  
 RL J. Biol. Chem. 266:23399-23406(1991).  
 DR PIR: A41589; A41589. 1  
 FT NON\_TER 1  
 FT NON\_TER 1  
 SQ SEQUENCE 14 AA; 1754 MW; 96CA3586B99D1C6A CRC64;  
 Query Match 26.9%; Score 21; DB 2; Length 14;  
 Best Local Similarity 50.0%; Pred. No. 1.3e+04;  
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 7 NDYSKN 12  
 DB 6 DDFEKN 11

RESULT 58  
 ID MK1\_PALPR STANDARD; PRT; 15 AA.  
 AC P80408;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 13-SEP-2005 (Rel. 48, Last annotation update)  
 DE Metanikowin I.  
 OS Palomena prasina (Green shield bug).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Paraneoptera; Hemiptera; Heteroptera;  
 OC Pentatomeroidea; Pentatomorpha; Pentatomidae; Pentatomidae;  
 ON NCBI\_TaxID=55431;  
 RN [1]  
 RP PROTEIN SEQUENCE.  
 RC TISSUE=Hemolymph;  
 RA Chernysh S., Cociancich S., Briand J.-P., Hetru C., Bulet P.;  
 RT "The inducible antibacterial peptides of the hemipteran insect  
 Palomena prasina: identification of a unique family of proline-rich  
 peptides and of a novel insect defensin.";  
 RL J. Insect Physiol. 42:81-89(1996)  
 CC -1- FUNCTION: Antibacterial peptide active against Gram-negative  
 bacteria.  
 CC -1- INDUCTION: By bacterial infection.  
 CC -----  
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC -----  
 CC Antilotic; Antimicrobial; Direct protein sequencing; Immune response;  
 KM Innate immunity.  
 KM Innate immunity.  
 SQ SEQUENCE 15 AA; 1838 MW; 21407B663CE46299 CRC64;

Query Match 26.9%; Score 21; DB 1; Length 15;  
 Best Local Similarity 44.4%; Pred. No. 1.4e+04;  
 Matches 4; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 5 DHNDYSKNP 13  
 DB 2 DKPDYRPRP 10

RESULT 59  
 ID MK2A\_PALPR STANDARD; PRT; 15 AA.  
 AC P80409;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)



DT 13-SEP-2005 (Rel. 48, Last annotation update)  
 DE Metalkowin IIA.  
 OS Palomona prasinia (Green shield bug).  
 CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 CC Neoptera; Paraneoptera; Hemiptera; Euhemiptera; Heteroptera;  
 CC Panheteroptera; Pentatomomorpha; Pentatomidae; Pentatomidae;  
 CC Pentatominae; Palomona.  
 CC NCB1\_TaxID=55431;  
 RN [1]  
 RP PROTEIN SEQUENCE.  
 RC TISSUE=Hemolymph.  
 RA Chermesh S., Cociancich S., Briand J.-P., Hecru C., Bulet P.;  
 RT "The inducible antibacterial peptides of the hemipteran insect  
 RT Palomona prasinia: identification of a unique family of proline-rich  
 RT peptides and of a novel insect defensein."  
 RL J. Insect Physiol. 42:81-89(1996).  
 CC -1- FUNCTION: Antibacterial peptide active against Gram-negative  
 CC bacteria.  
 CC -1- INDUCTION: By bacterial infection.  
 CC -----  
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 CC removed.  
 CC  
 CC Antibiotic; Antimicrobial; Direct protein sequencing; Immune response;  
 CC Innate immunity.  
 KW IMMATE IMMUNITY.  
 KW SEQUENCE 15 AA; 1893 MW; 23835D063B946299 CRC64;  
 SQ  
 Query Match 26.9%; Score 21; DB 1; Length 15;  
 Best Local Similarity 44.4%; Pred. No. 1.4e+04;  
 Matches 4; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
 QY 5 DHNDYSKNP 13  
 DB 2 DKPDYRPRP 10  
 RESULT 60  
 TX12B\_BUNCA STANDARD; PRT; 15 AA.  
 AC P84473;  
 DT 10-MAY-2005 (Rel. 47, Created)  
 DT 10-MAY-2005 (Rel. 47, Last sequence update)  
 DT 10-MAY-2005 (Rel. 47, Last annotation update)  
 DE Neurotoxin T1-2 B chain (Fragment).  
 OS Bungarus candidus (Malayan krait).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Lepidodermata; Squamata; Scleroglossa; Serpentes; Colubroidae;  
 CC Elapidae; Bungarinae; Bungarus.  
 CC NCB1\_TaxID=92438;  
 RN [1]  
 RP PROTEIN SEQUENCE, FUNCTION, SUBUNIT, SUBCELLULAR LOCATION, TISSUE  
 RP SPECIFICITY, AND LETHAL DOSE.  
 RC TISSUE=Venom.  
 RX PubMed=14769867; DOI=10.1093/jb/mwg187;  
 RA Know O., Chahome L., Omori-Sato T., Ogawa Y., Yanoshita R.,  
 RA Samejima Y., Kuch U., Mobs D., Sltprija V.;  
 RT "Isolation, toxicity and amino terminal sequences of three major  
 RT neurotoxins in the venom of Malayan krait (Bungarus candidus) from  
 RT Thailand."  
 RL J. Biochem. 134:799-804(2003).  
 CC -1- FUNCTION: Neurotoxin T1-2 is a presynaptic neurotoxin of the venom  
 CC that exhibits indirect hemolytic activity against human  
 CC erythrocytes. The B chain is homologous to venom basic protease  
 CC inhibitors but has no protease inhibitor activity and is non-  
 CC toxic.  
 CC -1- SUBUNIT: Heterodimer; disulfide-linked. The A chains have  
 CC phospholipase A2 activity and the B chains show homology with the  
 CC basic protease inhibitors.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: Expressed by the venom gland.

CC -1- TOXIC DOSE: LD(50) is 0.22 mg/kg by intravenous injection in mice.  
 CC -1- SIMILARITY: Contains 1 BPPI/Kunitz inhibitor domain.  
 CC -----  
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 CC  
 CC InterPro; IPR002223; Prot\_inh\_Kunz-m.  
 DR PROSITE; PS00280; BPPI\_KUNITZ\_1; PARTIAL.  
 DR PROSITE; PS00279; BPPI\_KUNITZ\_2; PARTIAL.  
 KW Direct protein sequencing; Neurotoxin; Presynaptic neurotoxin; Toxin.  
 FT NON\_TER 15  
 SQ SEQUENCE 15 AA; 1736 MW; 829370B198A971A0 CRC64;  
 Query Match 26.9%; Score 21; DB 1; Length 15;  
 Best Local Similarity 36.4%; Pred. No. 1.4e+04;  
 Matches 4; Conservative 2; Mismatches 5; Indels 0; Gaps 0;  
 QY 3 KRHDYSKNP 13  
 DB 1 RQRHPDCKRP 11  
 RESULT 61  
 UP02\_METAN STANDARD; PRT; 15 AA.  
 AC P83439;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Unknown 70 kDa protein (Fragment).  
 OS Metarhizium anisopliae.  
 CC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 CC Hypocreomycetidae; Hypocreales; Clavicipitaceae;  
 CC Clavicipitaceae; Metarhizium.  
 CC NCB1\_TaxID=5530;  
 RN [1]  
 RP PROTEIN SEQUENCE.  
 RC STRAIN=54A-1b;  
 RX MEDLINE=22343006; PubMed=12455610; DOI=10.1139/w02-074;  
 RA Kamp A.M., Bidochka M.J.;  
 RT "Protein analysis in a pleomorphically deteriorated strain of the  
 RT insect-pathogenic fungus Metarhizium anisopliae."  
 RL Can. J. Microbiol. 48:787-792(2002).  
 CC -1- MISCELLANEOUS: On the 2D-gel the determined MW of this unknown  
 CC protein is: 70 kDa.  
 CC -----  
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 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC  
 CC Direct protein sequencing.  
 KW NON\_TER 15  
 FT NON\_TER 15  
 SQ SEQUENCE 15 AA; 1483 MW; 2BD474FD7C6BB153 CRC64;  
 Query Match 26.9%; Score 21; DB 1; Length 15;  
 Best Local Similarity 57.1%; Pred. No. 1.4e+04;  
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 7 NDYSKNP 13  
 DB 9 NDLSPPG 15  
 RESULT 62  
 G9UC17\_HUMAN PRELIMINARY; PRT; 15 AA.  
 ID G9UC17\_HUMAN PRELIMINARY; PRT; 15 AA.  
 AC G9UC17;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
 DE 38 kDa MYELOPEROXIDASE (Fragment).  
 OS Homo sapiens (human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;  
 OC Homo.  
 NCBI\_TaxID=9606;  
 RN [1]  
 RP PROTEIN SEQUENCE.  
 RX MEDLINE=93094240; PubMed=1334087;  
 RA Taylor K.L., Pohl J., Kinkade J.M.Jr.;  
 RT "Unique autocatalytic cleavage of human myeloperoxidase. Implications for  
 the involvement of active site MET409".  
 RL J. Biol. Chem. 267.25282-25288(1992).  
 DR GO:0004601; P:peroxidase activity; IEA.  
 DR InterPro: IPR02007; AnIm\_peroxidase.  
 DR PROSITE: PS50292; PEROXIDASE\_3; 1.  
 SQ SEQUENCE 15 AA; 1791 MW; 8B76949B5D0E7321 CRC64;

Query Match 26.9%; Score 21; DB 2; Length 15;  
 Best Local Similarity 75.0%; Pred. No. 1.4e+04;  
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 RDHN 7  
 DB 12 REHN 15

RESULT 63  
 ID 07MOG8\_9MURI PRELIMINARY; PRT; 15 AA.  
 AC 07MOG8\_9MURI  
 DT 01-MAR-2004 (TREMBLrel. 26, Created)  
 DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)  
 DE 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
 DE CD3 antigen homolog (Fragment).  
 OS Mus sp.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Murinae; Mus.  
 NCBI\_TaxID=10095;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=94298870; PubMed=8026526;  
 RA Chies J.A., Lembezat M.P., Freitas A.A.;  
 RT "Entry of B lymphocytes into the persistent cell pool in non-immunized  
 mice is not accompanied by somatic mutation of VH genes."  
 RL Eur. J. Immunol. 24:1657-1664(1994).  
 DR PIR: I67525; I67525.  
 FT NON\_TER 1 1  
 FT NON\_TER 15 15  
 SQ SEQUENCE 15 AA; 1823 MW; 1C9A91068FP27916 CRC64;

Query Match 26.9%; Score 21; DB 2; Length 15;  
 Best Local Similarity 75.0%; Pred. No. 1.4e+04;  
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 KRDH 6  
 DB 4 RRDH 7

RESULT 64  
 ID 09PKC5\_TEV PRELIMINARY; PRT; 15 AA.  
 AC 09PKC5\_TEV  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)  
 DE Small nuclear inclusion polypeptide cleavage product.  
 OS Tobacco etch virus (TEV).  
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;

OC Potyvirus.  
 OC NCBI\_TaxID=12227;  
 RN [1]  
 RP PROTEIN SEQUENCE.  
 RX MEDLINE=91306428; PubMed=1853555;  
 RA Dougherty W.G., Parks T.D.;  
 RT "Post-translational processing of the tobacco etch virus 49-kDa small  
 RT nuclear inclusion polypeptide: identification of an internal cleavage  
 RT site and delimitation of VPg and proteinase domains."  
 RL Virology 183:449-456(1991).  
 SQ SEQUENCE 15 AA; 1680 MW; 2273B6E461D0F28C CRC64;

Query Match 26.9%; Score 21; DB 2; Length 15;  
 Best Local Similarity 57.1%; Pred. No. 1.4e+04;  
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 RDHNDYS 10  
 DB 9 RDYNPIS 15

RESULT 65  
 ID MK2B\_PALPR STANDARD; PRT; 16 AA.  
 AC P80410;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 13-SEP-2005 (Rel. 48, Last annotation update)  
 DE Metainikowin IIB.  
 OS Palomena prasina (Green shield bug).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Paraneoptera; Hemiptera; Euhemiptera; Heteroptera;  
 OC Pentheteroptera; Pentatomomorpha; Pentatomidae; Pentatomidae;  
 OC Pentatominae; Palomena.  
 NCBI\_TaxID=55431;  
 RN [1]  
 RP PROTEIN SEQUENCE.  
 RC TISSUE=Hemolymph;  
 RA Cherrysh S., Cociancich S., Briand J.-P., Hetru C., Bulet P.;  
 RT "The inducible antibacterial peptides of the hemipteran insect  
 RT Palomena prasina: identification of a unique family of proline-rich  
 RT peptides and of a novel insect defensin."  
 RL J. Insect Physiol. 42:81-89(1996).  
 CC -1- FUNCTION: Antibacterial peptide active against Gram-negative  
 CC bacteria.  
 CC -1- INDUCTION: By bacterial infection.

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 CC -----  
 CC Antibiotic; Antimicrobial; Direct protein sequencing; Immune response;  
 CC Innate immunity.  
 KW Innate immunity.  
 SQ SEQUENCE 16 AA; 2040 MW; AF21407D063B9462 CRC64;

Query Match 26.9%; Score 21; DB 1; Length 16;  
 Best Local Similarity 44.4%; Pred. No. 1.5e+04;  
 Matches 4; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5 DHNDYSKNP 13  
 DB 2 DKPDYRPRP 10

RESULT 66  
 ID MK3\_PALPR STANDARD; PRT; 16 AA.  
 AC P80411;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 13-SEP-2005 (Rel. 48, Last annotation update)

```

DE Metalkowin III.
OS Palomona prasinus (green shield bug).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pserygota;
OC Neoptera; Paraneoptera; Hemiptera; Euhemiptera; Heteroptera;
OC Pentheteroptera; Pentatomomorpha; Pentatomidae; Pentatomidae;
OC Pentatominae; Palomona.
NCBI_TaxID=55431;
RN [1]
RP PROTEIN SEQUENCE.
RC TISSUE=Hemolymph;
RA Cherysh S., Coccianich S., Briand J.-P., Hetru C., Bulet P.;
RT "The inducible antibacterial peptides of the hemipteran insect
RT Palomona prasinus: identification of a unique family of proline-rich
RT peptides and of a novel insect defensin."
RL J. Insect Physiol. 42:81-89(1996).
CC -1- FUNCTION: Antibacterial peptide active against Gram-negative
CC bacteria.
CC -1- INDUCTION: By bacterial infection.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC KW Antibiotic; Antimicrobial; Direct protein sequencing; Immune response;
KW Innate immunity.
SQ SEQUENCE 16 AA; 2024 MW; A9B3835D063B9462 CRC64;

Query Match 26.9%; Score 21; DB 1; Length 16;
Best Local Similarity 44.4%; Pred. No. 1.5e+04;
Matches 4; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5 DHNDYSKRP 13
DB 2 DKPDYRPRP 10

RESULT 67
Q6LEL3 MOUSE
ID Q6LEL3 MOUSE PRELIMINARY; PRT; 16 AA.
AC Q6LEL3
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE J1 region (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=BALB/c; TISSUE=Myeloma;
RX MEDLINE=8019926; PubMed=6769593; DOI=10.1016/0092-8674(80)90089-6;
RA Early P., Huang H., Davis M., Calame K., Hood L.;
RT "An immunoglobulin heavy chain variable region gene is generated from
RT three segments of DNA: VH, D and JH."
RL Cell 19:981-992(1980).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=BALB/c; TISSUE=Myeloma;
RX MEDLINE=8101213; PubMed=6774258;
RA Sakano H., Maki R., Korsawa Y., Roeder W., Tonggawa S.;
RT "Two types of somatic recombination are necessary for the generation
RT of complete immunoglobulin heavy-chain genes."
RL Nature 286:676-683(1980).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=BALB/c; TISSUE=Myeloma;
RX MEDLINE=80258493; PubMed=6250219;
RA Newell N., Richards J.E., Tucker P.W., Blattner F.R.;

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RT "J genes for heavy chain immunoglobulins of mouse."
RL Science 209:1128-1132(1980).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=BALB/c; TISSUE=Myeloma;
RX MEDLINE=93358330; PubMed=6101208; DOI=10.1016/0092-8674(81)90399-8;
RA Kim S., Davis M., Sim E., Patten P., Hood L.;
RT "Antibody diversity: somatic hypermutation of rearranged VH genes."
RL Cell 27:573-581(1981).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=BALB/c; TISSUE=Myeloma;
RX MEDLINE=81173073; PubMed=6783961;
RA Sakano H., Korsawa Y., Weigert M., Tonggawa S.;
RT "Identification and nucleotide sequence of a diversity DNA segment (D)
RT of immunoglobulin heavy-chain genes."
RL Nature 290:562-565(1981).
DR EMBL; J00440; AAB59646.1; -, Genomic_DNA.
FT NON_TER 1
FT NON_TER 16
SQ SEQUENCE 16 AA; 1914 MW; 30AFA12F20B5D464 CRC64;

Query Match 26.9%; Score 21; DB 2; Length 16;
Best Local Similarity 75.0%; Pred. No. 1.5e+04;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 KRDH 6
DB 8 RRDH 11

RESULT 68
Q9RSR6 STAAU
ID Q9RSR6 STAAU PRELIMINARY; PRT; 18 AA.
AC Q9RSR6
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE 40-kDa elastin-binding protein (Fragment).
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=1280;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=92078218; PubMed=1744133;
RA Park P.W., Roberts D.D., Groso L.E., Parks W.C., Rosenblum J.,
RA Abrams W.R., Mecham R.P.;
RT "Binding of elastin to Staphylococcus aureus."
RL J. Biol. Chem. 266:23399-23406(1991).
DR PIR; B41589; B41589.
FT NON_TER 1
FT NON_TER 18
SQ SEQUENCE 18 AA; 2162 MW; EAA30A4FAFA3586 CRC64;

Query Match 26.9%; Score 21; DB 2; Length 18;
Best Local Similarity 50.0%; Pred. No. 1.7e+04;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 7 NDYSKN 12
DB 6 DDFEKN 11

RESULT 69
O26062 HELPY
ID O26062 HELPY PRELIMINARY; PRT; 18 AA.
AC O26062
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein HP1536.
GN OrderedLocNames=HP1536;
OS Helicobacter pylori (Campylobacter pylori).

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OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;  
OC Helicobacteraceae; Helicobacter.  
OX NCBI\_TaxID=210;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=2695 / ATCC 700392;  
RX MEDLINE=9739467; PubMed=9252185; DOI=10.1038/41483;  
RA Tomb J.-F., White O., Kariavage A.R., Clayton R.A., Sutton G.G.,  
RA Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S.R.,  
RA Dougherty B.A., Nelson K.E., Quackenbush J., Zhou L., Kirkness E.F.,  
RA Peterson S.N., Loftus B.J., Richardson D.L., Dodson R.V., Khalak H.G.,  
RA Glick E.K., McKenney K., Fitzgerald L.M., Lee N., Adams M.D.,  
RA Hickley E.K., Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D.,  
RA Kelley J.M., Cotton M.D., Meldrum J.F., Fujii C., Bowman C.,  
RA Matthey L., Wallin E., Hayes W.S., Borodovsky M., Karp P.D.,  
RA Smith H.O., Fraser C.M., Venter J.C.,  
RT "The complete genome sequence of the gastric pathogen Helicobacter  
RT pylori."  
RL Nature 388:539-547(1997).  
DR EMBL; AEO00651; AAO08578.1; -; Genomic\_DNA.  
DR PIR; H64711; H64711.  
DR TIGR; Hsp536; -;  
KW Complete proteome; Hypothetical protein.  
SQ SEQUENCE 18 AA; 2236 MW; AC0B5A3DPD9CD482 CRC64;

Query Match 26.9%; Score 21; DB 2; Length 18;  
Best Local Similarity 57.1%; Pred. No. 1.7e+04;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 7 NDYSKNP 13  
DB 9 NHPSRNP 15

RESULT 70  
O4X617 PLACH  
ID O4X617 PLACH PRELIMINARY; PRT; 19 AA.  
AC O4X617;  
DT 13-SEP-2005 (TReMBLrel. 31, Created)  
DT 13-SEP-2005 (TReMBLrel. 31, Last sequence update)  
DT 13-SEP-2005 (TReMBLrel. 31, Last annotation update)  
DE Hypothetical protein (Fragment).  
GN ORFNames=Pc405777.00.0;  
OS Plasmodium chabaudi.  
OC Eukaryota; Alveolata; Apicomplexa; Haemosporidia; Plasmodium.  
OX NCBI\_TaxID=5825;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Hall N., Kariava M., Raine J.D., Carlton J.M., Kool J.T.W.A.,  
RA Berthman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,  
RA James K., Rutherford K., Harris B., Harris D., Churcher C.,  
RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,  
RA Bidwell S.L., Rajandream M.A., Carucci D.O., Yates J.R., Kallatos F.C.,  
RA Janse C.J., Barrett B., Turner C.M.R., Waters A.P., Sinden R.S.,  
RT "A comprehensive survey of the Plasmodium life cycle by genomic,  
RT transcriptomic, and proteomic analyses."  
RL Science 307:82-86(2005).  
CC -1- CAUTION: The sequence shown here is derived from an  
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
CC preliminary data.  
DR EMBL; CAJ01009496; CHA87489.1; -; Genomic\_DNA.  
KW Hypothetical protein.  
FT NON\_TER 1  
SQ SEQUENCE 19 AA; 2278 MW; FA6AC117648FE8A9 CRC64;

Query Match 26.9%; Score 21; DB 2; Length 19;  
Best Local Similarity 50.0%; Pred. No. 1.8e+04;  
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 2 IKRDHNDY 9  
DB 11 IKQDMARY 18

RESULT 71  
O9QW83 RAT  
ID O9QW83 RAT PRELIMINARY; PRT; 19 AA.  
AC O9QW83;  
DT 01-MAY-2000 (TReMBLrel. 13, Created)  
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)  
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)  
DE PHOSPHORHORN=PERITIDE fragment 12-44 (Fragment).  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OX Muridae; Murinae; Rattus.  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=91291127; PubMed=2064607;  
RA Sabsey B., Stetler-Stevenson W.G., Lechner J.H., Vets A.,  
RT "Domain structure and sequence distribution in dentin phosphophoryn."  
RL Biochem. J. 276:699-707(1991).  
FT NON\_TER 1  
SQ SEQUENCE 19 AA; 2195 MW; 744603FE729FDE0C CRC64;

Query Match 26.9%; Score 21; DB 2; Length 19;  
Best Local Similarity 33.3%; Pred. No. 1.8e+04;  
Matches 3; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 6 HNDYSKNP 14  
DB 4 HPSYNSNTL 12

RESULT 72  
O905F6 9HIV1  
ID O905F6 9HIV1 PRELIMINARY; PRT; 19 AA.  
AC O905F6;  
DT 01-DEC-2001 (TReMBLrel. 19, Created)  
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)  
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)  
DE Tat protein (Fragment).  
OS Human immunodeficiency virus 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus;  
OC Primate lentivirus group.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=21663216; PubMed=11804559; DOI=10.1089/08922202753394745;  
RA Taniguchi Y., Takehisa J., Bikanou B., Mboudjeka I.,  
RA N'Doundou-N'Kodia M.-Y., Obengul, M'Pandi M., M'Pele P., Harada Y.,  
RA Ido E., Hayami M., Ichimura H., Parra H. Joseph.,  
RT "Genetic subtypes of HIV type 1 based on the vpu/env sequences in the  
RT AIDS Res. Hum. Retroviruses 18:79-83(2002).  
DR EMBL; AF410450; AAL10266.1; -; Genomic\_DNA.  
FT NON\_TER 1  
SQ SEQUENCE 19 AA; 2333 MW; 22A23385A9068236 CRC64;

Query Match 26.9%; Score 21; DB 2; Length 19;  
Best Local Similarity 33.3%; Pred. No. 1.8e+04;  
Matches 4; Conservative 4; Mismatches 0; Indels 4; Gaps 1;

OY 3 KRDHNDYSKNP 14  
DB 10 RDXH-----ONPV 17

RESULT 73  
MEFP\_MYTED  
ID MEFP\_MYTED STANDARD; PRT; 20 AA.  
AC P83148;  
DT 05-JUL-2004 (Rel. 44, Created)

DT 05-JUN-2004 (Rel. 44, Last sequence update)  
 DT 13-SEP-2005 (Rel. 48, Last annotation update)  
 DE Major extracellular fluid protein (BP protein) (Fragment).  
 OS Mytilus edulis (Blue mussel).  
 OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Mytiloidea;  
 OC Mytiloidea; Mytilidae; Mytilinae; Mytilus.  
 ON NCBI\_TaxId=6550;  
 RX [1]  
 RP PROTEIN SEQUENCE, SUBUNIT, GLYCOSYLATION, AND MASS SPECTROMETRY.  
 RC TRISU-EXTRACELLULAR FLUID;  
 RX MEDLINE=1264951; PubMed=11084027; DOI=10.1074/jbc.M006803200;  
 RA Hatan S.J., Laue T.M., Chasteen N.D.;  
 RT "Purification and characterization of a novel calcium-binding protein  
 from the extracellular fluid of the mussel, Mytilus edulis.";  
 RT J. Biol. Chem. 276:4461-4468(2001).  
 CC -1- FUNCTION: Appears to be a building block of the soluble organic  
 CC matrix of the shell. The protein binds calcium.  
 CC -1- SUBUNIT: Homodimer.  
 CC -1- PTM: Glycosylated.  
 CC -1- MASS SPECTROMETRY: MW=28340; METHOD=MALDI; RANGE=1-7; NOTE=Ref.1.  
 CC -----  
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 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC -----  
 DR GO/GO:0005509; P:calcium ion binding; TAS.  
 KW Calcium; Direct protein sequencing; Glycoprotein.  
 FT NON TER 20  
 SQ SEQUENCE 20 AA; 2351 MW; CBB0C9E0D86F7451 CRC64;

Query Match 26.9%; Score 21; DB 1; Length 20;  
 Best Local Similarity 75.0%; Pred. No. 1.9e+04;  
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RESULT 74  
 Q9UC00 HUMAN PRELIMINARY; PRT; 20 AA.  
 ID Q9UC00 HUMAN PRELIMINARY; PRT; 20 AA.  
 AC Q9UC00;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Beta 2 microglobulin pI 5.1 isoform (Fragment).  
 OS Homo sapiens (human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;  
 OC Homo.  
 ON NCBI\_TaxId=9606;  
 RX [1]  
 RP PROTEIN SEQUENCE.  
 RX MEDLINE=9315819; PubMed=1336137;  
 RA Aggeler A., Derancourt J., Jauregui-Adell J., Mion C., Demaille J.G.;  
 RT "Biochemical characterization of serum and urinary beta 2  
 RT microglobulin in end-stage renal disease patients.";  
 RT Nephrol. Dial. Transplant. 7:1106-1110(1992).  
 DR HSRP; P61769; JUNT; 2310 MW; 9D01DE622DE2B283 CRC64;  
 SQ SEQUENCE 20 AA; 2310 MW; 9D01DE622DE2B283 CRC64;

Query Match 26.9%; Score 21; DB 2; Length 20;  
 Best Local Similarity 60.0%; Pred. No. 1.9e+04;  
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 9 YSKNP 13  
 DB 10 YSRHP 14

RESULT 75  
 Q9TPB8 NAEGR PRELIMINARY; PRT; 20 AA.  
 ID Q9TPB8 NAEGR PRELIMINARY; PRT; 20 AA.  
 AC Q9TPB8;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Cysteine protease (Fragment).  
 OS Naegleria gruberi.  
 OC Eukaryota; Heterolobosea; Schizopyrenida; Vahlkampfiidae; Naegleria.  
 ON NCBI\_TaxId=5762;  
 RX [1]  
 RP PROTEIN SEQUENCE.  
 RX MEDLINE=94164273; PubMed=8119377; DOI=10.1006/expr.1994.1023;  
 RA Aldape K., Huizinga H., Bouvier J., McKerrow J.;  
 RT "Naegleria fowleri: characterization of a secreted histolytic cysteine  
 RT protease.";  
 RT Exp. Parasitol. 78:230-241(1994).  
 SQ SEQUENCE 20 AA; 2325 MW; 010FC692737EEB0 CRC64;

Query Match 26.9%; Score 21; DB 2; Length 20;  
 Best Local Similarity 75.0%; Pred. No. 1.9e+04;  
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RESULT 76  
 Q4Y0U7 PLABR PRELIMINARY; PRT; 20 AA.  
 ID Q4Y0U7 PLABR PRELIMINARY; PRT; 20 AA.  
 AC Q4Y0U7;  
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
 DE Hypothetical protein (Fragment).  
 GN ORFNames=FBI07515.00.0;  
 OS Plasmodium berghei.  
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporidia; Plasmodium.  
 ON NCBI\_TaxId=5821;  
 RX [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Hall N., Karrae M., Raine J.D., Carlton J.M., Kooij T.N.A.,  
 RA Berrihan M., Florens L., Janssen C.S., Pain A., Christophides G.K.,  
 RA James K., Rutherford K., Harris B., Harris D., Churche C.,  
 RA Quail M.A., Ormond D., Doggett J., Trueman H.B., Mendoza J.,  
 RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,  
 RA Unse C.J., Bartell B., Turner C.M.R., Waters A.P., Sinden R.S.;  
 RT "A comprehensive survey of the Plasmodium life cycle by genomic,  
 RT transcriptomic, and proteomic analyses.";  
 RT Science 307:82-86(2005).  
 CC -1- CAUTION: The sequence shown here is derived from an  
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
 CC preliminary data.  
 DR EMBL; CA01002901; CAH99610.1; -; Genomic\_DNA.  
 KW Hypothetical protein.  
 FT NON TER 1  
 SQ SEQUENCE 20 AA; 2444 MW; C5D999B1DE5452CD CRC64;

Query Match 26.9%; Score 21; DB 2; Length 20;  
 Best Local Similarity 45.5%; Pred. No. 1.9e+04;  
 Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

RESULT 77  
 Q9R5E1 ABRHY PRELIMINARY; PRT; 20 AA.  
 ID Q9R5E1 ABRHY PRELIMINARY; PRT; 20 AA.  
 AC Q9R5E1;

DT 01-MAY-2000 (Tremblrel. 13, Created)  
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)  
 DT 01-JUN-2000 (Tremblrel. 14, Last annotation update)  
 DE Outer-membrane channel-forming protein IV (Fragment).  
 OS Aeromonas hydrophila.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;  
 OC Aeromonadaceae; Aeromonas.  
 OX NCBI\_TaxID=644;  
 RP [1]  
 RP PROTEIN SEQUENCE.  
 RX MEDLINE=9313115; PubMed=1283000;  
 RA Jeanneau D., Gletu N., Ratus F., Buckley J.T.;  
 RT "Purification of Aeromonas hydrophila major outer-membrane proteins:  
 N-terminal sequence analysis and channel-forming properties.";  
 RL Mol. Microbiol. 6:335-363(1992).  
 SQ SEQUENCE 20 AA; 2458 MW; EEDFCBAEECC66D00 CRC64;

Query Match 26.9%; Score 21; DB 2; Length 20;  
 Best Local Similarity 60.0%; Pred. No. 1.9e+04;  
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 7 NDYSK 11  
 Db 10 NDYKR 14

RESULT 78  
 ID Q9QVC1\_9MURI PRELIMINARY; PRT; 20 AA.  
 AC Q9QVC1;  
 DT 01-MAY-2000 (Tremblrel. 13, Created)  
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)  
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)  
 DE Kallikrein heavy chain N terminus (Fragment).  
 OS Rattus sp.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10118;  
 RN [1]  
 RP PROTEIN SEQUENCE.  
 RX MEDLINE=93329502; PubMed=1320938; DOI=10.1016/0167-4838(92)90162-7;  
 RA Wang C., Tang C.Q., Zhou G.X., Chao L., Chao J.;  
 RT "Biochemical characterization and substrate specificity of rat  
 RT prostatic kallikrein (93): comparison with tissue kallikrein, conin and  
 RT T-kallinogenase."; Acta 1121:309-316(1992).  
 RL Biochim. Biophys. Acta 1121:309-316(1992).  
 FT NON\_TER 1  
 FT NON\_TER 20  
 SQ SEQUENCE 20 AA; 2282 MW; A2402D52573B2D1D CRC64;

Query Match 26.9%; Score 21; DB 2; Length 20;  
 Best Local Similarity 75.0%; Pred. No. 1.9e+04;  
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 5 DHND 8  
 Db 3 DHNN 6

RESULT 79  
 ID Q34694\_HOMAM PRELIMINARY; PRT; 20 AA.  
 AC Q34694;  
 DT 01-NOV-1996 (Tremblrel. 01, Created)  
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)  
 DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)  
 DE Cytochrome oxidase subunit I (Fragment).  
 GN Name=COI;  
 OS Homo sapiens (Homo sapiens).  
 OS Homo sapiens (Homo sapiens).  
 OS Mitochondrion.  
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 OC Decapoda; Decapoda; Pleocyemata; Astacidea;  
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;

OC Nephropidae; Nephropidae; Homarus.  
 OX NCBI\_TaxID=6706;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=95327187; PubMed=7603565; DOI=10.1038/376163a0;  
 RA Moore J.L., Collins T.M., Stanton D., Daehler L.L., Brown W.M.;  
 RT "Deducing the pattern of arthropod phylogeny from mitochondrial DNA  
 RT rearrangements."; Nature 376:163-165 (1995).  
 RL Nature 376:163-165 (1995).  
 DR EMBL: U29717; AAA82245.1; Genomic\_DNA.  
 DR GO: GO:0016020; C:membrane; IEA.  
 DR GO: GO:0005739; C:mitochondrion; IEA.  
 DR GO: GO:0004129; F:cytochrome-c oxidase activity; IEA.  
 DR GO: GO:0006118; P:electron transport; IEA.  
 DR InterPro: IPR000883; COX1.  
 DR PANTHER: PTHR10422; COX1 1.  
 KW Mitochondrion.  
 FT NON\_TER 1  
 SQ SEQUENCE 20 AA; 2379 MW; 1A3FE5395AF32008 CRC64;

Query Match 26.3%; Score 20.5; DB 2; Length 20;  
 Best Local Similarity 50.0%; Pred. No. 2.3e+04;  
 Matches 5; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

Qy 5 DHNDYSKNPM 14  
 Db 8 DHS-YMEIPM 16

RESULT 80  
 ID Q15893\_HUMAN PRELIMINARY; PRT; 8 AA.  
 AC Q15893;  
 DT 01-NOV-1996 (Tremblrel. 01, Created)  
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)  
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)  
 DE Homo sapiens (clone XP587A) (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;  
 OC Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Placenta;  
 RA Lee C.-C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,  
 RA Caskey C.T.H.;  
 RT "Isolation of chromosome-specific genes by reciprocal probing of  
 RT arrayed cDNAs and cosmid libraries."; Hum. Mol. Genet. 0:0-0(1995).  
 RL Hum. Mol. Genet. 0:0-0(1995).  
 FT EMBL: L32073; AAA73883.1; mRNA.  
 FT NON\_TER 1  
 FT NON\_TER 8  
 SQ SEQUENCE 8 AA; 874 MW; DAA1B6D7376456C5 CRC64;

Query Match 25.6%; Score 20; DB 2; Length 8;  
 Best Local Similarity 60.0%; Pred. No. 2.2e+06;  
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 10 SKNPM 14  
 Db 1 SQNPL 5

RESULT 81  
 ID Q9UDZ4\_HUMAN PRELIMINARY; PRT; 8 AA.  
 AC Q9UDZ4;  
 DT 01-MAY-2000 (Tremblrel. 13, Created)  
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)  
 DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)  
 DE RHD protein (Fragment).

```
GN Name=RHD;
OC Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Blood;
RX MEDLINE=93066356; PubMed=1438298;
RA le van Kim C., Mouru I., Cherif-Zahar B., Raynal V., Cherrier C.,
RA Carton J.-P., Colin Y.;
RT "Molecular cloning and primary structure of the human blood group Rhd
RT polypeptide.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:10925-10929 (1992).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Blood;
RX MEDLINE=97260406; PubMed=9106526;
RA Metasni G., Cherif-Zahar B., Mouru I., Carton J.P.;
RT "Characterization of the recombination hot spot involved in the
RT genomic rearrangement leading to the hybrid D-CE-D gene in the DVI
RT phenotype.";
RL Am. J. Hum. Genet. 60:808-817 (1997).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Blood;
RA Flegel W.A.;
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z97031; CAB09727.1; -; Genomic DNA.
DR GO; GO:0016021; C:Integral to membrane; NAS.
FT NON_TER 1 8
SQ SEQUENCE 8 AA; 1042 MW; D296944691FB5AB1 CRC64;

Query Match 25.6%; Score 20; DB 2; Length 8;
Best Local Similarity 57.1%; Pred. No. 2.2e+06;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 8 DYKRP 14
DB 2 DYKRP 8

RESULT 82
Q5RLS1_PIG PRELIMINARY; PRT; 8 AA.
ID Q5RLS1_PIG PRELIMINARY; PRT; 8 AA.
AC Q5RLS1;
DT 01-FEB-2005 (TReMBLrel. 29, Created)
DT 01-FEB-2005 (TReMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TReMBLrel. 29, Last annotation update)
DE S13-domain binding protein 4 (Fragment).
OS Name=S13BP4;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC Sus.
OX NCBI_TaxID=9823;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Ear;
RA Du H.L., Chen J., Zhang Y.S., Cui J.X., He C., Zhang X.Q.;
RT "Improving the comparative map of SSC1q21-q26 containing QTL for
RT reproduction in swine.";
RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY805698; AAV65974.1; -; Genomic DNA.
DR EMBL; AY805699; AAV65975.1; -; Genomic DNA.
DR EMBL; AY805700; AAV65976.1; -; Genomic DNA.
DR EMBL; AY805697; AAV65973.1; -; Genomic DNA.
FT NON_TER 1 1
SQ SEQUENCE 8 AA; 998 MW; F942DB5AAB6DAA6 CRC64;

Query Match 25.6%; Score 20; DB 2; Length 8;
```

```
Best Local Similarity 60.0%; Pred. No. 2.2e+06;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 DHNDY 9
DB 2 DDDY 6

RESULT 83
Q93SR0_STAEP PRELIMINARY; PRT; 8 AA.
ID Q93SR0_STAEP PRELIMINARY; PRT; 8 AA.
AC Q93SR0;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Beta-lactamase repressor Blal (Fragment).
OS Name=blal;
OS Staphylococcus epidermidis.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1282;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21680477; PubMed=11822776; DOI=10.1089/10766290152773374;
RA Sidhu M.S., Heir B., Sorum H., Holck A.;
RT "Genetic linkage between resistance to quaternary ammonium compounds
RT and beta-lactam antibiotics in food-related Staphylococcus spp.";
RL Microb. Drug Resist. 7:363-371 (2001).
DR EMBL; AY028779; AAK8453.1; -; Genomic DNA.
KM Plasmid.
FT NON_TER 1 1
SQ SEQUENCE 8 AA; 930 MW; 4E3325B05AA44720 CRC64;

Query Match 25.6%; Score 20; DB 2; Length 8;
Best Local Similarity 80.0%; Pred. No. 2.2e+06;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 NDYSK 11
DB 3 NDISK 7

RESULT 84
P82136_SPIOL PRELIMINARY; PRT; 10 AA.
ID P82136_SPIOL PRELIMINARY; PRT; 10 AA.
AC P82136;
DT 01-JUN-2000 (TReMBLrel. 14, Created)
DT 01-JUN-2000 (TReMBLrel. 14, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Chloroplast 30S ribosomal protein S18 beta (Fragment).
OS Spinacia oleracea (Spinach).
OS Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC Caryophyllales; Amaranthaceae; Spinacia.
OX NCBI_TaxID=3562;
RN [1]
RP PROTEIN SEQUENCE.
RC STRAIN=cv. Alvaro; TISSUE=Leaf;
RX MEDLINE=20435797; PubMed=10874039; DOI=10.1074/jbc.M004350200;
RA Yamaguchi K., von Knochlauch K., Subramanian A.R.;
RT "The plastid ribosomal proteins. Identification of all the proteins in
RT the 30S subunit of an organelle ribosome (chloroplast)."
RL J. Biol. Chem. 275:28455-28465 (2000).
CC -1- SUBCELLULAR LOCATION: Chloroplast.
CC -1- TISSUE SPECIFICITY: Expressed in all plant tissues.
CC -1- MISCELLANEOUS: S18 alpha and beta forms differ in pI. Beta is the
CC least basic form.
CC -1- MISCELLANEOUS: ON THE 2D-GEL ITS MW IS: 14 kDa.
CC -1- SIMILARITY: BELONGS TO THE S1P FAMILY OF RIBOSOMAL PROTEINS.
DR GO; GO:0009507; C:chloroplast; IEA.
DR GO; GO:0003735; F:structural constituent of ribosome; IEA.
DR InterPro; IPR001648; Ribosomal_S18.
```

DR PROSITE; PS00057; RIBOSOMAL\_S18; PARTIAL.  
 KM Chloroplast; Ribosomal protein.  
 FT NON TER 10 10  
 SQ SEQUENCE 10 AA; 1250 MW; 403B60D7740325B3 CRC64;

Query Match 25.6%; Score 20; DB 2; Length 10;  
 Best Local Similarity 66.7%; Pred. No. 1.3e+04;  
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 DYSKRP 13  
 DB 2 DYSKRP 7

RESULT 85  
 Q9QVK7\_9MURI PRELIMINARY; PRT; 10 AA.  
 ID Q9QVK7;  
 AC Q9QVK7;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE MEPRIN=METALLOENDOPRITIDASE (Fragment).  
 OS Mus sp.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Murinae; Mus.  
 NCBI\_TaxID=10095;  
 RN [1]  
 RP PROTEIN SEQUENCE.  
 RX MEDLINE=91363409; PubMed=1886759; DOI=10.1016/0167-4838(91)90032-U;  
 RA Flannery A.V., Macadam G.C., Beynon R.J.;  
 RT "Immunological characterisation of different meprin species in mice."  
 RL Biochim. Biophys. Acta 1079:119-122(1991).  
 FT NON TER 1 1  
 FT NON TER 10 10  
 SQ SEQUENCE 10 AA; 1138 MW; FC01BF5BA866D1 CRC64;

Query Match 25.6%; Score 20; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+04;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 DHN 7  
 DB 8 DHN 10

RESULT 86  
 P96319\_DESDE PRELIMINARY; PRT; 11 AA.  
 ID P96319;  
 AC P96319;  
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)  
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)  
 DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)  
 DE Coded portion of proteolysis tag (Fragment).  
 OS Desulfovibrio desulfuricans.  
 OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfovibrionales;  
 OC Desulfovibrionaceae; Desulfovibrio.  
 NCBI\_TaxID=876;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=ATCC 27774;  
 RX MEDLINE=97128184; PubMed=8972778;  
 RA Williams K.P., Bartel D.P.;  
 RT "Phylogenetic analysis of tmRNA secondary structure."  
 RL RNA 2:1306-1310(1996).  
 DR EMBL; U68081; AAB48023.1; -; Genomic\_DNA.  
 FT NON TER 1 1  
 FT NON TER 11 AA; 1250 MW; 85776D58CB5A8B5A CRC64;

Query Match 25.6%; Score 20; DB 2; Length 11;  
 Best Local Similarity 75.0%; Pred. No. 1.5e+04;  
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 HNDY 9  
 DB 2 HNDY 5

RESULT 87  
 O6LBJ0\_MOUSE PRELIMINARY; PRT; 11 AA.  
 ID O6LBJ0\_MOUSE;  
 AC O6LBJ0;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Topoisomerase I (Fragment).  
 GN Name=Top1; Synonyms=TOP1;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=Balb/c; TISSUE=Liver;  
 RX MEDLINE=94250690; PubMed=8193161;  
 RA Baumgartner B., Heiland S., Kunze N., Richter A., Krippers R.;  
 RT "Conserved regulatory elements in the type I DNA topoisomerase gene promoters of mouse and man."  
 RL Biochim. Biophys. Acta 1218:123-127(1994).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=Balb/c; TISSUE=Liver;  
 RX MEDLINE=94250690; PubMed=8193161;  
 RA Baumgartner B., Heiland S., Kunze N., Richter A., Krippers R.;  
 RT "Submitted (FE8-1993) to the EMBL/GenBank/DBJ databases."  
 DR EMBL; X70958; CA50294.1; -; Genomic\_DNA.  
 DR MGI; MGI:98788; Top1.  
 DR GO; GO:0006260; P:DNA replication; IMP.  
 KW isomerase.  
 FT NON TER 11 11  
 SQ SEQUENCE 11 AA; 1240 MW; 95183A9D41B721EA CRC64;

Query Match 25.6%; Score 20; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+04;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 HND 8  
 DB 7 HND 9

RESULT 88  
 Q7MOD4\_RAT PRELIMINARY; PRT; 11 AA.  
 ID Q7MOD4\_RAT;  
 AC Q7MOD4;  
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Cytochrome-c oxidase (EC 1.9.3.1) chain VIIa-H, cardiac (Fragment).  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Murinae; Rattus.  
 NCBI\_TaxID=10116;  
 RN [1]  
 RP PROTEIN SEQUENCE.  
 RA Schaeffer H., Noack H., Halangk W., Brandt U., von Jagow G.;  
 RT "Cytochrome-c oxidase in developing rat heart. Enzymic properties and amino-terminal sequences suggest identity of the fetal heart and the adult liver isoform."  
 RL Eur. J. Biochem. 230:235-241(1995).  
 RN [2]  
 RP PROTEIN SEQUENCE.  
 RX PubMed=7601105;  
 RA Schaeffer H., Noack H., Halangk W., Brandt U., von Jagow G.;



RT "Cytochrome-c oxidase in developing rat heart. Enzymic properties and  
 RT and no-terminal sequences suggest identity of the fetal heart and the  
 RL adult liver isoform".  
 DR Bur. J. Biochem. 230:235-241(1995).  
 DR PIR; S65377; S65377.  
 DR GO; GO:0004129; F:cytochrome-c oxidase activity; IEA.  
 FT NON\_TER 1 1  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA, 927 MW, 4F3E57D71EAA873 CRC64;  
 Query Match 25.6%; Score 20; DB 2; Length 11;  
 Best Local Similarity 66.7%; Pred. No. 1.5e+04;  
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 SIKRDH 6  
 DB 2 SAKGDH 7

RESULT 89  
 Q6LDS1\_BPT3 PRELIMINARY; PRT; 13 AA.  
 ID Q6LDS1;  
 AC Q6LDS1;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE RNA polymerase III (Fragment).  
 OS Bacteriophage T3.  
 OC Bacteriophage T3.  
 OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Podoviridae;  
 OC T7-like viruses.  
 CX NCBI\_TaxID=10759;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=86221699; PubMed=3011596; DOI=10.1016/0378-1119(86)90098-3;  
 RA Morita C.E., Klement J.F., McCallister W.T.;  
 RT "Cloning and expression of the bacteriophage T3 RNA polymerase gene";  
 RL Gene 41:193-200(1986).  
 DR EMBL; M22609; AAA63781.1; -; Genomic\_DNA.  
 FT NON\_TER 13 13  
 FT NON\_TER 13 13  
 SQ SEQUENCE 13 AA, 1567 MW, 16F2BDD5EAD021054 CRC64;  
 Query Match 25.6%; Score 20; DB 2; Length 13;  
 Best Local Similarity 50.0%; Pred. No. 1.8e+04;  
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 DHNDYS 10  
 DB 8 EKNDPS 13

RESULT 90  
 Q51605\_9222Z PRELIMINARY; PRT; 13 AA.  
 ID Q51605\_9222Z PRELIMINARY;  
 AC Q51605;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE ColE7 protein (Fragment).  
 GN Name=colE7;  
 OS Plasmid ColE7.  
 OC other sequences; plasmids.  
 CX NCBI\_TaxID=2450;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=92293113; PubMed=1603061;  
 RA Soong B.W., Lu F.M., Chak K.-F.;  
 RT "Characterization of the cea gene of the ColE7 plasmid";  
 RL Mol. Gen. Genet. 233:177-183(1992).  
 DR EMBL; M62409; AAA98055.1; -; Genomic DNA.  
 DR GO; GO:0015643; F:coxin binding; IEA.  
 DR GO; GO:0030153; P:bacteriocin immunity; IEA.  
 DR InterPro; IPR000290; Colicin\_pycocin.

DR Pfam; PF01320; Colicin\_Pycocin; 1.  
 KM Plasmid.  
 FT NON\_TER 13 13  
 FT NON\_TER 13 13  
 SQ SEQUENCE 13 AA, 1501 MW, 9E75F892148CB045 CRC64;  
 Query Match 25.6%; Score 20; DB 2; Length 13;  
 Best Local Similarity 30.0%; Pred. No. 1.8e+04;  
 Matches 3; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 2 IKRDNDYSK 11  
 DB 3 LKNSIDSYTE 12

RESULT 91  
 HY14\_PIG STANDARD; PRT; 14 AA.  
 ID HY14\_PIG  
 AC P01155;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Hypothalamic tetradecapeptide.  
 OS Sus scrofa (pig).  
 OC Bkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suidae;  
 OC Sus.  
 CX NCBI\_TaxID=9823;  
 RN [1]  
 RP PROTEIN SEQUENCE.  
 RA Schleginger D.H., Niall H.D., Linthicum G.L., Dupont A., Schally A.V.;  
 RL Submitted (NOV-1976) to the PIR data bank.

CC -----  
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 CC -----  
 DR PIR; A01419; NYFG14.  
 KM Amidation; Direct protein sequencing.  
 FT MOD RES 14 14  
 FT MOD RES 14 14  
 SQ SEQUENCE 14 AA, 1648 MW, 3DDF87B2419DB47 CRC64;  
 Query Match 25.6%; Score 20; DB 1; Length 14;  
 Best Local Similarity 60.0%; Pred. No. 1.9e+04;  
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 9 YSKNP 13  
 DB 3 YGKSP 7

RESULT 92  
 Q5XVM8\_9MOLU PRELIMINARY; PRT; 14 AA.  
 ID Q5XVM8\_9MOLU PRELIMINARY;  
 AC Q5XVM8;  
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
 DE Ribosomal protein S19 (Fragment).  
 GN Name=rps19;  
 OS Candidatus Barley phytoplasma.  
 OC Bacteria; Firmicutes; Mollicutes; Acholeplasmatales;  
 OC Acholeplasmataceae; Candidatus Phytoplasma;  
 OC Candidatus Phytoplasma asteris.  
 CX NCBI\_TaxID=297014;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=Badel;  
 RA Uptonavienne L., Jomantienne R., Davis R.E.;  
 RT "First report of Barley as host of a phytoplasma belonging to group  
 RL 16Srl. subgroup B ";  
 DR Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.

DR EMBL: AY735448; AAU81712.1; -; Genomic DNA.  
 DR GO: GO:0003735; F:structural constituent of ribosome; IEA.  
 KW Ribosomal protein.  
 FT NON\_TER  
 SQ SEQUENCE 14 AA; 1771 MW; 4CC8BBE94FE747A3 CRC64;

Query Match 25.6%; Score 20; DB 2; Length 14;  
 Best Local Similarity 50.0%; Pred. No. 1.9e+04;  
 Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 RDHNDYSK 11  
 Db 2 RGHKKDK 9

RESULT 93  
 O6KXW1\_9MOLU PRELIMINARY; PRT; 14 AA.

AC O6KXW1;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DE Ribosomal protein S19 (Fragment).  
 GN Name=rpS19;  
 OS Chryseantheum yellows phytoplasma.  
 OC Bacteria; Firmicutes; Mollicutes; Acholeplasmatales;  
 OC Acholeplasmataceae; Candidatus Phytoplasma;  
 OC Candidatus Phytoplasma asteris.  
 NCBI\_TaxID=238674;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=CHRYM;  
 RA Lee I.-M., Gundersen-Rindal D.E., Davis R.E., Bottner K.D.,  
 RA Marcone C., Seemuller E.;  
 RT "Candidatus Phytoplasma asteris", a novel phytoplasma taxon  
 RT associated with aster yellows and related diseases.";  
 RL Int. J. Syst. Evol. Microbiol. 54:1037-1048(2004).  
 DR EMBL: AY264869; AAP91867.1; -; Genomic DNA.  
 DR GO: GO:0003735; F:structural constituent of ribosome; IEA.  
 KW Ribosomal protein.  
 FT NON\_TER  
 SQ SEQUENCE 14 AA; 1789 MW; 4CC8BBE94FE747A3 CRC64;

Query Match 25.6%; Score 20; DB 2; Length 14;  
 Best Local Similarity 50.0%; Pred. No. 1.9e+04;  
 Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 RDHNDYSK 11  
 Db 2 RGHKKDK 9

RESULT 94  
 O6KXW4\_9MOLU PRELIMINARY; PRT; 14 AA.

AC O6KXW4;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DE Ribosomal protein S19 (Fragment).  
 GN Name=rpS19;  
 OS Hydrangea phyllody phytoplasma.  
 OC Bacteria; Firmicutes; Mollicutes; Acholeplasmatales;  
 OC Acholeplasmataceae; Candidatus Phytoplasma;  
 OC Candidatus Phytoplasma asteris.  
 NCBI\_TaxID=238673;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=HYDP;  
 RA Lee I.-M., Gundersen-Rindal D.E., Davis R.E., Bottner K.D.,  
 RA Marcone C., Seemuller E.;  
 RT "Candidatus Phytoplasma asteris", a novel phytoplasma taxon  
 RT associated with aster yellows and related diseases.";

RL Int. J. Syst. Evol. Microbiol. 54:1037-1048(2004).  
 DR EMBL: AY264869; AAP91864.1; -; Genomic DNA.  
 DR GO: GO:0003735; F:structural constituent of ribosome; IEA.  
 KW Ribosomal protein.  
 FT NON\_TER  
 SQ SEQUENCE 14 AA; 1789 MW; 4CC8BBE94FE747A3 CRC64;

Query Match 25.6%; Score 20; DB 2; Length 14;  
 Best Local Similarity 50.0%; Pred. No. 1.9e+04;  
 Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 RDHNDYSK 11  
 Db 2 RGHKKDK 9

RESULT 95  
 O6KXW7\_9MOLU PRELIMINARY; PRT; 14 AA.

AC O6KXW7;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DE Ribosomal protein S19 (Fragment).  
 GN Name=rpS19;  
 OS Plantago virescens phytoplasma.  
 OC Bacteria; Firmicutes; Mollicutes; Acholeplasmatales;  
 OC Acholeplasmataceae; Candidatus Phytoplasma;  
 OC Candidatus Phytoplasma asteris.  
 NCBI\_TaxID=238672;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=PVM;  
 RA Lee I.-M., Gundersen-Rindal D.E., Davis R.E., Bottner K.D.,  
 RA Marcone C., Seemuller E.;  
 RT "Candidatus Phytoplasma asteris", a novel phytoplasma taxon  
 RT associated with aster yellows and related diseases.";  
 RL Int. J. Syst. Evol. Microbiol. 54:1037-1048(2004).  
 DR EMBL: AY264867; AAP91861.1; -; Genomic DNA.  
 DR GO: GO:0003735; F:structural constituent of ribosome; IEA.  
 KW Ribosomal protein.  
 FT NON\_TER  
 SQ SEQUENCE 14 AA; 1789 MW; 4CC8BBE94FE747A3 CRC64;

Query Match 25.6%; Score 20; DB 2; Length 14;  
 Best Local Similarity 50.0%; Pred. No. 1.9e+04;  
 Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 RDHNDYSK 11  
 Db 2 RGHKKDK 9

RESULT 96  
 O6KXW0\_9MOLU PRELIMINARY; PRT; 14 AA.

AC O6KXW0;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DE Ribosomal protein S19 (Fragment).  
 GN Name=rpS19;  
 OS Apricot aster yellows phytoplasma.  
 OC Bacteria; Firmicutes; Mollicutes; Acholeplasmatales;  
 OC Acholeplasmataceae; Candidatus Phytoplasma;  
 OC Candidatus Phytoplasma asteris.  
 NCBI\_TaxID=238671;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=ACLR-AY;  
 RA Lee I.-M., Gundersen-Rindal D.E., Davis R.E., Bottner K.D.,  
 RA Marcone C., Seemuller E.;  
 RT "Candidatus Phytoplasma asteris", a novel phytoplasma taxon  
 RT associated with aster yellows and related diseases.";

RL Int. J. Syst. Evol. Microbiol. 54:1037-1048(2004).  
DR EMBL: AY264866; AAP91858.1; -; Genomic DNA.  
DR GO: 0003735; F: structural constituent of ribosome; IEA.  
KW Ribosomal protein.  
FT NON TER 1  
SQ SEQUENCE 14 AA; 1771 MW; 4CC88B8F8FE747A3 CRC64;  
Query Match 25.6%; Score 20; DB 2; Length 14;  
Best Local Similarity 50.0%; Pred. No. 1.9e+04;  
Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 4 RDHNDYSK 11  
DB 2 RGHNKDK 9  
RESULT 97  
Q6WXX3\_9MOLU PRELIMINARY; PRT; 14 AA.  
ID Q6WXX3\_9MOLU PRELIMINARY;  
AC Q6WXX3;  
DT 05-JUL-2004 (TREMBlrel. 27, Created)  
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)  
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)  
DE Ribosomal protein S19 (Fragment).  
GN Name=rp919;  
OS Leafhopper-borne phytoplasma.  
OC Bacteria; Firmicutes; Mollicutes; Acholeplasmatales;  
OC Acholeplasmataceae; Candidatus Phytoplasma.  
OX NCBI\_Taxid=238670;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=CVB;  
RA Lee I.-M., Gundersen-Rindal D.E., Davis R.E., Bottner K.D.,  
RA Marcone C., Seemuller E.;  
RT "Candidatus Phytoplasma asteris", a novel phytoplasma taxon  
RT associated with aster yellows and related diseases.";  
RL Int. J. Syst. Evol. Microbiol. 54:1037-1048(2004).  
DR EMBL: AY264865; AAP91855.1; -; Genomic DNA.  
DR GO: 0003735; F: structural constituent of ribosome; IEA.  
KW Ribosomal protein.  
FT NON TER 1  
SQ SEQUENCE 14 AA; 1771 MW; 4CC88B8F8FE747A3 CRC64;  
Query Match 25.6%; Score 20; DB 2; Length 14;  
Best Local Similarity 50.0%; Pred. No. 1.9e+04;  
Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 4 RDHNDYSK 11  
DB 2 RGHNKDK 9  
RESULT 98  
Q6WXX6\_9MOLU PRELIMINARY; PRT; 14 AA.  
ID Q6WXX6\_9MOLU PRELIMINARY;  
AC Q6WXX6;  
DT 05-JUL-2004 (TREMBlrel. 27, Created)  
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)  
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)  
DE Ribosomal protein S19 (Fragment).  
GN Name=rp919;  
OS Grey dogwood 'witches'-broom phytoplasma.  
OC Bacteria; Firmicutes; Mollicutes; Acholeplasmatales;  
OC Acholeplasmataceae; Candidatus Phytoplasma.  
OX NCBI\_Taxid=238669;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=GD1;  
RA Lee I.-M., Gundersen-Rindal D.E., Davis R.E., Bottner K.D.,  
RA Marcone C., Seemuller E.;  
RT "Candidatus Phytoplasma asteris", a novel phytoplasma taxon  
RT associated with aster yellows and related diseases.";  
RL Int. J. Syst. Evol. Microbiol. 54:1037-1048(2004).

DR EMBL: AY264864; AAP91852.1; -; Genomic DNA.  
DR GO: 0003735; F: structural constituent of ribosome; IEA.  
KW Ribosomal protein.  
FT NON TER 1  
SQ SEQUENCE 14 AA; 1789 MW; 4CC88B894FE747A3 CRC64;  
Query Match 25.6%; Score 20; DB 2; Length 14;  
Best Local Similarity 50.0%; Pred. No. 1.9e+04;  
Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 4 RDHNDYSK 11  
DB 2 RGHNKDK 9  
RESULT 99  
Q6WXX9\_9MOLU PRELIMINARY; PRT; 14 AA.  
ID Q6WXX9\_9MOLU PRELIMINARY;  
AC Q6WXX9;  
DT 05-JUL-2004 (TREMBlrel. 27, Created)  
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)  
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)  
DE Ribosomal protein S19 (Fragment).  
GN Name=rp919;  
OS Blueberry stunt phytoplasma.  
OC Bacteria; Firmicutes; Mollicutes; Acholeplasmatales;  
OC Acholeplasmataceae; Candidatus Phytoplasma;  
OC Candidatus Phytoplasma asteris.  
OX NCBI\_Taxid=37695;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=BBS3;  
RA Lee I.-M., Gundersen-Rindal D.E., Davis R.E., Bottner K.D.,  
RA Marcone C., Seemuller E.;  
RT "Candidatus Phytoplasma asteris", a novel phytoplasma taxon  
RT associated with aster yellows and related diseases.";  
RL Int. J. Syst. Evol. Microbiol. 54:1037-1048(2004).  
DR EMBL: AY264863; AAP91849.1; -; Genomic DNA.  
DR GO: 0003735; F: structural constituent of ribosome; IEA.  
KW Ribosomal protein.  
FT NON TER 1  
SQ SEQUENCE 14 AA; 1789 MW; 4CC88B894FE747A3 CRC64;  
Query Match 25.6%; Score 20; DB 2; Length 14;  
Best Local Similarity 50.0%; Pred. No. 1.9e+04;  
Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 4 RDHNDYSK 11  
DB 2 RGHNKDK 9  
RESULT 100  
Q6WXX8\_9MOLU PRELIMINARY; PRT; 14 AA.  
ID Q6WXX8\_9MOLU PRELIMINARY;  
AC Q6WXX8;  
DT 05-JUL-2004 (TREMBlrel. 27, Created)  
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)  
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)  
DE Ribosomal protein S19 (Fragment).  
GN Name=rp919;  
OS Clover phyllody phytoplasma.  
OC Bacteria; Firmicutes; Mollicutes; Acholeplasmatales;  
OC Acholeplasmataceae; Candidatus Phytoplasma;  
OC Candidatus Phytoplasma asteris.  
OX NCBI\_Taxid=35777;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=KV6, KVE, and CPH;  
RA Lee I.-M., Gundersen-Rindal D.E., Davis R.E., Bottner K.D.,  
RA Marcone C., Seemuller E.;  
RT "Candidatus Phytoplasma asteris", a novel phytoplasma taxon  
RT associated with aster yellows and related diseases.";

RL Int. J. Syst. Evol. Microbiol. 54:1037-1048 (2004).  
 DR EMBL: AY264860; AAP91840.1; -; Genomic DNA.  
 DR EMBL: AY264861; AAP91843.1; -; Genomic DNA.  
 DR EMBL: AY264862; AAP91846.1; -; Genomic DNA.  
 DR GO: GO:0003735; F:structural constituent of ribosome; IEA.  
 KW Ribosomal protein.  
 FT NON TER 1  
 SQ SEQUENCE 14 AA; 1771 MW; 4CC8B8EF8FE747A3 CRC64;  
 Query Match 25.6%; Score 20; DB 2; Length 14;  
 Best Local Similarity 50.0%; Pred. No. 1.9e+04;  
 Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 QY 4 RDHNDYSK 11  
 DB 2 RGHKKDK 9

Search completed: January 20, 2006, 19:11:01  
 Job time : 49.5769 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 20, 2006, 18:54:14 ; Search time 75.5769 Seconds

(without alignments)  
116.273 Million cell updates/sec

Title: US-09-662-293-2

Perfect score: 114  
Sequence: 1 DYEPGSRGPNPKAPLYKRP 20

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 880474

Minimum DB seq length: 0  
Maximum DB seq length: 20

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 100 summaries

Database :

A\_GeneSeq\_21:\*  
1: geneseqp1980s:\*  
2: geneseqp1980s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*  
9: geneseqp2005s:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	114	100.0	20	3	AA552511 House dms
2	114	100.0	20	5	AAU96315 Der HMW-m
3	39	34.2	14	4	AA000360 Human pro
4	38	33.3	10	5	AAU92321 PHOR1-FSD
5	38	33.3	10	5	AAU92321 PHOR1-FSD
6	38	33.3	10	5	AAU92517 PHOR1-FSD
7	37	32.5	16	9	AAU92613 PHOR1-FSD
8	36	31.6	20	2	AAW71598 Human ade
9	36	31.6	20	3	AAW71598 Peptide f
10	36	31.6	20	3	AAW71598 Peptide d
11	35	30.7	9	9	ADW23014 SARS coro
12	35	30.7	15	9	ADW78056 Human inf
13	35	30.7	15	9	ADW77792 Human can
14	34.5	30.3	18	2	AAW77792 Collagen-
15	34.5	30.3	18	2	AAW77792 Collagen-
16	34.5	30.3	18	2	AAW77792 Collagen-
17	34	29.8	14	4	AAW77792 Collagen-
18	34	29.8	15	8	ADW77792 Collagen-
19	34	29.8	20	7	ADW77792 Collagen-
20	34	29.8	20	7	ADW77792 Collagen-
21	33.5	29.4	15	9	AAW78278 Rat neuro
22	33	28.9	9	5	AAU92598 PHOR1-FSD
23	33	28.9	10	5	AAU92855 PHOR1-FSD
24	33	28.9	14	8	ADW92104 Human odo

25	33	28.9	16	6	ABP55617 Human cyt
26	33	28.9	16	7	ADD24038 Breast ca
27	33	28.9	17	1	AAW80012 Sequence
28	33	28.9	17	1	AAW80012 Sequence
29	33	28.9	18	2	AAW32877 Fibronect
30	33	28.9	18	2	AAW32877 Fibronect
31	33	28.9	19	4	AAW32865 Fibronect
32	33	28.9	19	4	AAW32865 Fibronect
33	33	28.9	19	4	AAW32865 Fibronect
34	33	28.9	19	4	AAW32865 Fibronect
35	33	28.9	19	4	AAW32865 Fibronect
36	33	28.9	19	4	AAW32865 Fibronect
37	33	28.9	19	4	AAW32865 Fibronect
38	33	28.9	19	4	AAW32865 Fibronect
39	33	28.9	19	4	AAW32865 Fibronect
40	33	28.9	19	4	AAW32865 Fibronect
41	33	28.9	19	4	AAW32865 Fibronect
42	33	28.9	19	4	AAW32865 Fibronect
43	33	28.9	19	4	AAW32865 Fibronect
44	33	28.9	19	4	AAW32865 Fibronect
45	33	28.9	19	4	AAW32865 Fibronect
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47	33	28.9	19	4	AAW32865 Fibronect
48	33	28.9	19	4	AAW32865 Fibronect
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92	33	28.9	19	4	AAW32865 Fibronect
93	33	28.9	19	4	AAW32865 Fibronect
94	33	28.9	19	4	AAW32865 Fibronect
95	33	28.9	19	4	AAW32865 Fibronect
96	33	28.9	19	4	AAW32865 Fibronect
97	33	28.9	19	4	AAW32865 Fibronect

98	31	27.2	20	7	ADJ90130	Human pap
99	30.5	26.8	13	6	ABR00752	HCV nonet
100	30	26.3	9	9	ADU70749	Human hep

## ALIGNMENTS

## RESULT 1

AAVS2511

ID AAVS2511 standard; peptide; 20 AA.

XX AAVS2511;

XX 22-FEB-2000 (first entry)

XX House dust mite allergen protein (map) A/B fragment map(1).

XX Mite allergen protein; map; high molecular weight; HMW-map; allergy;

XX house dust mite; IGE; immunoglobulin E; allergen; mapA; mapB;

XX hypersensitivity reaction; therapy; treatment; diagnosis; human; feline;

XX canine; veterinary; antibody; vaccine; immunisation.

XX Dermatophagoides farinae.

XX WO954349-A2.

XX 28-OCT-1999.

XX 16-APR-1999; 99WO-US008524.

XX 17-APR-1998; 98US-00062013.

XX 13-MAY-1998; 98US-0085295P.

XX 02-SEP-1998; 98US-0098909P.

XX (HESK-) HESKA CORP.

XX Mccall CA, Hunter SW, Weber ER,

XX WPI, 2000-052700/04.

XX Novel high molecular weight Dermatophagoides nucleic acid polypeptides

XX used to modify an animal's hypersensitivity to mite allergens.

XX Claim 3; Page 69; 154pp; English.

XX Sequences AAVS2510-Y52522 represent proteolytic fragments of

XX Dermatophagoides farinae high molecular weight mite allergen protein (HMW

XX -map) composition. The HMW-map composition was isolated from a D. farinae

XX homogenate by gel filtration, with each fraction being analysed for the

XX presence of proteins that bound to IGE present in mite-allergic dog

XX antiserum. The HMW-map composition comprises mapA (a 109 kD protein) and

XX mapB (98 kD). Mite allergenic proteins and peptides, and nucleic acids

XX encoding them, may be used in therapeutic compositions to modify an

XX animal's hypersensitivity reaction to mite allergens. Animals that may be

XX treated include mammals and birds, especially felines, canines, equines,

XX humans, other pets, and work or domestic animals. The proteins or

XX fragments may also be used to diagnose allergies via a skin test. The

XX proteins and peptides can also be used to raise antibodies, which have a

XX variety of potential uses. For example, they can be used as vaccines to

XX passively immunise animals against dust mite hypersensitivity, as

XX positive controls in test kits and as tools to recover desired dust mite

XX allergens from a mixture of proteins

XX SQ Sequence 20 AA;

XX Query Match 100.0%; Score 114; DB 3; Length 20;

XX Best Local Similarity 100.0%; Pred. No. 2.1e-10;

XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX QY 1 DVEYPSRLGNPKAPLYKRP 20

XX DB 1 DVEYPSRLGNPKAPLYKRP 20

RESULT 2  
AAU96315  
ID AAU96315 standard; peptide; 20 AA.

XX AAU96315;

XX 15-UTL-2002 (first entry)

XX Der HMW-map polypeptide #2.

XX Der HMW-map; American house dust mite; antiallergic; mite; IGE;

XX mite allergenic protein; immunoglobulin E; hypersensitivity;

XX immunocomplex formation.

XX Dermatophagoides farinae.

XX WO200222807-A2.

XX 21-MAR-2002.

XX 14-SEP-2001; 2001WO-US028730.

XX 14-SEP-2000; 2000US-00622293.

XX (HESK-) HESKA CORP.

XX Mccall CA, Hunter SW, Weber ER,

XX WPI, 2002-351888/38.

XX New mite allergenic protein isolated from Dermatophagoides, designated

XX Der HMW-map protein, useful as a vaccine for treating mite allergy.

XX Claim 12; Page 70; 161pp; English.

XX The invention relates to an isolated mite allergenic protein of

XX Dermatophagoides, designated Der HMW-map protein, and its related nucleic

XX acid. The Der HMW-map protein is useful for eliciting an immune response

XX against Der HMW-map protein. The protein or a reagent comprising a non-

XX proteinaceous epitope is useful for identifying an animal (e.g., dog,

XX cat) susceptible to or having an allergic response to a mite. A

XX therapeutic composition is useful for desensitising a host animal to an

XX allergic response to a mite. The DNA and protein can be used in the

XX detection of anti-Der HMW-map antibodies in animal fluids, and inhibition

XX of immunoglobulin (Ig)E or Der HMW-map protein activity associated with a

XX disease. Antibodies that bind to Der HMW-map are useful for inhibiting

XX binding of proteins to IGE, to prevent immunocomplex formation, thus

XX reducing hypersensitivity responses to mite allergens, and as vaccines

XX against mite allergen hypersensitivity. Sequences AAU96314-AAU96342

XX represent Der HMW-map polypeptides of the invention

XX SQ Sequence 20 AA;

XX Query Match 100.0%; Score 114; DB 5; Length 20;

XX Best Local Similarity 100.0%; Pred. No. 2.1e-10;

XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX QY 1 DVEYPSRLGNPKAPLYKRP 20

XX DB 1 DVEYPSRLGNPKAPLYKRP 20

XX RESULT 3

XX AAM00360

XX ID AAM00360 standard; peptide; 14 AA.

XX AC AAM00360;

XX 01-OCT-2001 (first entry)

XX Human protein fragment SEQ ID NO: 906.

XX Human; single nucleotide polymorphism; SNP; paternity test;  
KW forensic test; aberrant protein expression.  
XX Homo sapiens.  
OS WO200151670-A2.  
PN 19-JUL-2001.  
PD 05-JAN-2001; 2001WO-US000322.  
PP 07-JAN-2000; 2000US-0174962P.  
PR (CURA-) CURAGEN CORP.  
PA Shinkets RA, Leach MD;  
PI WPI; 2001-451871/48.  
DR N-FSD6; AAH89475.  
DR Isolated human polynucleotides containing single nucleotide  
PT polymorphisms, useful for the treatment and diagnosis of e.g. cancer,  
PI infection and diabetes.  
XX Disclousure; Page 364; 475pp; English.  
XX The present invention relates to human nucleic acids containing single  
CC nucleotide polymorphisms (SNPs). These can be used in forensic and  
CC paternity tests, and to aid in the treatment of diseases associated with  
CC aberrant protein expression, including cancer, amyloidosis, diabetes,  
CC Alzheimer's disease, Down's syndrome, oedema, lupus (SLE), vasculitis,  
CC glomerulonephritis, haemolytic anaemia, thrombocytopenia, arthritis,  
CC meningitis, muscular disorders, dementia, neurological diseases, tubercous  
CC sclerosis, male infertility, hypercalcaemia, blood pressure disorders,  
CC osteoporosis, pathogenic infections, hypercholesterolaemia, obesity or  
CC autoimmunity. The present sequence is a peptide encoded by a  
CC polymorphism-containing oligonucleotide fragment of the invention  
CC  
SQ Sequence 14 AA;  
Query Match 34.2%; Score 39; DB 4; Length 14;  
Best Local Similarity 63.6%; Pred. No. 65;  
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 1 DYBYPGSRIGN 11  
Db 4 DYRYPPRLAN 14  
RESULT 4  
AAU92321  
ID AAU92321 standard; peptide; 10 AA.  
AC AAU92321;  
DT 02-JUL-2002 (first entry)  
XX PHOR1-FSD6 peptide #59 tested for HLA binding.  
DE Human; PHOR1-A11; PHOR1-FSD6; prostate cancer; cytostatic.  
KW Homo sapiens.  
OS WO200214501-A2.  
PN 21-FEB-2002.  
PD 17-AUG-2001; 2001WO-US025862.  
PP 17-AUG-2000; 2000US-0226241P.  
PR (AGEN-) AGENSYS INC.  
PA

XX Hubert RS, Raitano AB, Paris M, Challita-Bid PM, Ge W;  
PI Jakobovits A;  
XX WPI; 2002-269193/31.  
DR Monitoring PHOR1-A11/PHOR1-FSD6 gene products for monitoring presence of  
PT cancer in subject, by determining status of PHOR1-A11/PHOR1-FSD6 gene  
PT products in tissue sample from subject and comparing it to normal sample.  
XX Claim 49; Page 177; 250pp; English.  
XX The present invention relates to the isolation of novel human genes  
CC designated PHOR1-A11 and PHOR1-FSD6 and their encoded proteins. The gene  
CC encoding PHOR1-A11 maps to chromosome 1q23, and the gene encoding PHOR1-  
CC FSD6 maps to chromosome 7q33-q35. The PHOR1-A11 and PHOR1-FSD6  
CC polynucleotide and polypeptide sequences are useful in diagnostic and  
CC therapeutic methods, and compositions for various cancers such as  
CC prostate cancer. The sequences are useful for inhibiting the growth of  
CC cancer cells that express PHOR1-A11 or PHOR1-FSD6 and for treating  
CC cancer. The PHOR1-A11 or PHOR1-FSD6 polypeptide or a fragment thereof can  
CC be used to elicit an immune response. AAU91563-AAU92962 represent PHOR1-  
CC A11 or PHOR1-FSD6 peptides tested for HLA binding  
XX  
SQ Sequence 10 AA;  
Query Match 33.3%; Score 38; DB 5; Length 10;  
Best Local Similarity 70.0%; Pred. No. 64;  
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 4 YPGSRIGNPK 13  
Db 1 YVGRYGNPK 10  
RESULT 5  
AAU92517  
ID AAU92517 standard; peptide; 10 AA.  
AC AAU92517;  
DT 02-JUL-2002 (first entry)  
XX PHOR1-FSD6 peptide #255 tested for HLA binding.  
DE Human; PHOR1-A11; PHOR1-FSD6; prostate cancer; cytostatic.  
KW Homo sapiens.  
OS WO200214501-A2.  
PN 21-FEB-2002.  
PD 17-AUG-2001; 2001WO-US025862.  
PP 17-AUG-2000; 2000US-0226241P.  
PR (AGEN-) AGENSYS INC.  
PA Hubert RS, Raitano AB, Paris M, Challita-Bid PM, Ge W;  
PI Jakobovits A;  
XX WPI; 2002-269193/31.  
DR Monitoring PHOR1-A11/PHOR1-FSD6 gene products for monitoring presence of  
PT cancer in subject, by determining status of PHOR1-A11/PHOR1-FSD6 gene  
PT products in tissue sample from subject and comparing it to normal sample.  
XX Claim 49; Page 185; 250pp; English.  
XX The present invention relates to the isolation of novel human genes  
CC designated PHOR1-A11 and PHOR1-FSD6 and their encoded proteins. The gene  
CC encoding PHOR1-A11 maps to chromosome 1q23, and the gene encoding PHOR1-

CC F5D6 maps to chromosome 7q33-q35. The PHOR1-A11 and PHOR1-F5D6  
CC polynucleotide and polypeptide sequences are useful in diagnostic and  
CC therapeutic methods, and compositions for various cancers such as  
CC prostate cancer. The sequences are useful for inhibiting the growth of  
CC cancer cells that express PHOR1-A11 or PHOR1-F5D6 and for treating  
CC cancer. The PHOR1-A11 or PHOR1-F5D6 polypeptide or a fragment thereof can  
CC be used to elicit an immune response. AAU91563-AAU92962 represent PHOR1-  
CC A11 or PHOR1-F5D6 peptides tested for HLA binding  
XX  
SQ Sequence 10 AA;

Query Match 33.3%; Score 38; DB 5; Length 10;  
Best Local Similarity 70.0%; Pred. No. 64;  
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 YPGSRIGNPK 13  
DB 1 YVGPRTYGNPK 10

RESULT 6  
AAU92613  
ID AAU92613 standard; peptide; 10 AA.

AC AAU92613;  
XX  
XX 02-JUL-2002 (first entry)  
XX  
XX PHOR1-F5D6 peptide #351 tested for HLA binding.

XX Human; PHOR1-A11; PHOR1-F5D6; prostate cancer; cytostatic.  
XX  
XX Homo sapiens.  
XX  
XX WO200214501-A2.

XX  
XX 21-FEB-2002.  
XX  
XX 17-AUG-2001; 2001WO-US025862.

XX  
XX 17-AUG-2000; 2000US-0226241P.  
XX  
XX (AGEN-) AGENSYS INC.

XX PI Hubert RS, Raitano AB, Faris M, Challita-Eid PM, Ge W;  
XX PI Jakobovics A;  
XX  
XX WPI; 2002-269193/31.

XX Monitoring PHOR1-A11/PHOR1-F5D6 gene products for monitoring presence of  
XX cancer in subject, by determining status of PHOR1-A11/PHOR1-F5D6 gene  
XX products in tissue sample from subject and comparing it to normal sample.  
XX  
XX Claim 49; Page 188; 250pp; English.

XX The present invention relates to the isolation of novel human genes  
XX designated PHOR1-A11 and PHOR1-F5D6 and their encoded proteins. The gene  
XX encoding PHOR1-A11 maps to chromosome 1q23, and the gene encoding PHOR1-  
XX F5D6 maps to chromosome 7q33-q35. The PHOR1-A11 and PHOR1-F5D6  
XX polynucleotide and polypeptide sequences are useful in diagnostic and  
XX therapeutic methods, and compositions for various cancers such as  
XX prostate cancer. The sequences are useful for inhibiting the growth of  
XX cancer cells that express PHOR1-A11 or PHOR1-F5D6 and for treating  
XX cancer. The PHOR1-A11 or PHOR1-F5D6 polypeptide or a fragment thereof can  
XX be used to elicit an immune response. AAU91563-AAU92962 represent PHOR1-  
XX A11 or PHOR1-F5D6 peptides tested for HLA binding  
XX  
SQ Sequence 10 AA;

Query Match 33.3%; Score 38; DB 5; Length 10;  
Best Local Similarity 70.0%; Pred. No. 64;  
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 YPGSRIGNPK 13  
DB 1 YVGPRTYGNPK 10

RESULT 7  
ADMW21182  
ID ADMW21182 standard; peptide; 16 AA.

AC ADMW21182;  
XX  
XX 24-MAR-2005 (first entry)  
XX  
XX Human adenovirus type 37 third beta repeat of the fiber shaft protein.

XX Human adenovirus type 37 third beta repeat of the fiber shaft protein.  
XX  
XX vector; gene therapy; retinopathy; ophthalmological; fiber shaft.  
XX  
XX Human adenovirus type 37.  
XX  
XX WO2004111251-A2.

XX  
XX 23-DEC-2004.  
XX  
XX 10-JUN-2004; 2004WO-US018623.

XX  
XX 11-JUN-2003; 2003US-0478008P.  
XX  
XX (SCRI) SCRIPPS RES INST.

XX PA (REGC) UNIV CALIFORNIA.  
XX  
XX Nemerow GR, Wu E, Stewart P;  
XX  
XX WPI; 2005-040114/04.

XX  
XX New modified adenovirus fiber that bind to Coxsackie-Adenovirus Receptor  
XX (CAR) comprises a modification to the fiber protein shaft, useful for  
XX developing targeted adenoviruses for therapeutic uses, e.g. gene therapy  
XX of retinal disorders.  
XX  
XX Claim 12; SEQ ID NO 58; 171pp; English.

XX This invention relates to a novel modified adenovirus fiber that bind to  
XX the Coxsackie-Adenovirus Receptor (CAR) in vivo and comprises a  
XX modification to the fiber protein shaft. Specifically, it refers to a  
XX modified adenovirus fiber that binds to CAR with less than 50%  
XX preferably less than 1% of the binding affinity of the unmodified fiber,  
XX and furthermore is shorter and more rigid than its unmodified  
XX counterpart. As such, the present invention describes recombinant  
XX de-targeted adenovirus viral particles and vectors that can be used as a  
XX base vectors to develop targeted adenoviruses for specific therapeutic a  
XX uses. Accordingly, by addition of a heterologous nucleic acid encoding a  
XX therapeutic product and a targeting ligand in the capsid of the  
XX adenoviral particle, the modified adenovirus vector can be used in gene  
XX therapy in order to treat retinal disorders. As such, these compositions  
XX exhibit ophthalmological activity. This peptide sequence is a beta repeat  
XX motif of a human adenovirus fiber shaft protein that can be modified to  
XX reduce CAR binding, given in an exemplification of the invention.

XX  
SQ Sequence 16 AA;

Query Match 32.5%; Score 37; DB 9; Length 16;  
Best Local Similarity 72.7%; Pred. No. 1,5e+02;  
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 6 GSRLGNPKAPL 16  
DB 1 GSLTVNPKAPL 11

RESULT 8  
AAW71598  
ID AAW71598 standard; peptide; 20 AA.

XX



```
AC AA071598;
XX XX
DT 24-NOV-1998 (first entry)
DE Protein tyrosine phosphatase peptide PTP PEPT.
XX XX
KW Mouse; tyrosine phosphorylated cleavage furrow-associated protein;
KM PSTPIP, PEPT family; protein tyrosine phosphatase; murine;
KV polymerisation; actin monomer; eukaryotic cell; identification;
antagonist.
XX XX
OS Synthetic.
XS Mus sp.
XX XX
FN WO9835037-A1.
XX PD 13-AUG-1998.
XX PF 30-JAN-1998; 98WO-US001774.
XX PR 07-FEB-1997; 97US-00798419.
PR 29-SEP-1997; 97US-00938829.
XX PA (GETH ) GENENTECH INC.
PI Laeky LA, Dowbenko DJ;
DR WPL, 1998-447234/38.
XX PT New PEPT-type protein tyrosine phosphatase interacting polypeptide -
XX nucleic acids and vectors; for inducing the polymerisation of actin
PT monomers in eukaryotic cells and identifying antagonists.
PS Disclosure; Page 37; 11pp; English.
XX XX
CC The present sequence represents a peptide from the present invention
CC which describes murine tyrosine phosphorylated cleavage furrow-
CC associated protein (PSTPIP), which is a PEPT-type protein tyrosine
CC phosphatase (PTP)-interacting polypeptide. PSTPIP induces the
CC polymerisation of actin monomers in a eukaryotic cell, by introducing a
CC vector containing the nucleic acid sequence encoding PSTPIP into the
CC cell. Assays for identifying (anti)agonists of PSTPIP comprise contacting
CC PSTPIP with the agent and monitoring the ability of PSTPIP to induce
CC actin polymerisation
XX XX
SQ Sequence 20 AA;

Query Match      31.6%; Score 36; DB 2; Length 20;
Best Local Similarity    60.0%; Pred.No. 2.8e+02;
Matches   6; Conservative     1; Mismatches   3; Indels    0; Gaps    0;

OY        6 GSRLGNPKAP 15          |.:|.|.|.|
Db         3 GNRCCKPKGP 12          |||||.

RESULT 9
AAAY81932
ID AAAY81932 standard; protein; 20 AA.
XX AC AAAY81932;
XX DT 27-JUN-2000 (first entry)
DE Peptide fragment of PXP-HSCF.
XX PS PEST phosphatase interacting protein; PSTPIP; tumour therapy;
KV krrotein tyrosine phosphatase; PTP.
XX OS Unidentified.
XX FN US6040437-A.
XX XX
```

PD 21-MAR-2000 .  
XX  
PF 29-SEP-1997; 97US-00938830 .  
XX  
PR 17-APR-1997; 97US-0104590P .  
XX  
PA (GETH ) GENENTECH INC .  
XX  
PI Dowdenko DJ, Laasky LA;  
XX  
DR WPI, 2000-282393/24 .  
XX  
PT Novel genes encoding protein tyrosine phosphatase binding proteins useful  
PT for isolating homologous genes, e.g. in tumor cells, which provide more  
PI specific targets for tumor therapy.  
XX  
PS Disclosure; Col 35; 65pp; English.  
XX  
CC This sequence represents a fragment of a protein tyrosine phosphatase  
CC (PTP). It was used to isolate the P57 phosphatase interacting protein  
CC (P57IP) sequence of the invention. The protein is a protein tyrosine  
CC phosphatase that possesses a non-catalytic domain comprising a proline,  
CC serine and threonine rich region and a C-terminal segment of 20 amino  
CC acid (aa's) rich in proline, and defines an SH3 binding domain. Nucleic  
CC acids encoding native P57IP molecules can be used to isolate homologous  
CC genes specifically expressed in tumour cells, which might provide more  
CC specific targets for tumour therapy. The DNA is also useful for the  
CC preparation of P57IP polypeptides by recombinant techniques and as  
CC hybridisation probes for searching cDNA and genomic libraries for the  
CC coding sequence of other P57IP polypeptide analogues in other species  
XX  
SQ Sequence 20 AA;

```

Query Match      31.6%; Score 36; DB 3; Length 20;
Best Local Similarity 60.0%; Pred. No. 2.8e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY      6 GSRIGNPKAP 15
      ||| |||
Db      3 GNRCKPKP 12

RESULT 10
AAB08489
ID      AAB08489 standard; peptide: 20 AA.
XX
AC      AAB08489;
XX
DT      20-DEC-2000 (first entry)
XX
DB      Peptide derived from a protein tyrosine phosphatase.
XX
KW      protein tyrosine phosphatase; PTP; phosphatase interacting protein;
KM      PSTRIP, PSTR family; protein tyrosine phosphatase; actin monomer;
XX      tissue typing; tumour cell; tumour imaging.
XX
OS      Synthetic.
XX
PN      US611073-A.
XX
PD      29-AUG-2000.
XX
PP      06-FEB-1998; 98US-00020222.
XX
PR      17-APR-1997; 97US-0104590P.
XX
PA      (GERTH ) GENENTECH INC.
XX
PI      LabKey LA;
XX
DR      WPI, 2000-586378/55.
XX
PT      Novel PST phosphatase interacting protein useful for inducing

```

PT polymerization of actin monomers and for identifying homolog of PST  
 PT phosphatase interacting protein.

PS Disclosure; Col 34; 48pp; English.

XX  
 CC AAB08487-90 represent peptides derived from protein tyrosine phosphatase  
 CC (PTP). They were used to identify interaction domains of a murine protein  
 CC tyrosine phosphatase (PTP) phosphatase interacting protein (PSPIP).  
 CC PSPIP polypeptides are bound by and dephosphorylated by the PEST family  
 CC of protein tyrosine phosphatase. PSPIP associates with actin. PSPIP is  
 CC useful for inducing the polymerisation of actin monomer in eukaryotic  
 CC cells by introducing the polypeptide into the cell. The polypeptide is  
 CC useful for identifying and isolating PSPIP homologues in another  
 CC mammalian species, in screening assays to identify antagonists and  
 CC agonists of native PSPIP polypeptide and as molecular weight markers on  
 CC protein gels. The PSPIP nucleic acid is useful for tissue typing of  
 CC specific mammalian tissues, for preparing PSPIP polypeptides by  
 CC recombinant techniques, as hybridisation probes for searching cDNA and  
 CC genomic libraries for the coding sequence of other PSPIP analogues and  
 CC to isolate homologous genes specifically expressed in tumour cells.  
 CC Antagonists of PSPIP peptide are useful for inhibiting biological  
 CC activity of the peptide. Antibodies of PSPIP are useful to identify  
 CC rapidly dividing cells and are used to image tumours comprising such  
 CC rapidly dividing cells

SQ Sequence 20 AA;

Query Match 31.6%; Score 36; DB 3; Length 20;  
 Best Local Similarity 60.0%; Pred. No. 2.8e+02;  
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 6 GSRLGNPKAP 15  
 Db 3 GNRCKPKKP 12

RESULT 11  
 ADM23014  
 ID ADM23014 standard; peptide; 9 AA.

XX AC ADM23014;  
 XX DT 10-MAR-2005 (first entry)

DE SARS coronavirus T-cell epitope SEQ ID 70.

KM SARS coronavirus infection; infection; respiratory disease;  
 KM epitope mapping; vaccine; diagnosis; T-lymphocyte; virucide.

OS SARS coronavirus.

PN WO2004110349-A2.

PD 23-DEC-2004.

PF 14-MAY-2004; 2004WO-US015026.

PR 14-MAY-2003; 2003DK-00000725.

XX (SIGA-) SIGA TECHNOLOGIES INC.

PI Nielsen M, Lund O, Lundegaard C, Worning P, Buus S, Brunak S,  
 PI Justesen S, Sylvestre-Hvid C, Roder GA, Lamberth K;

DR WPI; 2005-048689/05.

XX New Severe Acute Respiratory Syndrome (SARS) virus T-cell epitope  
 PT comprising 407 peptide sequences, each having 9 amino acids, useful in  
 PT preparing a vaccine against SARS infection.

PS Claim 1; SEQ ID NO 70; 103pp; English.

XX The invention relates to a new Severe Acute Respiratory Syndrome (SARS)

CC virus T-cell epitope comprising 407 peptide sequences appearing as  
 CC ADM22945-ADM23351. Also included are predicting peptides that are  
 CC epitopes (or that can be used as diagnostic tools), a vaccine using a  
 CC limited number of the SARS virus peptides, e.g., 1, 2, 3, 4, 5, 8, 16,  
 CC 32, 64, 128, 256 or 512, given in the specification, or a diagnostic tool  
 CC using a limited number of the SARS virus peptides, e.g., 1, 2, 3, 4, 5,  
 CC 8, 16, 32, 64, 128, 256 or 512, given in the specification. Predicting  
 CC peptides that are epitopes or that can be used as diagnostic tools  
 CC comprises predicting which peptides bind to a MHC (major  
 CC histocompatibility complex) molecule with high affinity using a method  
 CC with at least one or two of the following features: using a Gibbs sampler  
 CC to derive binding motif weight matrices; using a Gibbs sampler including  
 CC sequences weighting to derive binding motif weight matrices; or using a  
 CC Gibbs sampler including pseudo counts to correct for low counts to derive  
 CC binding motif weight matrices. The prediction of the Gibbs sampler weight  
 CC matrix is combined with prediction or measurement of proteasomal cleavage  
 CC sites, major histocompatibility complex (MHC) binding, presence or  
 CC related sequences in patent databases, TAP binding, gene or protein  
 CC expression level, function of the protein, localization of the protein,  
 CC similarity to self proteins or sequence conservation. The new Severe  
 CC Acute Respiratory Syndrome (SARS) virus T-cell epitope is useful in  
 CC preparing a vaccine against SARS infection. The present sequence is a  
 CC SARS virus epitope of the invention.

SQ Sequence 9 AA;

Query Match 30.7%; Score 35; DB 9; Length 9;  
 Best Local Similarity 75.0%; Pred. No. 2e+06;  
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 11 NPKAPLYK 18  
 Db 1 NPKTPKPK 8

RESULT 12  
 ADM78056  
 ID ADM78056 standard; peptide; 15 AA.

XX AC ADM78056;

XX DT 07-APR-2005 (first entry)

DE Human inflammation therapy target peptide CEBA.

KM DEF domain; MAP kinase; cytosolic; cardiovascular-gen.; cardiac;  
 KM vasoactive; hypotensive; antiarteriosclerotic; antiinflammatory;  
 KM antiallergic; immunosuppressive; antibacterial; antiasthmatic;  
 KM dermatological; antidiabetic; gastrointestinal-gen.; antitumor;  
 KM thrombolytic; neuroprotective; ophthalmological; antirheumatic;  
 KM antipyretic; uropathic; antiparasitic; hepatotropic; antianemic;  
 KM muscular-gen.; thyromimetic; antithyroid; gynecological; nephrotropic;  
 KM hepatotropic; virucide; anti-HIV; anabolic; hypertensive; anorectic;  
 KM endocrine-gen.; neuroleptic; nootropic; antiparkinsonian; anticonvulsant;  
 KM antidepressant; antidiabetic; sedative; hypnotic; CNS-gen.;

KM antiferility; cancer; cardiovascular disease; inflammation;  
 KM metabolic disorder; neuropathy; sleep disorder.

OS Homo sapiens.

PN WO2005007090-A2.

PD 27-JAN-2005.

PF 02-JUL-2004; 2004WO-US021514.

PR 03-JUL-2003; 2003US-0484761P.

XX (HARD) HARVARD COLLEGE.

XX Blenis J, Murphy IO;

PI WPI; 2005-112720/12.

XX Identification of compound for treating e.g. cancer by culturing cells  
PT expressing target protein in the presence of growth factor, cytokine,  
PT tumor promoter or oncogene and assessing binding after contacting with  
PT the compound.  
XX  
PS Claim 12; Page 59; 104pp; English.  
XX  
CC The invention relates to a novel method for the identification of a  
CC therapeutic compound. The method involves providing test cells that  
CC express a target protein containing a D5F domain and MAP kinase;  
CC culturing the cells in the presence of growth factor, cytokine, tumor  
CC promoter or oncogene; contacting the cells with a candidate compound; and  
CC assessing the binding of the MAP kinase to the D5F domain relative to the  
CC binding in the absence of the candidate compound. The invention further  
CC comprises a method for the identification of a therapeutic compound; a  
CC method for treatment of cancer, which involves administering a compound  
CC that inhibits the binding of a MAP kinase to the D5F domain of a target  
CC protein; and an antibody that specifically binds to phospho-T-325 c-Fos  
CC (preferably polyclonal or monoclonal). The novel therapeutic compounds  
CC have the following activities: cytostatic, cardiovascular-gen., cardiant,  
CC vasoactive, hypotensive, antiarteriosclerotic, antiinflammatory,  
CC antiallergic, immunosuppressive, antibacterial, antiasthmatic,  
CC dermatological, antidiabetic, gastroenteral-gen., antitumor,  
CC thrombolytic, neuroprotective, ophthalmological, antirheumatic,  
CC antipyretic, uropathic, antiparasitic, hepatotropic, antianemic, muscular  
CC -gen., thyromimetic, antihypertensive, antiparkinsonian, anorectic,  
CC hepatotropic, virucide, anti-HIV, anabolic, hypertensive, anorectic,  
CC endocrine-gen., neuroleptic, nootropic, antiparkinsonian, anticonvulsant,  
CC antidepressant, antidiabetic, sedative, hypnotic, CNS-gen., and  
CC antifertility. The therapeutic compound may be used in the treatment  
CC of: cancer, cardiovascular disorders, inflammatory disorders, metabolic  
CC disorders, neuropathy or a behavioural disorder, and a sleep disorder.  
CC This sequence represents a cardiovascular therapy target peptide of the  
CC invention.  
XX  
SQ Sequence 15 AA;  
XX  
Query Match 30.7%; Score 35; DB 9; Length 15;  
Best Local Similarity 50.0%; Pred. No. 2.9e+02;  
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
QY 1 DYRYPSRLG 10  
|::|||:|  
DB 4 DFDYPPAPAG 13  
  
RESULT 13  
ADW77792  
ID ADW77792 standard; peptide; 15 AA.  
XX  
AC ADW77792;  
XX  
DT 07-APR-2005 (first entry)  
XX  
DE Human cancer therapy target peptide CBRA #2.  
XX  
KM D5F domain; MAP kinase; cytostatic; cardiovascular-gen.; cardiant;  
KM vasoactive; hypotensive; antiarteriosclerotic; antiinflammatory;  
KM antiallergic; immunosuppressive; antibacterial; antiasthmatic;  
KM dermatological; antidiabetic; gastroenteral-gen.; antitumor;  
KM thrombolytic; neuroprotective; ophthalmological; antirheumatic;  
KM antipyretic; uropathic; antiparasitic; hepatotropic; antianemic;  
KM muscular-gen.; thyromimetic; antihypertensive, antiparkinsonian;  
KM hepatotropic; virucide; anti-HIV; anabolic; hypertensive; anorectic;  
KM endocrine-gen.; neuroleptic; nootropic; antiparkinsonian; anticonvulsant;  
KM antidepressant; antidiabetic; sedative; hypnotic; CNS-gen.;  
KM antifertility; cancer; cardiovascular disease; inflammation;  
KM metabolic disorder; neuropathy; sleep disorder.  
XX  
XX Homo sapiens.  
OS  
XX WO2005007090-A2.

XX  
PD 27-JUN-2005.  
XX  
XX 02-JUL-2004; 2004WO-US021514.  
PP  
XX  
PR 03-JUL-2003; 2003US-0484761P.  
PR  
XX  
PA (HARD ) HARVARD COLLEGE.  
PI  
PI Blenis J, Murphy LO;  
XX  
DR WPI; 2005-112720/12.  
XX  
PT Identification of compound for treating e.g. cancer by culturing cells  
PT expressing target protein in the presence of growth factor, cytokine,  
PT tumor promoter or oncogene and assessing binding after contacting with  
PT the compound.  
XX  
PS Claim 11; Page 49; 104pp; English.  
XX  
CC The invention relates to a novel method for the identification of a  
CC therapeutic compound. The method involves providing test cells that  
CC express a target protein containing a D5F domain and MAP kinase;  
CC culturing the cells in the presence of growth factor, cytokine, tumor  
CC promoter or oncogene; contacting the cells with a candidate compound; and  
CC assessing the binding of the MAP kinase to the D5F domain relative to the  
CC binding in the absence of the candidate compound. The invention further  
CC comprises a method for the identification of a therapeutic compound; a  
CC method for treatment of cancer, which involves administering a compound  
CC that inhibits the binding of a MAP kinase to the D5F domain of a target  
CC protein; and an antibody that specifically binds to phospho-T-325 c-Fos  
CC (preferably polyclonal or monoclonal). The novel therapeutic compounds  
CC have the following activities: cytostatic, cardiovascular-gen., cardiant,  
CC vasoactive, hypotensive, antiarteriosclerotic, antiinflammatory,  
CC antiallergic, immunosuppressive, antibacterial, antiasthmatic,  
CC dermatological, antidiabetic, gastroenteral-gen., antitumor,  
CC thrombolytic, neuroprotective, ophthalmological, antirheumatic,  
CC antipyretic, uropathic, antiparasitic, hepatotropic, antianemic,  
CC -gen., thyromimetic, antihypertensive, antiparkinsonian, anorectic,  
CC hepatotropic, virucide, anti-HIV, anabolic, hypertensive, anorectic,  
CC endocrine-gen., neuroleptic, nootropic, antiparkinsonian, anticonvulsant,  
CC antidepressant, antidiabetic, sedative, hypnotic, CNS-gen., and  
CC antifertility. The therapeutic compound may be used in the treatment  
CC of: cancer, cardiovascular disorders, inflammatory disorders, metabolic  
CC disorders, neuropathy or a behavioural disorder, and a sleep disorder.  
CC This sequence represents a cancer therapy target peptide of the  
CC invention.  
XX  
SQ Sequence 15 AA;  
XX  
Query Match 30.7%; Score 35; DB 9; Length 15;  
Best Local Similarity 50.0%; Pred. No. 2.9e+02;  
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
QY 1 DYRYPSRLG 10  
|::|||:|  
DB 4 DFDYPPAPAG 13  
  
RESULT 14  
AAR37725  
ID AAR37725 standard; peptide; 18 AA.  
XX  
AC AAR37725;  
XX  
DT 25-MAR-2003 (revised)  
DT 07-SEP-1993 (first entry)  
XX  
DE Collagen-like polymer #8.  
XX  
KM Recombinant; collagen-like polymer; CRP; tripeptide; helix; membrane;  
KM fibre; film; coating; triad sequence; collagen; mammalian; moulding;  
KM hydrogel; interchain linkage; colloid suspension.

XX OS Synthetic.  
 XX PN WO9310154-A1.  
 XX PD 27-MAY-1993.  
 XX PF 04-NOV-1992; 92WO-US009485.  
 XX PR 12-NOV-1991; 91US-00791960.  
 XX (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
 XX PA Cappello J, Ferrari FA;  
 XX PI Cappello J, Ferrari FA;  
 XX DR WPI, 1993-182496/22.  
 XX High mol. wt. collagen-like protein polymers - capable of being produced  
 PT in unicellular microorganisms.  
 XX  
 PS Disclosure; Page 11; 82pp; English.  
 CC The sequences given in AAR37718-32 are examples of recombinantly produced  
 CC collagen-like polymers (CLPs) which consist of repeated tripeptide  
 CC sequences selected from a wide range of GXY sequences, where X and Y can  
 CC be any amino acid. These polymers have molecular weights of >30 kD and  
 CC are able to form helices due to interchain linkages. These polymers pref.  
 CC contain a proportion of tripeptide triad sequences found in natural  
 CC collagens, pref. mammalian collagens. The CLPs impart unique  
 CC characteristics to materials such as fibres, membranes, films, coatings,  
 CC hydrogels, colloid suspensions and moulded articles. (Updated on 25-MAR-  
 CC 2003 to correct PN field.)  
 XX  
 SQ Sequence 18 AA;

Query Match 30.3%; Score 34.5; DB 2; Length 18;  
 Best Local Similarity 72.7%; Pred. No. 4.3e+02;  
 Matches 8; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 5 PGRSLGNPKAP 15  
 ||||| :|||  
 DB 6 PGRS-GDPGAP 15

## RESULT 15

AAR93232 standard; peptide; 18 AA.  
 ID AAR93232  
 XX  
 AC AAR93232;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 24-FEB-1996 (first entry)

XX Collagen-like polymer repetitive motif 8.  
 XX  
 KM collagen; repetitive triad motif; recombinant production; photographic;  
 KM medical; structural; fibre.

XX OS Synthetic.  
 XX  
 XX US5496712-A.  
 XX PN  
 XX PD 05-MAR-1996.  
 XX PF 05-NOV-1992; 92US-00972032.  
 XX PR 06-NOV-1990; 90US-00609716.  
 XX PR 12-NOV-1991; 91US-00791960.

XX (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
 XX PA Cappello J, Ferrari FA;  
 XX PI  
 XX

XX

DR WPI, 1996-150728/15.  
 XX  
 XX Collagen-like polymers comprising repetitive triads - produced in  
 PT unicellular organisms with improved characteristics, useful in, e.g.  
 PT photographic and medical fibres.  
 XX  
 PS Disclosure; Col 5; 43pp; English.  
 XX

CC The invention concerns collagen-like polymers having repetitive triads  
 CC with reduced proline content, and where glycine is the initial amino acid  
 CC and the subsequent amino acids are varied. The choice of triads utilised  
 CC in a recombinant collagen-like polymer are chosen in order to affect  
 CC properties such as helix stability, hydration, solubility, gel point,  
 CC biodegradation and immunogenicity. Also considered is the level of  
 CC guanidine and cytosine nucleotides (due to levels of glycine and proline)  
 CC present in the genes encoding the polymers. As the gene is synthesised  
 CC there is opportunity for strands to loop out, single-stranded DNA to be  
 CC excluded, recombination events to occur which can result in loss of  
 CC segments of the gene, and inefficient transcription and/or translation  
 CC (due to the presence of self-complementary sequences), hence genes of the  
 CC invention are designed to provide the advantageous properties of  
 CC collagen, while at the same time allowing for stable expression of high  
 CC mol. wt. collagen-like proteins. Triads of particular interest include  
 CC GAP, GPP, GAS, GPG, GAO, GSP, GLO, GPR, GAK, GAR, GBR,  
 CC GDR, GRP, GDA, GAN and GEA. The collagen-like polymers may impart new  
 CC characteristics, finding wide use in photographic, medical, structural  
 CC and fibre applications, and are capable of being produced in unicellular  
 CC microorganisms at high mol. wts. and in high efficiency. AAR3225-34 are  
 CC peptides defining a variety of repetitive triad motifs. The peptides are  
 CC useful as happens, to produce antisera or monoclonal antibodies specific  
 CC to the sequences which are then used for affinity purification,  
 CC identification of the polymers, etc. (Updated on 25-MAR-2003 to correct  
 CC PF field.)  
 XX  
 SQ Sequence 18 AA;

Query Match 30.3%; Score 34.5; DB 2; Length 18;  
 Best Local Similarity 72.7%; Pred. No. 4.3e+02;  
 Matches 8; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 5 PGRSLGNPKAP 15  
 ||||| :|||  
 DB 6 PGRS-GDPGAP 15

## RESULT 16

AAM57681 standard; peptide; 18 AA.  
 ID AAM57681  
 XX  
 AC AAM57681;  
 XX  
 DT 27-AUG-1998 (first entry)

XX Collagen-like polymer fragment.  
 XX  
 KM Collagen-like polymer; synthetic polymer; fibre coating;  
 KM prosthetic device; catalytic substance.

XX OS Synthetic.  
 XX  
 XX US5773249-A.  
 XX PN  
 XX PD 30-JUN-1998.  
 XX PF 02-MAY-1996; 96US-00642255.  
 XX PR 04-NOV-1986; 86US-00927258.  
 XX PR 29-OCT-1987; 87US-00114618.  
 XX PR 09-NOV-1988; 88US-00259429.  
 XX PR 06-NOV-1990; 90US-00609716.  
 XX PR 12-NOV-1991; 91US-00791960.  
 XX PR 05-NOV-1992; 92US-00972032.  
 XX PR 22-DEC-1995; 95US-00577046.

XX

```

XX PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
XX XX
XX P1 Ferrarri FA, Cappello J;
XX DR WPI, 1998-387004/33.
XX PT Recombinant collagen-like polymers - useful for making gels, films,
XX PT fibres, etc.
XX PS Diaclosure; Col 6, 93pp; English.
XX CC This sequence represents a fragment of a unnatural collagen-like polymer
CC CC of the invention. The products may be used as films, fibres, moulded
CC CC objects and admixed with other natural or synthetic polymers or coatings
CC CC on fibres, films, labware or other surfaces, e.g. prosthetic devices. The
CC CC polymers may be used for binding a wide variety of specific binding
CC CC materials, as catalytic substances (where the amino acid sequence may
CC CC specifically chelate a wide variety of elements), as purification media,
CC CC composites, laminates or adhesives. They may also be combined with
CC CC inorganic or organic materials such as carbon fibres, nylon fibres,
CC CC nitrocellulose, etc., as flask coatings or in synthetic matrices for the
CC CC growth and study of cells, as affinity columns or as supports for
CC CC biological materials. The polymers have collagen-like properties, but may
CC CC be easily expressed in micro-organisms in high efficiency. The new
CC CC sequences can be tailored to give the desired properties
XX SO Sequence 18 AA;

Query Match 30.3%; Score 34.5; DB 2; Length 18;
Best Local Similarity 72.7%; Pred. No. 4.3e+02;
Matches 8; Conservative 1; Mismatches 1; Indels 1; Gaps 1.

Qy 5 PGSRLGNPKAP 15
Db ||||| |:|||
6 PGSR-GDPCAP 15

RESULT 17
AAM00359
AAM00359 standard; peptide; 14 AA.
AC AAM00359;
DX 01-OCT-2001 (first entry)
DT Human protein fragment SEQ ID NO: 905.
DE Human, single nucleotide polymorphism; SNP; paternity test;
KW forensic test; aberrant protein expression.
XX Homo sapiens.
OS WO200151670-A2.
PN 19-JUL-2001.
PD 05-JAN-2001; 2001WO-US0000322.
PF 07-JAN-2000; 2000US-0174962P.
PR (CURA-) CURAGEN CORP.
PA Shinketsu RA, Leach MD;
XX N-PBDB; AAH89474.
DR WPI, 2001-451871/48.
XX N-PBDB; AAH89474.
XX Isolated human polynucleotides containing single nucleotide
PT polymorphisms, useful for the treatment and diagnosis of e.g. cancer,
PT infection and diabetes.
PS Disclosure; Page 364, 475pp; English.
```

XX	The present invention relates to human nucleic acids containing single
CC	nucleotide polymorphisms (SNPs). These can be used in forensic and
CC	paternity tests, and to aid in the treatment of diseases associated with
CC	aberrant protein expression, including cancer, amyloidosis, diabetes,
CC	Alzheimer's disease, Down's syndrome, oedema, lupus (SLE), vasculitis,
CC	glomerulonephritis, haemolytic anaemia, thrombocytopenia, arthritis,
CC	meningitis, muscular disorders, dementia, neurological diseases, tubercous
CC	scleriosis, male infertility, hypercalcaemia, blood pressure disorders,
CC	osteoporosis, pathogenic infections, hypercholesterolaemia, obesity or
CC	autoimmunity. The present sequence is a peptide encoded by a
CC	polymorphism-containing oligonucleotide fragment of the invention
XX	
SQ	Sequence 14 AA:
Oy	1 DYEYPSRLGN 11    : 4 DYRHPPEPLAN 14
Db	
Query Match	29.8%; Score 34; DB 4; Length 14;
Best Local Similarity	54.5%; Pred. No. 3.9e+02;
Matches	6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
RESULT 18	
ID	ADS71368 standard; peptide; 15 AA.
XX	
AC	ADS71368;
DT	02-DEC-2004 (first entry)
XX	
DB	Extensin peptide #1.
XX	
KW	Extensin; hydroxyproline-rich glycoprotein; HRGP; infection; cancer;
XX	immune response; synergistic effect; antimicrobial; cytostatic.
OS	Unidentified.
XX	
FH	Key Location/Qualifiers
FT	Modified-site 2..3 /label= Hyp
FT	Modified-site /note= "Hydroxyproline"
FT	Modified-site 9..10 /label= Hyp
FT	Modified-site /note= "Hydroxyproline"
FT	Modified-site 12 /label= Hyp
FT	Modified-site /note= "Hydroxyproline"
XX	
PN	US6794495-B1.
XX	
PD	21-SEP-2004.
XX	
PP	18-OCT-1999; 99US-00419927.
XX	
PR	19-OCT-1998; 98US-0104720P.
XX	
PA	(NEWMN-) NEW NORDIC DANMARK APS.
PI	
DR	Sorensen MB;
WI	2004-666364/65.
PT	Composition comprising an extensin and at least one pectin, is useful in
PS	the treatment of cancer.
XX	
PS	Claim 1; Col 8; 5pp; English.
CC	The invention relates to the composition which comprises the protein
CC	extensin [which is a hydroxyproline-rich glycoprotein (HRGP)] or a
CC	combination of pectin or polysaccharides found in the pectic molecule and
CC	extensin. The invention is useful for preventing or treating a broad

CC variety of disorders including infections and cancers that are associated  
CC with a modulation of immune responses and has improved synergistic  
CC effect. The present sequence is an extensin peptide.

XX Sequence 15 AA;

Query Match 29.8%; Score 34; DB 8; Length 15;  
Best Local Similarity 41.2%; Pred. No. 4.2e+02;  
Matches 7; Conservative 2; Mismatches 2; Indels 6; Gaps 1;

QY 2 YEPGSRGNPKAPLYK 18  
:|||:|:|:  
Db 5 HEXP-----PPRPVYK 15

RESULT 19

ADL5704  
ID ADE15704 standard; peptide; 20 AA.

XX ADE15704;

XX 29-JAN-2004 (first entry)

DE E. coli tridegin fragment SEQ ID 21.

XX tridegin; anticoagulant; inhibition; thrombin; factor Xa;  
XX platelet aggregation; acetylsalicylic acid; heparin; heparinoid; hirudin;  
XX bivalirudin; melagatran; eptifibatide; streptokinase; staphylokinase;  
XX eminase; hementin; plasmin; tissue plasminogen activator; tPA; urokinase;  
XX thrombolytic activity; transglutaminase inhibitor; factor XIII;  
XX blood coagulation cascade.

XX Escherichia coli.

XX WO2003054194-A2.

XX 03-JUL-2003.

XX 20-DEC-2002; 2002WO-EP014684.

XX 21-DEC-2001; 2001DE-01063333.

XX 12-DEC-2002; 2002DE-01058159.

XX (CURA-) CURACYTE AG.

XX Giersefien H, Stoeckel J, Pamp T, Ohlmann M;

XX WPI; 2003-533140/50.

XX New variants of tridegin, useful as anticoagulant and thrombolytic  
XX agents, inhibit factor 13a and have e.g. improved stability against  
XX aggregation.

XX Example 3; SEQ ID NO 21; 54pp; German.

XX This invention describes novel variants of the tridegin polypeptide which  
XX may be formulated with at least one other agent, especially an  
XX anticoagulant that acts by inhibition of thrombin, factor Xa and/or  
XX platelet aggregation. The agent can be any of the following compounds  
XX acetylsalicylic acid, (low-molecular weight) heparin, heparinoid,  
XX hirudin, bivalirudin, melagatran, streptokinase, staphylokinase,  
XX eminase, hementin, plasmin, tissue plasminogen activator (tPA) and  
XX urokinase. The products of the invention have anticoagulant and  
XX thrombolytic activity and inhibit transglutaminases, specifically factor  
XX XIII, the last enzyme in the blood coagulation cascade. Compared with  
XX wild-type tridegin the novel variants may be less prone to form  
XX aggregates when expressed in Escherichia coli, form aggregates more  
XX slowly when stored at lower temperatures, be protected against  
XX proteolysis when expressed in Pichia pastoris, have greater inhibitory  
XX activity, be produced in greater yield, have reduced immunogenicity  
XX and/or have slower metabolic degradation after injection. Compositions  
XX containing tridegin variants and other anticoagulants, specifically  
XX tissue plasminogen activator and urokinase, show a synergistic effect for

CC lysis of blood clots. This sequence represents a wild-type tridegin  
CC protein fragment used to construct the variants of the invention.

XX Sequence 20 AA;

Query Match 29.8%; Score 34; DB 7; Length 20;  
Best Local Similarity 43.8%; Pred. No. 5.8e+02;  
Matches 7; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 5 PGRSLGNPKAPLYKRP 20  
:|||:|:|:  
Db 2 PRSELKPKMDIYQRP 17

RESULT 20

ADL5703  
ID ADE15703 standard; peptide; 20 AA.

XX ADE15703;

XX 29-JAN-2004 (first entry)

DE E. coli tridegin fragment SEQ ID 20.

XX tridegin; anticoagulant; inhibition; thrombin; factor Xa;  
XX platelet aggregation; acetylsalicylic acid; heparin; heparinoid; hirudin;  
XX bivalirudin; melagatran; eptifibatide; streptokinase; staphylokinase;  
XX eminase; hementin; plasmin; tissue plasminogen activator; tPA; urokinase;  
XX thrombolytic activity; transglutaminase inhibitor; factor XIII;  
XX blood coagulation cascade.

XX Escherichia coli.

XX WO2003054194-A2.

XX 03-JUL-2003.

XX 20-DEC-2002; 2002WO-EP014684.

XX 21-DEC-2001; 2001DE-01063333.

XX 12-DEC-2002; 2002DE-01058159.

XX (CURA-) CURACYTE AG.

XX Giersefien H, Stoeckel J, Pamp T, Ohlmann M;

XX WPI; 2003-533140/50.

XX New variants of tridegin, useful as anticoagulant and thrombolytic  
XX agents, inhibit factor 13a and have e.g. improved stability against  
XX aggregation.

XX Example 3; SEQ ID NO 20; 54pp; German.

XX This invention describes novel variants of the tridegin polypeptide which  
XX may be formulated with at least one other agent, especially an  
XX anticoagulant that acts by inhibition of thrombin, factor Xa and/or  
XX platelet aggregation. The agent can be any of the following compounds  
XX acetylsalicylic acid, (low-molecular weight) heparin, heparinoid,  
XX hirudin, bivalirudin, melagatran, streptokinase, staphylokinase,  
XX eminase, hementin, plasmin, tissue plasminogen activator (tPA) and  
XX urokinase. The products of the invention have anticoagulant and  
XX thrombolytic activity and inhibit transglutaminases, specifically factor  
XX XIII, the last enzyme in the blood coagulation cascade. Compared with  
XX wild-type tridegin the novel variants may be less prone to form  
XX aggregates when expressed in Escherichia coli, form aggregates more  
XX slowly when stored at lower temperatures, be protected against  
XX proteolysis when expressed in Pichia pastoris, have greater inhibitory  
XX activity, be produced in greater yield, have reduced immunogenicity  
XX and/or have slower metabolic degradation after injection. Compositions  
XX containing tridegin variants and other anticoagulants, specifically  
XX tissue plasminogen activator and urokinase, show a synergistic effect for  
XX lysis of blood clots. This sequence represents a wild-type tridegin

CC protein fragment used to construct the variants of the invention.  
 XX  
 XX Sequence 20 AA;  
 Query Match 29.8%; Score 34; DB 7; Length 20;  
 Best Local Similarity 43.8%; Pred. No. 5.8e+02;  
 Matches 7; Conservative 2; Mismatches 7; Indels 0; Gaps 0;  
 Db 5 PGSRLGNPKAPLYRKP 20  
 4 PRSELIRKMDIYQRP 19  
 RESULT 21  
 ADM78278  
 ID ADM78278 standard; peptide; 15 AA.  
 XX  
 XX ADM78278;  
 XX  
 XX 07-APR-2005 (first entry)  
 DT  
 XX  
 XX Rat neuropathic therapy target peptide SHK2.  
 DE  
 XX  
 XX DEF domain; MAP kinase; cytosolic; cardiovascular-gen.; cardiac;  
 KM vasotrophic; hypotensive; antiarteriosclerotic; antiinflammatory;  
 KM antiallergic; immunosuppressive; antibacterial; antitumoric;  
 KM dermatological; antidiabetic; gastrointestinal-gen.; antitumor;  
 KM thrombolytic; neuroprotective; ophthalmological; antirheumatic;  
 KM antipruritic; uropathic; antipsoriatic; hepatotropic; antianemic;  
 KM muscular-gen.; thyromimetic; antithyroid; gynecological; nephrotropic;  
 KM hepatotropic; virologic; antihiv; anabolic; hypertensive; anorectic;  
 KM endocrine-gen.; neuroleptic; nootropic; antiparkinsonian; anticonvulsant;  
 KM antidepressant; antidiabetic; sedative; hypnotic; CNS-gen.;  
 KM antifertility; cancer; cardiovascular disease; inflammation;  
 KM metabolic disorder; neuropathy; sleep disorder.  
 KM  
 XX  
 XX Rattus norvegicus.  
 OS  
 XX  
 XX WO2005007090-A2.  
 PN  
 XX  
 XX 27-JAN-2005.  
 PD  
 XX  
 XX 02-JUL-2004; 2004WO-US021514.  
 PF  
 XX  
 XX 03-JUL-2003; 2003US-0484761P.  
 PR  
 XX  
 XX (HARD) HARVARD COLLEGE.  
 PA  
 XX  
 XX Bientle J, Murphy LO;  
 PI  
 XX  
 XX WPI; 2005-112720/12.  
 DR  
 XX  
 XX Identification of compound for creating e.g. cancer by culturing cells  
 PT expressing target protein in the presence of growth factor, cytokine,  
 PT tumor promoter or oncogene and assessing binding after contacting with  
 PT the compound.  
 PT  
 XX  
 XX Claim 15; Page 67; 104pp; English.  
 PS  
 XX  
 XX The invention relates to a novel method for the identification of a  
 CC therapeutic compound. The method involves providing test cells that  
 CC express a target protein containing a DEF domain and MAP kinase;  
 CC culturing the cells in the presence of growth factor, cytokine, tumor  
 CC promoter or oncogene; contacting the cells with a candidate compound; and  
 CC assessing the binding of the MAP kinase to the DEF domain relative to the  
 CC binding in the absence of the candidate compound. The invention further  
 CC comprises a method for the identification of a therapeutic compound; a  
 CC method for treatment of cancer, which involves administering a compound  
 CC that inhibits the binding of a MAP kinase to the DEF domain of a target  
 CC protein; and an antibody that specifically binds to phospho-T-325 c-Fos  
 CC (preferably polyclonal or monoclonal). The novel therapeutic compounds  
 CC have the following activities: cytostatic, cardiovascular-gen., cardiac,  
 CC vasotrophic, hypotensive, antiarteriosclerotic, antiinflammatory,

CC antiallergic, immunosuppressive, antibacterial, antiaslarmatic,  
 CC dermatological, antidiabetic, gastrointestinal-gen., antitumor,  
 CC thrombolytic, neuroprotective, ophthalmological, antirheumatic,  
 CC antipruritic, uropathic, antipsoriatic, hepatotropic, antianemic,  
 CC -gen., thyromimetic, antithyroid, gynecological, nephrotropic,  
 CC hepatotropic, virologic, antihiv, anabolic, hypertensive, anorectic,  
 CC endocrine-gen., neuroleptic, nootropic, antiparkinsonian, anticonvulsant,  
 CC antidepressant, antidiabetic, sedative, hypnotic, CNS-gen., and  
 CC antifertility. The therapeutic compound may be used in the treatment  
 CC of: cancer, cardiovascular disorders, inflammatory disorders, metabolic  
 CC disorders, neuropathy or a behavioral disorder, and a sleep disorder.  
 CC This sequence represents a neuropathic therapy target peptide of the  
 CC invention.  
 XX  
 XX Sequence 15 AA;  
 SQ  
 Query Match 29.4%; Score 33.5; DB 9; Length 15;  
 Best Local Similarity 43.8%; Pred. No. 5e+02;  
 Matches 7; Conservative 2; Mismatches 2; Indels 5; Gaps 1;  
 Db 2 YRPGSRLGNPKAPLY 17  
 5 FEYPG-----PRKLY 15  
 RESULT 22  
 AAU92598  
 ID AAU92598 standard; peptide; 9 AA.  
 XX  
 XX AAU92598;  
 XX  
 XX 02-JUL-2002 (first entry)  
 DT  
 XX  
 XX PHOR1-F5D6 peptide #336 tested for HLA binding.  
 DE  
 XX  
 XX Human; PHOR1-A11; PHOR1-F5D6; prostate cancer; cytostatic.  
 KM  
 XX  
 XX Homo sapiens.  
 OS  
 XX  
 XX WO200214501-A2.  
 PN  
 XX  
 XX 21-FEB-2002.  
 PD  
 XX  
 XX 17-AUG-2001; 2001WO-US025862.  
 PF  
 XX  
 XX 17-AUG-2000; 2000US-0226241P.  
 PR  
 XX  
 XX (AGEN-) AGENSYS INC.  
 PA  
 XX  
 XX Hubert RS, Raitano AB, Faris M, Challita-Bid PM, Ge W,  
 PI Jakobovits A;  
 PI  
 XX  
 XX WPI; 2002-269193/31.  
 DR  
 XX  
 XX Monitoring PHOR1-A11/PHOR1-F5D6 gene products for monitoring presence of  
 PT cancer in subject, by determining status of PHOR1-A11/PHOR1-F5D6 gene  
 PT products in tissue sample from subject and comparing it to normal sample.  
 PT  
 XX  
 XX Claim 49; Page 188; 250pp; English.  
 PS  
 XX  
 XX The present invention relates to the isolation of novel human genes  
 CC designated PHOR1-A11 and PHOR1-F5D6 and their encoded proteins. The gene  
 CC encoding PHOR1-A11 maps to chromosome 1q23, and the gene encoding PHOR1-  
 CC F5D6 maps to chromosome 7q33-q35. The PHOR1-A11 and PHOR1-F5D6  
 CC polynucleotide and polypeptide sequences are useful in diagnostic and  
 CC therapeutic methods, and compositions for various cancers such as  
 CC prostate cancer. The sequences are useful for inhibiting the growth of  
 CC cancer cells that express PHOR1-A11 or PHOR1-F5D6 and for treating  
 CC cancer. The PHOR1-A11 or PHOR1-F5D6 polypeptide or a fragment thereof can  
 CC be used to elicit an immune response. AAU91563-AAU92962 represent PHOR1-  
 CC A11 or PHOR1-F5D6 peptides tested for HLA binding  
 XX  
 XX Sequence 9 AA;  
 SQ

Query Match 28.9%; Score 33; DB 5; Length 9;  
Best Local Similarity 75.0%; Pred. No. 26+06;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 GSRLGNPK 13  
| | | | |  
DB 2 GPRYGNPK 9

## RESULT 23

AAU92855  
ID AAU92855 standard; peptide; 10 AA.

XX  
AC AAU92855;

DT 02-JUL-2002 (first entry)

DE PHOR1-F5D6 peptide #593 tested for HLA binding.

XX Human; PHOR1-A11; PHOR1-F5D6; prostate cancer; cytostatic.

OS Homo sapiens.

PN WO200214501-A2.

PD 21-FEB-2002.

PF 17-AUG-2001; 2001WO-US025862.

PR 17-AUG-2000; 2000US-0226241P.

PA (AGEN-) AGENSYS INC.

PI Hubert RS, Raitano AB, Farris M, Challita-Bid PM, Ge W;

PI Jakobovits A;

DR WPI; 2002-269193/31.

PT Monitoring PHOR1-A11/PHOR1-F5D6 gene products for monitoring presence of  
PT cancer in subject, by determining status of PHOR1-A11/PHOR1-F5D6 gene  
PT products in tissue sample from subject and comparing it to normal sample.

PS Claim 49; Page 198; 250pp; English.

XX The present invention relates to the isolation of novel human genes  
CC designated PHOR1-A11 and PHOR1-F5D6 and their encoded proteins. The gene  
CC encoding PHOR1-A11 maps to chromosome 1q23, and the gene encoding PHOR1-  
CC F5D6 maps to chromosome 7q33-q35. The PHOR1-A11 and PHOR1-F5D6  
CC polynucleotide and polypeptide sequences are useful in diagnostic and  
CC therapeutic methods, and compositions for various cancers such as  
CC prostate cancer. The sequences are useful for inhibiting the growth of  
CC cancer cells that express PHOR1-A11 or PHOR1-F5D6 and for treating  
CC cancer. The PHOR1-A11 or PHOR1-F5D6 polypeptide or a fragment thereof can  
CC be used to elicit an immune response. AAU91563-AAU92962 represent PHOR1-  
CC A11 or PHOR1-F5D6 peptides tested for HLA binding  
XX  
SQ Sequence 10 AA;

Query Match 28.9%; Score 33; DB 5; Length 10;  
Best Local Similarity 75.0%; Pred. No. 3.8e+02;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 GSRLGNPK 13  
| | | | |  
DB 1 GPRYGNPK 8

## RESULT 24

ADS92104  
ID ADS92104 standard; peptide; 14 AA.

XX  
AC ADS92104;

XX 02-DEC-2004 (first entry)

DT Human odorant receptor (OR) peptide fragment SeqID9.

XX antibody; antibody complex; modulating chemosensation; transgenic animal;

KW antigenic site; chemosensation enhancement; taste sensation;

XX smell sensation; OR; odorant receptor; human.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 1 /note= "Optionally absent"

FN WO2003102030-A1.

PD 11-DEC-2003.

PF 20-MAY-2003; 2003WO-IL000409.

PR 20-MAY-2002; 2002US-0382059P.

PA 04-MAR-2003; 2003US-0451639P.

PI (TVDI-) TWD TASTE VIRTUAL DIMENSIONS INC.

PI Ben-Sasson S;

DR WPI; 2004-053430/05.

PT New antibody or complex of two or more antibodies, useful for preparing a

PT composition for modulating chemosensation.

PS Disclosure; SEQ ID NO 9; 48pp; English.

XX This invention relates to a novel antibody or complex of two or more  
CC antibodies for modulating chemosensation. Claims were also included for a  
CC composition comprising the antibody or complex of antibodies; making an  
CC antibody or complex of antibodies; a transgenic non-human animal that is  
CC genetically engineered to produce an antibody that modulates  
CC chemosensation; selecting a candidate antigenic site; and enhancing  
CC chemosensation. The antibody or complex of two or more antibodies is  
CC useful for preparing a composition for modulating chemosensation, in  
CC particular for use in modulating taste sensation or smell sensation. The  
CC present sequence is that of a human peptide which is related to the  
CC invention.  
XX  
SQ Sequence 14 AA;

Query Match 28.9%; Score 33; DB 8; Length 14;  
Best Local Similarity 75.0%; Pred. No. 5.6e+02;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 GSRLGNPK 13  
| | | | |  
DB 2 GPRYGNPK 9

## RESULT 25

ABP55617  
ID ABP55617 standard; peptide; 16 AA.

XX  
AC ABP55617;

DT 20-FEB-2003 (first entry)

DE Human cytokine peptide IL17beta.

XX DPP10; dipeptidyl peptidase; prolyl oligopeptidase; enzyme; asthma;  
KW antiinflammatory; antiaesthetic; antipsoriatic; antitachytic;  
KW antirheumatic; vaccine; gene therapy; inflammatory disease;  
KW inflammatory bowel disease; atopy; rheumatoid arthritis; psoriasis;  
KW chromosome 2q14.



XX Homo sapiens.  
 OS  
 XX  
 PN MO200286113-A2.  
 PD  
 XX 31-OCT-2002.  
 PF 24-APR-2002; 2002MO-GB001887.  
 XX  
 XX 24-APR-2001; 2001GB-00010044.  
 PR 24-APR-2001; 2001GB-00010046.  
 PR 12-OCT-2001; 2001GB-00024575.  
 PR 12-OCT-2001; 2001GB-00024594.  
 XX  
 PA (ISIS-) ISIS INNOVATIONS LTD.  
 XX  
 PI Cookson WOCM, Moffat MF, Allen M, Iench N;  
 XX  
 DR MPI; 2003-093132/08.  
 XX  
 PT New nucleic acid sequence comprising DPP10 mRNA, useful for the  
 PT manufacture of a medicament for regulating DPP10 protein expression or  
 PT for preventing or treating inflammatory disease e.g., inflammatory bowel  
 PT disease.  
 XX  
 XX Example 2; Fig 19; 321pp; English.  
 PS  
 XX The present invention describes a new isolated nucleic acid sequence (I)  
 CC comprising a DPP10 mRNA sequence. DPP10 is a dipeptidyl peptidase (also  
 CC known as prolyl oligopeptidase). (I) has antiinflammatory, antiasthmatic,  
 CC antiproliferative, antitumor, antirheumatic and antineoplastic activities, and can be  
 CC used in vaccines and gene therapy. A composition comprising (I) can be  
 CC used for the manufacture of a medicament for regulating DPP10 expression  
 CC or for preventing or treating inflammatory disease e.g., inflammatory  
 CC bowel disease, asthma, atopy, rheumatoid arthritis or psoriasis. (I) can  
 CC also be used in an assay for detecting or measuring DPP10 in a sample. A  
 CC host cell comprising (I) can be used for producing recombinant DPP10 gene  
 CC products, or in drug screening systems to identify agents for diagnosis  
 CC or treatment of individuals having or susceptible to inflammatory  
 CC disease. Human DPP10 is located on chromosome 2, more specifically  
 CC chromosome 2q14. AB084254 to AB084612 and ABP55569 to ABP55629 represent  
 CC sequences used in the exemplification of the present invention  
 CC  
 XX Sequence 16 AA;  
 SQ  
 Query Match 28.9%; Score 33; DB 6; Length 16;  
 Best Local Similarity 54.5%; Pred. No. 6.5e+02;  
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
 QY 9 LGNPKRPLYKR 19  
 DB 5 LGQPRSPKSKR 15  
 RESULT 26  
 ADD24038  
 ID ADD24038 standard; peptide, 16 AA.  
 AC  
 XX ADD24038;  
 DT 15-JAN-2004 (first entry)  
 XX  
 DE Breast cancer membrane protein (BCMP) peptide SEQ ID NO:1004.  
 XX  
 KW breast cancer; screening; diagnosis; breast cancer therapy;  
 KW breast cancer membrane protein; BCMP; cytostatic; vaccine; human.  
 XX  
 OS Homo sapiens.  
 XX  
 KW WO2003087831-A2.  
 PN  
 XX 23-OCT-2003.  
 PD  
 XX

PF 10-APR-2003; 2003MO-GB001559.  
 XX  
 XX 11-APR-2002; 2002GB-00008331.  
 XX  
 XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.  
 PA  
 XX Hudson LJ, Stamps AC, Terrett JA;  
 PI  
 DR MPI; 2003-045381/78.  
 XX  
 XX Screening, diagnosing and/or treating breast cancer by detecting a change  
 PT in expression or activity of a breast cancer membrane protein (BCMP)  
 PT polypeptide or encoding nucleic acid molecule.  
 XX  
 PS Example; SEQ ID NO 1004, 81pp; English.  
 XX  
 XX The present invention describes a method of screening for and/or  
 CC diagnosing breast cancer in a subject, and/or monitoring the  
 CC effectiveness of breast cancer therapy. The method comprises detecting  
 CC and/or quantifying in a biological sample obtained from the subject a  
 CC breast cancer membrane protein (BCMP) polypeptide and a nucleic acid  
 CC molecule. Also described: (1) an antibody, its functionally-active  
 CC fragment, derivative or analogue, that specifically binds to one or more  
 CC of the BCMP polypeptide; (2) a diagnostic kit comprising a capture  
 CC reagent specific for an BCMP polypeptide, reagents and instructions for  
 CC use; (3) a method for screening for anti-breast cancer agents that  
 CC interact with the BCMP polypeptide, comprising contacting the polypeptide  
 CC with a candidate agent, and determining whether or not the candidate  
 CC agent interacts with the polypeptide; (4) a method for screening for anti-  
 CC breast cancer agents that modulate the expression or activity of an BCMP  
 CC polypeptide or the nucleic acid molecule cited above, comprising  
 CC comparing the expression or activity of the polypeptide or nucleic acid  
 CC molecule, in the presence and absence of a candidate agent or in the  
 CC presence of a control agent, and determining whether the candidate agent  
 CC causes the expression or activity of the polypeptide or nucleic acid  
 CC molecule to change; and (5) an agent identified by the method of (3) or  
 CC (4), which interacts with the polypeptide or causes the expression or  
 CC activity of the polypeptide, or the expression of the nucleic acid  
 CC molecule to change. BCMPs have cytostatic activities, and can be used in  
 CC vaccines. The BCMP polypeptide, nucleic acid molecule, antibody, agent or  
 CC their derivatives, are useful in the manufacture of a medicament for the  
 CC treatment of breast cancer, where the composition is a vaccine. The  
 CC present sequence represents a BCMP peptide which is used in the  
 CC exemplification of the present invention.  
 CC  
 XX Sequence 16 AA;  
 SQ  
 Query Match 28.9%; Score 33; DB 7; Length 16;  
 Best Local Similarity 50.0%; Pred. No. 6.5e+02;  
 Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
 QY 5 PCSRLGNPKRAPL 16  
 DB 4 PCGMAGTFLPL 15  
 RESULT 27  
 AAP80012  
 ID AAP80012 standard; protein, 17 AA.  
 AC  
 XX AAP80012;  
 DT 25-MAR-2003 (revised)  
 DT 19-SEP-1990 (first entry)  
 XX  
 DE Sequence of immunogenic synthetic peptide containing AAs 64 to 77 of  
 DE herpes simplex virus type 1 (HSV1) glycoprotein B (gB).  
 XX  
 XX Herpes simplex virus type 1 glycoprotein B; vaccines;  
 KW immunogenic synthetic peptide.  
 XX  
 OS Herpes simplex virus type 1.  
 XX

```

FH Key Location/Qualifiers
FT Misc-difference 1 /label= OTHER
FT /note= "Ac-Lys"
FT
FT Misc-difference 2 /label= Nle
FT /label= Nle
FT
FT Misc-difference 16 /label= Nle
FT /label= Nle
FT
FT Misc-difference 17 /label= OTHER
FT /note= "L-NH2"
FT
XX
XX US4761470-A.
XX
XX 02-AUG-1988.
XX
XX
XX 10-APR-1987; 87US-00036651.
XX
XX 16-DEC-1985; 85US-00809452.
XX
XX (MERI ) MERCK & CO INC.
XX
XX PA
XX PI Emini EA, Larson VM, Boger JS;
XX
XX WPI; 1988-234840/33.
XX
XX
XX New synthetic oligopeptide immunogens and their conjugates - used for
XX inducing prodn. of antibodies against herpes simplex virus type 1.
XX
XX Claim 3; Page 10; 6pp; English.
XX
XX Immunogenic synthetic peptides of this formula and their salts are new.
XX Also new are conjugates of the peptides covalently bonded to a carrier
XX protein or synthetic polymer. The peptides are immunogens for inducing
XX prodn. of HSV1 neutralising antibodies and so are useful in vaccines.
XX (Updated on 25-MAR-2003 to correct PD field.)
XX
XX SQ Sequence 17 AA;

Query Match 28.9%; Score 33; DB 1; Length 17;
Best Local Similarity 46.2%; Pred. No. 6.9e+02;
Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 8 RLGNPKAPLYKRP 20
   :||:| | | :|
Db 1 KLGDPRKKNKRP 13

RESULT 28
AAP80013
ID AAP80013 standard; protein; 17 AA.
XX
XX AAP80013;
XX
XX 25-MAR-2003 (revised)
XX 19-SBP-1990 (first entry)
XX
XX Sequence of immunogenic synthetic peptide containing AAs 64 to 77 of
XX herpes simplex virus type 1 (HSV1) glycoprotein B (gB).
XX
XX Herpes simplex virus type 1 glycoprotein B; vaccines;
XX immunogenic synthetic peptide.
XX
XX Herpes simplex virus type 1.
XX
XX Key Location/Qualifiers
XX Misc-difference 1 /label= OTHER
XX /note= "Ac-Lys"
XX
XX Misc-difference 2 /label= Nle
XX /label= Nle
XX
XX Misc-difference 2 /label= OTHER
XX /label= OTHER

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FT /note= "p-DenzyIbenzoYL-L"
FT Misc-difference 16 /label= Nle
FT /label= Nle
FT
FT Misc-difference 17 /label= OTHER
FT /note= "L-NH2"
FT
XX
XX US4761470-A.
XX
XX 02-AUG-1988.
XX
XX
XX 10-APR-1987; 87US-00036651.
XX
XX 16-DEC-1985; 85US-00809452.
XX
XX (MERI ) MERCK & CO INC.
XX
XX PA
XX PI Emini EA, Larson VM, Boger JS;
XX
XX WPI; 1988-234840/33.
XX
XX
XX New synthetic oligopeptide immunogens and their conjugates - used for
XX inducing prodn. of antibodies against herpes simplex virus type 1.
XX
XX Claim 3; Page 10; 6pp; English.
XX
XX Immunogenic synthetic peptides of this formula and their salts are new.
XX Also new are conjugates of the peptides covalently bonded to a carrier
XX protein or synthetic polymer. The peptides are immunogens for inducing
XX prodn. of HSV1 neutralising antibodies and so are useful in vaccines.
XX (Updated on 25-MAR-2003 to correct PD field.)
XX
XX SQ Sequence 17 AA;

Query Match 28.9%; Score 33; DB 1; Length 17;
Best Local Similarity 46.2%; Pred. No. 6.9e+02;
Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 8 RLGNPKAPLYKRP 20
   :||:| | | :|
Db 1 KLGDPRKKNKRP 13

RESULT 29
AAV32877
ID AAV32877 standard; peptide; 18 AA.
XX
XX AAV32877;
XX
XX 02-NOV-1999 (first entry)
XX
XX Fibronectin protein heparin II binding domain peptide H-1.
XX
XX Fibronectin; extracellular matrix. Open wound healing; IIRCS domain;
XX acute gaping cutaneous wound; chronic cutaneous ulcer; therapy;
XX wound healing promoter; cell binding domain; heparin II binding domain.
XX
XX Homo sapiens.
XX
XX WO9942117-A1.
XX
XX 26-AUG-1999.
XX
XX 10-FEB-1999; 99WO-US002872.
XX
XX 18-FEB-1998; 98US-00025622.
XX
XX (UWNY ) UNIV NEW YORK STATE RES FOUND.
XX
XX Clark RA, Greiling D;
XX
XX WPI; 1999-527415/44.
XX

```

PT New extracellular matrix used to accelerate healing of acute gaping  
 CC cutaneous wounds and chronic cutaneous ulcers.  
 XX  
 XX  
 PS Claim 10, Page 19, 43pp; English.  
 CC This sequence represents a fibronectin protein fragment used in the  
 CC extracellular matrix of the invention. The extracellular matrix comprises  
 CC two or more fibronectin domains in a backbone matrix, and is used to  
 CC enhance wound healing. The fibronectin domain peptides used are  
 CC preferably from the IICCS domain, the cell binding domain, or the heparin  
 CC II binding domain of human fibronectin. The matrix facilitates wound  
 CC healing by providing an environment that intrinsically recruits new  
 CC tissue cells to the wound site. The new matrix is useful for facilitating  
 CC wound healing, especially useful for treating open wounds such as acute  
 CC gaping cutaneous wounds and chronic cutaneous ulcers. The problem of  
 CC chronic, non-healing wounds is severe. These open wounds require long-  
 CC term care and procedures that are costly and labour intensive.  
 CC Furthermore, these wounds have a severe impact on the patients' quality of  
 CC life. Prior compositions and matrices have not been useful or cost  
 CC effective. The present invention provides a matrix for wound healing that  
 CC meets these requirements, and overcomes the deficiencies of the prior  
 CC matrices  
 CC  
 SQ Sequence 18 AA;  
 XX  
 XX  
 Query Match 28.9%; Score 33; DB 2; Length 18;  
 Best Local Similarity 42.1%; Pred. No. 7.4e+02;  
 Matches 8; Conservative 2; Mismatches 5; Indels 4; Gaps 1;  
 QY 2 YEYSGRLGNPKAPLYKRP 20  
 DB 1 YEKFGS---PRREVPRP 15  
 XX  
 XX  
 RESULT 30  
 ID AAY32865  
 XX AAY32865 standard; peptide; 18 AA.  
 AC AAY32865;  
 XX  
 DT 02-NOV-1999 (first entry)  
 XX  
 DE Fibronectin protein heparin II binding domain peptide H-I.  
 XX  
 KM Fibronectin; extracellular matrix; wound healing promoter; IICCS domain;  
 KM cell binding domain; heparin II binding domain; haemostasis; therapy;  
 KM surgical incisional wound; traumatic wound; radiation wound;  
 KM cancer extirpation; venous leg ulcer; diabetic ulcer; pressure ulcer.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO942126-A1.  
 XX  
 PD 26-AUG-1999.  
 XX  
 PF 10-FEB-1999; 99MO-US002873.  
 XX  
 PR 18-FEB-1998; 98US-00025706.  
 XX  
 XX (UNYNY ) UNIV NEW YORK STATE RES FOUND.  
 PA  
 XX  
 PI Clark RA, Grelling D, Gallit J;  
 XX  
 DR WPI; 1999-527421/44.  
 XX  
 PT Extracellular matrix for promoting wound healing containing recombinant  
 PT fibronectin-derived peptide and backbone matrix.  
 XX  
 PS Claim 10, Page 21, 48pp; English.  
 XX  
 CC This sequence represents a fibronectin protein fragment used in the  
 CC extracellular matrix (A) of the invention. (A) is used for promoting  
 CC wound healing, and comprises a recombinant fibronectin peptide.

CC containing peptide fragments from at least two fibronectin domains, and a  
 CC backbone matrix. The fibronectin domain peptides used are preferably from  
 CC the IICCS domain, the cell binding domain, or the heparin II binding  
 CC domain of human fibronectin. (A) provides haemostasis and an environment  
 CC that recruits new tissue cells to the site of the wound. (A) is used to  
 CC promote healing of acute or chronic wounds, e.g. surgical incisional  
 CC wounds, traumatic wounds, radiation wounds, cancer extirpations, venous  
 CC leg ulcers, diabetic ulcers and pressure ulcers  
 XX  
 SQ Sequence 18 AA;  
 XX  
 XX  
 Query Match 28.9%; Score 33; DB 2; Length 18;  
 Best Local Similarity 42.1%; Pred. No. 7.4e+02;  
 Matches 8; Conservative 2; Mismatches 5; Indels 4; Gaps 1;  
 QY 2 YEYSGRLGNPKAPLYKRP 20  
 DB 1 YEKFGS---PRREVPRP 15  
 XX  
 XX  
 RESULT 31  
 ID AAB62425  
 XX AAB62425 standard; peptide; 19 AA.  
 AC AAB62425;  
 XX  
 DT 09-JUL-2001 (first entry)  
 XX  
 DE Human SAPL peptide fragment.  
 XX  
 KM SAPL; SIT4; SIT4 associated proteins like; human; antidiabetic;  
 KM sporulation-induced transcript 4; SAPA; SAPb; gene therapy; IDDM;  
 KM insulin-dependent diabetes mellitus; epitope.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200129213-A1.  
 XX  
 PD 26-APR-2001.  
 XX  
 PF 19-OCT-2000; 2000MO-GB004027.  
 XX  
 PR 19-OCT-1999; 99US-0160400P.  
 XX  
 XX (WELL ) WELLCOME TRUST LTD.  
 PA (MERI ) MERCK & CO INC.  
 XX  
 PI Todd JA, Twells RCJ, Hess JW, Hey P, Hey P, Caskey CT;  
 PI Hammond H, Metzker ML;  
 XX  
 XX WPI; 2001-300338/31.  
 DR  
 XX  
 PT Isoforms of novel gene arising from alternative splicing and encoding  
 PT highly related proteins termed as SAPa and SAPb, from the IDDM locus  
 PT on human chromosome 11q13, useful for treating IDDM and other diseases.  
 XX  
 PS Claim 22, Page 106; 129pp; English.  
 XX  
 XX The invention relates to SAPL (SIT4-(sporulation-induced transcript4)  
 CC associated proteins-like) polypeptide, selected from SAPa polypeptide  
 CC isoforms and SAPb polypeptide isoforms. The SAPL polynucleotides are  
 CC useful in gene therapy for treating and preventing insulin-dependent  
 CC diabetes mellitus (IDDM). Fragments of the SAPL DNA are useful as primers  
 CC and probes. The SAPL polypeptides are useful in screening for a substance  
 CC e.g., a peptide or chemical compound, which interacts and/or binds with  
 CC them. The present sequence represents a fragment of the SAPL protein,  
 CC that can act as an epitope for raising antibodies  
 XX  
 SQ Sequence 19 AA;  
 XX  
 XX  
 Query Match 28.9%; Score 33; DB 4; Length 19;  
 Best Local Similarity 54.5%; Pred. No. 7.8e+02;  
 Matches 6; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 5 PGSRLGNPKAP 15  
| | | | |  
DB 5 PEQRTOQPSAP 15

RESULT 32

ABP74734  
ID ABP74734 standard; peptide; 19 AA.  
XX

AC ABP74734;

DT 03-FEB-2003 (first entry)

DE Proteome analysis related peptide #19.

KW Proteome analysis; isolation; determination; diagnostic assay; detection;  
KW protein marker; identification; metastatic; invasive cancer;  
KW differential expression; signalling pathway; chromatography.

OS Homo sapiens.  
XX Synthetic.

PN WO200277016-A2.

PD 03-OCT-2002.

PF 22-MAR-2002; 2002WO-EP003368.

PR 22-MAR-2001; 2001US-0278171P.

PR 12-SEP-2001; 2001US-0318749P.

PR 20-SEP-2001; 2001US-0323999P.

(VLA-) VLAAMS INTERNUNIVERSITAIR INST BIOTECHNOG.

PI Vandekerckhove J, Gevaert K;

DR WPI; 2003-067379/06.

PT Method for isolation of peptides from complex mixture of peptides  
PT involves specific chemical and/or enzymatic alteration of at least one  
PT type of peptide.

PS Example 19; Page 138; 193pp; English.

CC The present invention describes a method (M1) for the isolation of a  
CC subset of peptides from a protein peptide mixture (P1). M1 involves: (a)  
CC separating the protein peptide mixture into fractions of peptides via  
CC chromatography; (b) chemically, or enzymatically, or chemically and  
CC enzymatically, altering at least one amino acid of at least one of the  
CC peptides in each fraction, thereby generating a subset of altered  
CC peptides; and (c) isolating the altered (flagged) peptides out of each  
CC fraction via chromatography, where the chromatography of steps (a) and  
CC (c) is performed with the same type of chromatography. M1 can be used for  
CC the isolation and determination of peptides from protein peptide  
CC mixtures. M1 can also be used in diagnostic assays for detection of the  
CC presence, the absence or a variation in expression level of at least one  
CC protein marker or a specific set of proteins indicative of a disease  
CC state. M1 can be used for identifying target proteins present in  
CC metastatic and invasive cancers, in differential expression of proteins  
CC in transgenic mice, identification of proteins that are upregulated or  
CC down regulated in disease tissues, in identification of intracellular  
CC changes in cells with physiological changes such as metabolic shift, in  
CC the identification of biomarkers in cancers and in the identification of  
CC signalling pathways. The method is gel-free methodology for qualitative  
CC and quantitative proteome analysis without the need for multidimensional  
CC chromatography and without the use of affinity tags. ABP74714 to ABP75190  
CC represent peptide sequences used in the exemplification of the present  
CC invention

XX Sequence 19 AA;

Query Match 28.9%; Score 33; DB 6; Length 19;

Best Local Similarity 46.2%; Pred. No. 7.8e+02;  
Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

OY 1 DYEYPSRLGNPK 13  
| | | | |  
DB 7 DLSTPDVAVGNPK 19

RESULT 33

ADSI3312  
ID ADSI3312 standard; peptide; 19 AA.  
XX

AC ADSI3312;

DT 16-DEC-2004 (first entry)

DE Human rheumatoid arthritis marker peptide - SEQ ID 103.  
KW Rheumatoid arthritis; marker; antiinflammatory; antiarthritic.

OS Homo sapiens.  
XX

PN WO2004082617-A2.

PD 30-SEP-2004.

PF 15-MAR-2004; 2004WO-US007880.

PR 14-MAR-2003; 2003US-0455037P.

(SURRE-) SURREMED INC.

PI Kantor AB, Becker CH, Schulman H;

DR WPI; 2004-690929/67.

PT New isolated marker for rheumatoid arthritis, useful in preparing a  
PT composition for diagnosing or treating rheumatoid arthritis.  
PS Claim 1, SEQ ID NO 103; 184pp; English.

CC The invention relates to a novel isolated marker for rheumatoid arthritis  
CC selected from one of many (around 400) markers defined in the  
CC specification. Rheumatoid arthritis is a chronic inflammatory disorder of  
CC the small joints which is estimated to affect 2.1 million people in the  
CC United States alone. Current approaches to treat the disease include the  
CC use of non-steroidal antiinflammatory drugs (NSAIDs), which may reduce  
CC pain, swelling and inflammation, and disease-modifying anti-rheumatic  
CC drugs (DMARDs), which act to slow the progression of the disease and  
CC avoid further joint injury. These drugs are associated with a number of  
CC serious side effects and the search for improved therapeutics is a  
CC subject of active research. The marker of the invention demonstrates  
CC antiarthritic activity and may be useful in preparing a composition for  
CC diagnosing or treating rheumatoid arthritis. The current sequence is that  
CC of a human rheumatoid arthritis marker peptide of the invention.

XX Sequence 19 AA;

Query Match 28.9%; Score 33; DB 8; Length 19;  
Best Local Similarity 46.2%; Pred. No. 7.8e+02;  
Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

OY 1 DYEYPSRLGNPK 13  
| | | | |  
DB 7 DLSTPDVAVGNPK 19

RESULT 34

ADY39949  
ID ADY39949 standard; peptide; 19 AA.  
XX

AC ADY39949;

XX

DT 19-MAY-2005 (first entry)  
 XX  
 DE Human plasma polypeptide (HPP) fragment #129.  
 XX  
 KW Human plasma polypeptide; protein secretion; plasma protein; cancer;  
 KW hyperplasia; neurodegeneration; disorder of iron metabolism;  
 KW metabolic disorder; fibrosis; prostate hyperplasia;  
 KW congenital adrenal hyperplasia; psoriasis; inflammation;  
 KW spinal cord injury; Alzheimers disease; Parkinsons disease;  
 KW multiple sclerosis; motor neurone disease; peripheral neuropathy;  
 KW Guillain Barre syndrome; diabetic neuropathy; demyelinating disease;  
 KW hemochromatosis; thalassemia; iron overload; anemia; sickle cell anemia;  
 KW diabetes; amyloidosis; cystostatic; antiinflammatory; antiproliferative;  
 KW CNS-Gen.; neuroprotective; neurotropic; antiparaneoplastic; antidiabetic;  
 KW ophthalmological; hemostatic; antianemic.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2005019825-A2.  
 XX  
 PD 03-MAR-2005.  
 XX  
 PF 19-AUG-2004; 2004WO-EP009323.  
 XX  
 PR 20-AUG-2003; 2003US-0496966P.  
 XX  
 PA (XENO-) XENOVA LTD.  
 PA (NOVS ) NOVARTIS AG.  
 PA (NOVS ) NOVARTIS PHARMA GMBH.  
 XX  
 PI Argoud-Puy G, Bederr N, Bouguetere L, Cusin I, Mahe B;  
 PI Mknjad A, Riffas S, Rose K, Saudrats C, Scherer A, Papotian R;  
 PI Dengler UJ, Croft LJ;  
 XX  
 DR WPI; 2005-214290/22.  
 XX  
 PT Detecting a Human Plasma Polypeptide (HPP) comprises contacting a  
 PT biological sample with an HPP-binding adsorbent.  
 XX  
 PS Disclosure, SEQ ID NO 129; 284pp; English.  
 XX  
 CC The invention relates to a method of detecting a Human Plasma Polypeptide  
 CC (HPP) comprising contacting a biological sample with an HPP-binding  
 CC adsorbent and detecting and/or quantifying binding of an HPP to the HPP-  
 CC binding adsorbent. The invention also relates to a protein array  
 CC comprising an adsorbent specific for at least one HPP, a method of  
 CC detecting an abnormal concentration of at least one HPP in an individual,  
 CC a pharmaceutical composition comprising an amount of HPP-38, HPP-13,  
 CC HPP23 or GPR101 polypeptide and a pharmaceutical carrier, a method of  
 CC treating cancer, a disease or condition associated with hyperplasia,  
 CC neurodegeneration, iron balance or iron transport, a disease associated  
 CC with dysregulated serum glucose or a metabolic disorder, a method of  
 CC identifying a modulator of a cancer disease, a disease or condition  
 CC associated with hyperplasia, neurodegeneration, iron balance or iron  
 CC transport or a disease associated with dysregulated serum glucose, a  
 CC method of prognosing or diagnosing a cancer disease, a disease or  
 CC condition associated with hyperplasia, neurodegeneration, iron balance  
 CC and a method of reducing blood glucose levels in a mammal, including a  
 CC human. The method is useful for detecting an HPP. The polypeptides,  
 CC compositions and methods are useful for prognosing, diagnosing or  
 CC treating a cancer disease, a disease or condition associated with  
 CC hyperplasia (e.g. fibrosis, prostate hyperplasia, adrenal hyperplasia or  
 CC psoriasis), a disease or condition associated with neurodegeneration  
 CC (e.g. spinal cord injuries or CNS injuries, Alzheimers disease,  
 CC Parkinsons disease, multiple sclerosis, motor neurone disease,  
 CC neuropathy, Guillain Barre syndrome, diabetic neuropathy or demyelinating  
 CC disease), a disease or condition associated with iron balance or iron  
 CC transport (e.g. hemochromatosis, thalassemia, iron overload, anemia or  
 CC sickle cell anemia), a disease associated with dysregulated serum glucose  
 CC (e.g. diabetes) or a metabolic disorder (e.g. amyloidosis). This sequence  
 CC represents an HPP fragment of the invention.  
 XX

SO Sequence 19 AA;  
 Query Match 28.9%; Score 33; DB 9; Length 19;  
 Best Local Similarity 46.2%; Pred. No. 7.8e+02;  
 Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;  
 DB 7 DLSPTDVMGNPK 19  
 QY 1 DYEPGSRGNPK 13  
 DB 7 DLSPTDVMGNPK 19  
 RESULT 35  
 ID AEA33956 standard; peptide; 19 AA.  
 AC AEA33956;  
 DT 11-AUG-2005 (first entry)  
 DE Mass spectrometry peptide, SEQ ID NO:29.  
 XX  
 KW mass spectrometry; protein sequencing.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2005052563-A1.  
 XX  
 PD 09-JUN-2005.  
 XX  
 PF 19-NOV-2004; 2004WO-US83932.  
 XX  
 PR 20-NOV-2003; 2003US-0523643P.  
 XX  
 PA (INDV ) UNIV INDIANA RES & TECHNOLOGY CORP.  
 PA Reilly JP, Beardsley RL;  
 XX  
 DR WPI; 2005-418032/42.  
 XX  
 PT Preparing derivatized peptides to enhance mass spectral analysis of  
 PT peptide by providing composition comprising peptide and labeling N-  
 PT propionamide group.  
 XX  
 PS Example 3; SEQ ID NO 29; 53pp; English.  
 XX  
 CC The invention relates to a method of preparing (M1) derivatized peptides  
 CC to enhance mass spectral analysis of peptide-containing compositions,  
 CC comprising providing a composition comprising a peptide and labeling the  
 CC N-termini of the peptide with a compound chosen from an acetamide group  
 CC and a propionamide group. Also disclosed are: a set of modified tryptic  
 CC peptides (I) comprising a first and second pool of peptides, where the N-  
 CC termini of the first and second pooled peptides are labeled with an  
 CC acetamide group and a propionamide group, respectively; and a method  
 CC of identifying a protein or peptide by searching a genomic database using  
 CC sequence information derived by directly interpreting mass spectral data.  
 CC (M1) further involves blocking lysine residues of the peptide or protein  
 CC with lithiumfluoride or O-methylisourea. N-termini are labeled with an  
 CC methyliothiourea or O-methylisourea. N-termini are labeled with an  
 CC acetamide group utilizing S-methyl thioacetamide. N-termini are  
 CC labeled with a propionamide group utilizing S-methyl  
 CC thiopropionamide. (M1) further involves dividing the peptide  
 CC composition into first and second pool of peptides, where the labeling  
 CC step involves labeling the N-termini of the peptides of the first pool of  
 CC peptides with an acetamide or amide group and labeling the N-termini  
 CC of the peptides of the second pool of peptides with a propionamide or  
 CC amide group. The present sequence represents a peptide used to  
 CC demonstrate the method of the invention.  
 XX  
 XX Sequence 19 AA;  
 Query Match 28.9%; Score 33; DB 9; Length 19;  
 Best Local Similarity 46.2%; Pred. No. 7.8e+02;

Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 DYEYPSRLGNPK 13  
| : ||||  
Db 7 DUSTPDVWGNPK 19

RESULT 36  
ABJ00309  
ID ABJ00309 standard; peptide; 14 AA.

XX AC ABJ00309,  
XX DT 02-SEP-2002 (first entry)

DE Human IGE immunogenic peptide SEQ ID NO: 93.

KW Immunogen; human; IGE; immunoglobulin E; allergy; thio-ether linkage;  
XX vaccine; anti-allergic.

OS Homo sapiens.

PN WO200216409-A2.

PD 28-FEB-2002.

PF 17-AUG-2001; 2001WO-EP009576.

PR 22-AUG-2000; 2000GB-00020717.

PA (SMIR ) SMITHKLINE BEECHAM BIOLOGICALS.  
XX (PEPT-) PEPTIDE THERAPEUTICS LTD.

PI Friede M, Mason S, Turnell WG, Vinals Y BassolsC;

DR WPI; 2002-489648/52.

PT Conjugate for use in vaccine for treatment of allergy, comprises  
XX disulfide bridge cyclized peptide and immunogenic carrier.

PS Claim 4; Page 11; 45pp; English.

XX The present invention relates to conjugates suitable for use in vaccines,  
CC where the conjugate comprises a disulphide bridge cyclised peptide and an  
CC immunogenic carrier. The vaccines can be used in the treatment of  
CC allergies. The present sequence is a peptide immunogen derived from human  
CC immunoglobulin E (IGE) suitable to be cyclised and used in the invention

XX Sequence 14 AA;

Query Match 28.1%; Score 32; DB 5; Length 14;  
Best Local Similarity 75.0%; Pred. No. 8e+02;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DYEYPSR 8  
| : ||||  
Db 1 DPEWPSR 8

RESULT 37  
AAR94744  
ID AAR94744 standard; peptide; 15 AA.

XX AAR94744;

DT 06-NOV-1996 (first entry)

DE SPNE 19b-11-715.

KW Selected principle neutralisation epitope; SPNE; HIV; Neisseria; antigen;  
KW monoclonal antibody; HIV; gp120; outer membrane proteosome complex; OMPC;  
KW SPNE-OMPC conjugate; vaccine; passive immunisation; therapy.

OS Synthetic.

PN GB2294047-A.

PD 17-APR-1996.

PF 10-OCT-1995; 95GB-00020739.

PR 14-OCT-1994; 94US-00323338.

PA (MERI ) MERCK & CO INC.

PI Arnold BA, Boots LJ, Conley AJ, Keller PM;

DR WPI; 1996-181618/19.

PT New antigenic conjugate contg. HIV-specific neutralising epitopes - bound  
XX to Neisseria outer membrane proteosome, useful in vaccines to treat or  
XX prevent HIV infection.

PS Claim 1; Page 4; 49pp; English.

CC AAR94729-R94746 represent HIV-specific, selected principal neutralisation  
CC epitopes (SPNE). AAR94739-R94745 are SPNE's identified from phage  
CC sequences by selection with the monoclonal antibody (MAb) 19b in the  
CC presence of a competing peptide (see AAR94747 and AAR94748). MAb 19b is a  
CC neutralising antibody specific for HIV gp120. These sequences are  
CC covalently bound to the purified outer membrane proteosome complex (OMPC)  
CC of Neisseria, to form antigenic conjugates. The SPNE-OMPC conjugates are  
CC used in vaccines for prevention or treatment of HIV infections. The  
CC conjugates elicit specific HIV-neutralising antibodies which may also be  
CC used in passive immunisation. The conjugates, or one of these sequences  
CC can be used to screen blood, or can be used for clinical evaluation and  
CC diagnosis of AIDS and ARC (AIDS-related complex)

XX Sequence 15 AA;

Query Match 28.1%; Score 32; DB 2; Length 15;  
Best Local Similarity 71.4%; Pred. No. 8.6e+02;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 YEYPSR 8  
| : ||||  
Db 9 YHYPGR 15

RESULT 38  
ADO17459  
ID ADO17459 standard; peptide; 15 AA.

XX ADO17459;

DT 01-JUL-2004 (first entry)

DE Differentially expressed protein Iu1 immunogenic peptide #174.

KW Immunoestimulant; Cytostatic; Vaccine; Lu1; Lu2; Lu3; Lu4; Lu5;  
KW lung cancer target protein; lung cancer; hexabrachion; tenascine C;  
KW cytotoxicin.

OS Unidentified.

PN WO2004015390-A2.

PD 19-FEB-2004.

PF 08-AUG-2003; 2003WO-US024698.

PR 09-AUG-2002; 2002US-0402057P.

PA (APPL-) APPLERA CORP.  
XX Hoffman S, Wang R, Subramanian G;  
PI

XX WPI; 2004-180755/17.  
DR  
XX  
PT Eliciting an immune response, useful in diagnosing, preventing or  
PT treating lung cancer, comprises introducing into the subject a  
PT composition comprising lung cancer target proteins.  
XX  
PS Claim 1, Fig 3; 54pp; English.  
XX  
XX The present invention relates to a method for eliciting an immune  
CC response in a subject comprising introducing into the subject a  
CC composition comprising purified peptides from differentially expressed  
CC proteins lml (AD017766), lml2 (AD017767), lml3 (AD017768), lml4 (AD017769)  
CC and lml5 (AD017770). The differentially expressed proteins lml, lml2, lml3,  
CC lml4 and lml5 bind to a specific human leukocyte antigen (HLA) allele and  
CC are lung cancer target proteins. The method is useful in eliciting an  
CC immune response and in diagnosing, preventing or treating lung cancer.  
CC The present sequence is an immunogenic peptide from lml. This peptide is  
CC a Class I/II overlapping T-cell epitope. lml is hexabrachion (tenascine C  
CC or cycloactin).  
CC  
SQ Sequence 15 AA;  
Query Match 28.1%; Score 32; DB 8; Length 15;  
Best Local Similarity 60.0%; Pred. No. 8.6e+02;  
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 3 EYFGSRLGNP 12  
Db 3 EIPGLRAGTP 12  
RESULT 39  
ADJ90073  
ID ADJ90073 standard; peptide; 16 AA.  
XX  
XX ADJ90073;  
XX  
XX 06-MAY-2004 (first entry)  
DT  
XX Human papillomavirus minor capsid protein L2 peptide #220.  
DE  
XX Human papillomavirus infection; Tsg101; viral infection; HIV; AIDS;  
KM hepatitis B virus infection; human herpesvirus 1 infection;  
KM human herpesvirus 2 infection.  
XX  
OS Human papillomavirus type 6b.  
XX  
XX WO2003053332-A2.  
PN  
XX 03-JUL-2003.  
PD  
XX 20-AUG-2002; 2002WO-US026549.  
PF  
XX 20-AUG-2001; 2001US-0313695P.  
PR  
XX (MYRI-) MYRIAD GENETICS INC.  
PA  
XX Morham S, Zavitz K, Hobden A;  
PI  
XX WPI; 2003-586940/55.  
DR  
XX  
XX Peptides and hybrid polypeptides associated with a transporter that  
PT increases its uptake by a mammalian cell, useful for inhibiting viral  
PT budding or propagation, especially for treating e.g. AIDS or hepatitis B  
PT virus infection.  
XX  
PS Claim 35; SEQ ID NO 1541; 137pp; English.  
XX  
XX The invention comprises a composition which contains a peptide associated  
CC with a transporter that is capable of increasing the uptake of the  
CC peptide by a mammalian cell. The peptide of the invention contains the  
CC amino acid motif Pro-Xaa-Xaa-Pro and is capable of binding the URY domain

CC of Tsg101. The composition of the invention is useful in the manufacture  
CC of a medicament for the treatment of viral infections, such as: HIV  
CC infection (particularly AIDS), hepatitis B virus infection and human  
CC herpesvirus 1/2 infection. The present amino acid sequence represents a  
CC peptide of the invention.  
XX  
SQ Sequence 16 AA;  
Query Match 28.1%; Score 32; DB 7; Length 16;  
Best Local Similarity 31.2%; Pred. No. 9.2e+02;  
Matches 5; Conservative 5; Mismatches 6; Indels 0; Gaps 0;  
QY 1 DYVYSGRLGNPAPL 16  
Db 1 DTFPTAPMGTPSPV 16  
RESULT 40  
AAW17560  
ID AAW17560 standard; protein; 17 AA.  
XX  
XX AAW17560;  
XX  
XX 27-JAN-1998 (first entry)  
DT  
XX  
XX Beta-B2-crystallin fragment (amino acids 145-161).  
DE  
XX Beta-A3-crystallin; lens protein; cataract; antigen; autoimmune;  
KM epithelial cell; epitope.  
XX  
XX Synthetic.  
OS Homo sapiens.  
XX  
XX EP770398-A2.  
PN  
XX 02-MAY-1997.  
PD  
XX 10-OCT-1996; 96EP-00116212.  
PF  
XX 13-OCT-1995; 95JP-00291993.  
PR  
XX (SENP ) SENJU PHARM CO LTD.  
PA  
XX  
PI Inoue B;  
XX  
XX WPI; 1997-237935/22.  
DR  
XX  
XX Composition containing lens antigen or microorganism that expresses it -  
PT used to treat or prevent cataract by reducing the level of antibodies  
PT directed against lens protein.  
XX  
XX Example 4; Page 31; 36pp; English.  
XX  
XX This sequence is an internal fragment of human beta-B2-crystallin. 17  
CC peptides constituting beta-B2-crystallin were synthesized and subjected  
CC to competitive inhibition assay of beta-B2-crystallins and respective  
CC oligopeptides. As a result, only peptide fragment amino acid residues 157  
CC -173 showed a strong binding inhibitory effect on beta-B2-crystallin.  
CC This suggests that the binding site (epitope) of beta-B2-crystallin to  
CC the antibody was present in this region (157-173). Lens antigens of  
CC sequence of amino acids numbers 162-166 of beta-B2-crystallin or a  
CC microorganism that can express a lens antigen are used in a  
CC pharmaceutical composition. The composition can be used to prepare an  
CC inhibitor of an increase of anti-lens protein antibodies. The  
CC composition, and the inhibitor can be used to treat, prevent or delay the  
CC onset of cataract. Cataract is considered to be the result of autoimmune  
CC damage to lens epithelial cells induced by lens protein  
XX  
SQ Sequence 17 AA;  
Query Match 28.1%; Score 32; DB 2; Length 17;  
Best Local Similarity 71.4%; Pred. No. 9.9e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;





PX	
PN	WO2003053332-A2.
XX	
PD	03-JUL-2003.
XX	
PF	20-AUG-2002; 2002WO-US026549.
XX	
PR	20-AUG-2001; 2001US-0313695P.
XX	
PA	(MYRI-) MYRIAD GENETICS INC.
PI	Morham S, Zavitz K, Hobden A;
DR	WPI; 2003-586940/55.
XX	
PT	Peptides and hybrid polypeptides associated with a transporter that
PT	increases its uptake by a mammalian cell, useful for inhibiting viral
PT	budding or propagation, especially for treating e.g. AIDS or hepatitis B
PT	virus infection.
PS	
PS	Claim 35; SEQ ID NO 1555; 137pp; English.
CC	
CC	The invention comprises a composition which contains a peptide associated
CC	with a transporter that is capable of increasing the uptake of the
CC	peptide by a mammalian cell. The peptide of the invention contains the
CC	amino acid motif Pro-Xaa-Xaa-Pro and is capable of binding the URY domain
CC	of Tsg101. The composition of the invention is useful in the manufacture
CC	of a medicament for the treatment of viral infections, such as: HIV
CC	infection (particularly AIDS), hepatitis B virus infection and human
CC	hepatitis 1/2 infection. The present amino acid sequence represents a
CC	peptide of the invention.
XX	
XX	Sequence 17 AA;

Query Match	28.1%	Score 32;	DB 7;	Length 17;
Best Local Similarity	31.2%	Pred. No. 9.9e+02;		
Matches	5;	Conservative	5;	Mismatches 6;
				Indels 0;
				Gaps 0;

```
QY      1 DYEPGSRIGNPKAPL 16
         |:::|:::
Db      1 DTFPTAPMGTFPSV 16
```

## RESULT 44

ID ADP74618 standard; peptide; 17 AA.

AC ADP74618;

DT 26-AUG-2004 (First entry)

DE Amino acid sequence of a DEP-1 antigen peptide.

KW human; density enhanced phosphatase-1; DEP-1; DEP-1 complex;

KM HGF receptor; scatter factor receptor; SF receptor; Met; plakoglobin;

KW cell cycle regulation; contact inhibition; cellular differentiation;

1000

XX WO2004048549-A2  
PN

XX PD 10-JTN-2004-

XX  
PF 26-NOV-2003, 2003WO-115038089

XX  
PR 26-NOV-2002 1 2002US-0429746P.

XX  
PA (COLD-) COLD SPRING HARBOR LAB.

PI Palka-Hamblyn HL, Tonks NK,

XX WPI; 2004-450367/42  
DR

PT New isolated complex comprises Density Enhanced Phosphatase-1 (DEP-1)  
PT polypeptide, useful for manipulating biological signal transduction  
PT pathways, or determining additional molecular components of the pathways

PS Example 1; Page 61; 130pp; English.

CC The specification describes density enhanced phosphatase-1 (DEP-1)  
CC complexes, comprising DEP-1 and DEP-1 substrates. DEP-1 substrate  
CC polypeptides that interact specifically with the substrate-trapping  
CC mutant form of DEP-1 are isolated from human breast tumour cell lines.  
CC These polypeptides include the functional component of p120 catenin, the  
CC adaptor protein Gab 1, the hepatocyte growth factor (HGF)/scatter factor  
CC (sf) receptor Met, a plakoglobin polypeptide, and a beta-catenin  
CC polypeptide. The DEP-1 complexes are useful for manipulating biological  
CC signal transduction pathways, including defining therapeutic targets, or  
CC determining additional molecular components of such pathways. Agents  
CC which modulate the complexes are useful for therapeutic interventions  
CC which influence biological processes, e.g. cell growth or proliferation  
CC including cell cycle regulation and contact inhibition of cell growth,  
CC cellular differentiation including altered cellular morphogenesis or  
CC motility or other cellular activities characterized by alterations in  
CC cytoskeletal organization and/or cellular gene expression, or cell  
CC survival including cellular responses to apoptotic stimuli. The present  
CC sequence represents a DEP-1 extracellular domain peptide, derived from  
CC residues 292-307, which was used to raise polyclonal antibodies.

**SQ** Sequence 17 AA;

Query Match	28.1%	Score 32	DB 8	Length 17
Best Local Similarity	66.7%	Pred. NO.	9.9e+02	
Matches 6	Conservative 1	Mismatches 2	Indels 0	Gaps 0

QY	7	SRLGNPKAP	15
		:	
Db	9	SRAGSPTAP	17

## RESULT 45

ID	ADJ90100	standard; peptide; 18 AA.

AC ADJ90100;

DT 06-MAY-2004 (first entry)

DE Human papillomavirus minor capsid protein L2 peptide #247.

KW transporter peptide; UEV domain; Tsg101; viral infection; HIV; AIDS;

KW human herpesvirus 2 infection.

OS Human papillomavirus type 6b.

PN WO2003053332-A2.

PD 03-JUL-2003

PF 20-AUG-2002; 2002WO-US026549.  
YY

PR 20-AUG-2001; 2001US-0313695P.  
XX

PA (MYRI-) MYRIAD GENETICS INC.  
XX

Pl. Mornam S, Zavitz K, Hobden A,  
XX

WP1; 2003-586940/55

PT increases its uptake by a mammalian cell, useful for inhibiting viral

PT budding or propagation, especially for treating e.g. AIDS or hepatitis B

PT	virus infection.
XX	
PS	Claim 35; SEQ ID NO 1568; 137bp; English.
CC	The invention comprises a composition which contains a peptide associated
CC	with a transporter that is capable of increasing the uptake of the
CC	peptide by a mammalian cell. The peptide of the invention contains the
CC	amino acid motif Pro-Xaa-Xaa-Pro and is capable of binding the USV domain
CC	of Tsg101. The composition of the invention is useful in the manufacture
CC	of a medicament for the treatment of viral infections, such as: HIV
CC	infection (particularly AIDS), hepatitis B virus infection and human
CC	herpesvirus 1/2 infection. The present amino acid sequence represents a
CC	peptide of the invention.
XX	
SQ	Sequence 18 AA;
Query Match	28.1%; Score 32; DB 7; Length 18;
Best Local Similarity	31.2%; Pred. No. 1.1e+03;
Matches	5; Conservative 5; Mismatches 6; Indels 0; Gaps 0
Db	1 DYEYPSRLGNPKAPL 16   :   :   :   : 3 DTFFPAHPWGTFPSPV 18
RESULT 46	
ADJ90101	
ID	ADJ90101 standard; peptide; 18 AA.
XX	
AC	ADJ90101;
DT	06-MAY-2004 (first entry)
DE	Human papillomavirus minor capsid protein L2 peptide #248.
XX	
KM	transporter peptide; USV domain; Tsg101; viral infection; HIV; AIDS;
KW	hepatitis B virus infection; human herpesvirus 1 infection;
XX	human herpesvirus 2 infection.
OS	Human papillomavirus type 6b.
XX	
PN	WO2003053332-A2.
XX	
PD	03-JUL-2003.
XX	
PF	20-AUG-2002; 2002WC-US026549.
XX	
PR	20-AUG-2001; 2001US-0313695P.
XX	
PA	(MYRI-) MYRIAD GENETICS INC.
XX	
PI	Morham S, Zavitz K, Hobden A;
XX	
DR	WPI; 2003-586940/55.
XX	
PT	Peptides and hybrid polypeptides associated with a transporter that
PT	increases its uptake by a mammalian cell, useful for inhibiting viral
PT	budding or propagation, especially for treating e.g. AIDS or hepatitis B
PT	virus infection.
XX	
PS	Claim 35; SEQ ID NO 1569; 137bp; English.
XX	
CC	The invention comprises a composition which contains a peptide associated
CC	with a transporter that is capable of increasing the uptake of the
CC	peptide by a mammalian cell. The peptide of the invention contains the
CC	amino acid motif Pro-Xaa-Xaa-Pro and is capable of binding the USV domain
CC	of Tsg101. The composition of the invention is useful in the manufacture
CC	of a medicament for the treatment of viral infections, such as: HIV
CC	infection (particularly AIDS), hepatitis B virus infection and human
CC	herpesvirus 1/2 infection. The present amino acid sequence represents a
CC	peptide of the invention.
XX	
SQ	Sequence 18 AA;

[illegible]

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XX 06-MAY-2004 (first entry)
DT Human papillomavirus minor capsid protein L2 peptide #262.
DE
XX transporter peptide; UEV domain; Tsg101; viral infection; HIV; AIDS;
XX hepatitis B virus infection; human herpesvirus 1 infection;
KM human herpesvirus 2 infection.
XX
XX Human papillomavirus type 6b.
XX
XX WO2003053332-A2.
XX
XX 03-JUL-2003.
XX
XX 20-AUG-2002; 2002WO-US026549.
XX
XX 20-AUG-2001; 2001US-0313695P.
XX
XX (MYRI-) MYRIAD GENETICS INC.
XX
XX Morham S, Zavitz K, Hobden A;
XX
XX WPI; 2003-586940/55.
XX
XX Peptides and hybrid polypeptides associated with a transporter that
PT increases its uptake by a mammalian cell, useful for inhibiting viral
PT budding or propagation, especially for treating e.g. AIDS or hepatitis B
PT virus infection.
XX
XX Claim 35; SEQ ID NO 1583; 137bp; English.
XX
XX The invention comprises a composition which contains a peptide associated
CC with a transporter that is capable of increasing the uptake of the
CC peptide by a mammalian cell. The peptide of the invention contains the
CC amino acid motif Pro-Xaa-Xaa-Pro and is capable of binding the UEV domain
CC of Tsg101. The composition of the invention is useful in the manufacture
CC of a medicament for the treatment of viral infections, such as: HIV
CC infection (particularly AIDS), hepatitis B virus infection and human
CC herpesvirus 1/2 infection. The present amino acid sequence represents a
CC peptide of the invention.
XX
XX Sequence 19 AA;
SQ
Query Match 28.1%; Score 32; DB 7; Length 19;
Best Local Similarity 31.2%; Pred. No. 1.1e+03;
Matches 5; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
QY 1 DYKPSGRLGNPKAPL 16
DB 4 DTFPTAPMGTPSPV 19

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PF 20-AUG-2002; 2002WO-US026549.
XX
XX 20-AUG-2001; 2001US-0313695P.
XX
XX (MYRI-) MYRIAD GENETICS INC.
XX
XX Morham S, Zavitz K, Hobden A;
XX
XX WPI; 2003-586940/55.
XX
XX Peptides and hybrid polypeptides associated with a transporter that
PT increases its uptake by a mammalian cell, useful for inhibiting viral
PT budding or propagation, especially for treating e.g. AIDS or hepatitis B
PT virus infection.
XX
XX Claim 35; SEQ ID NO 1585; 137bp; English.
XX
XX The invention comprises a composition which contains a peptide associated
CC with a transporter that is capable of increasing the uptake of the
CC peptide by a mammalian cell. The peptide of the invention contains the
CC amino acid motif Pro-Xaa-Xaa-Pro and is capable of binding the UEV domain
CC of Tsg101. The composition of the invention is useful in the manufacture
CC of a medicament for the treatment of viral infections, such as: HIV
CC infection (particularly AIDS), hepatitis B virus infection and human
CC herpesvirus 1/2 infection. The present amino acid sequence represents a
CC peptide of the invention.
XX
XX Sequence 19 AA;
SQ
Query Match 28.1%; Score 32; DB 7; Length 19;
Best Local Similarity 31.2%; Pred. No. 1.1e+03;
Matches 5; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
QY 1 DYKPSGRLGNPKAPL 16
DB 2 DTFPTAPMGTPSPV 17

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RESULT 49
ADJ90117
ID ADJ90117 standard; peptide; 19 AA.
XX
XX ADJ90117;
AC
XX
XX 06-MAY-2004 (first entry)
DT
XX
XX Human papillomavirus minor capsid protein L2 peptide #264.
DE
XX transporter peptide; UEV domain; Tsg101; viral infection; HIV; AIDS;
XX hepatitis B virus infection; human herpesvirus 1 infection;
KM human herpesvirus 2 infection.
XX
XX Human papillomavirus type 6b.
XX
XX WO2003053332-A2.
XX
XX 03-JUL-2003.
XX

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RESULT 50
ADJ90118
ID ADJ90118 standard; peptide; 19 AA.
XX
XX ADJ90118;
AC
XX
XX 06-MAY-2004 (first entry)
DT
XX
XX Human papillomavirus minor capsid protein L2 peptide #265.
DE
XX transporter peptide; UEV domain; Tsg101; viral infection; HIV; AIDS;
XX hepatitis B virus infection; human herpesvirus 1 infection;
KM human herpesvirus 2 infection.
XX
XX Human papillomavirus type 6b.
XX
XX WO2003053332-A2.
XX
XX 03-JUL-2003.
XX
XX 20-AUG-2002; 2002WO-US026549.
XX
XX 20-AUG-2001; 2001US-0313695P.
XX
XX (MYRI-) MYRIAD GENETICS INC.
XX
XX Morham S, Zavitz K, Hobden A;
XX
XX WPI; 2003-586940/55.
XX
XX Peptides and hybrid polypeptides associated with a transporter that
PT increases its uptake by a mammalian cell, useful for inhibiting viral
PT budding or propagation, especially for treating e.g. AIDS or hepatitis B
PT virus infection.
XX

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XX 27-JUN-2000 (first entry)  
 DT Peptide fragment of PXXP-HSCF.  
 XX  
 DB PST phosphatase interacting protein; PSTPIP; tumour therapy;  
 XX protein tyrosine phosphatase; PTP.  
 XX  
 OS Unidentified.  
 XX  
 PN US6040437-A.  
 XX  
 PD 21-MAR-2000.  
 XX  
 XX 29-SEP-1997; 97US-00938830.  
 XX  
 PR 17-APR-1997; 97US-0104590P.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Dowbenko DJ, Lasky LA,  
 XX WPI; 2000-282393/24.  
 DR  
 PT Novel genes encoding protein tyrosine phosphatase binding proteins useful  
 PT for isolating homologous genes, e.g. in tumor cells, which provide more  
 PT specific targets for tumor therapy.  
 XX  
 PS Disclosure; Col 35; 65pp; English.  
 XX  
 CC This sequence represents a fragment of a protein tyrosine phosphatase  
 CC (PTP). It was used to isolate the PST phosphatase interacting protein  
 CC (PSTPIP) sequence of the invention. The protein is a protein tyrosine  
 CC phosphatase that possesses a non-catalytic domain comprising a proline,  
 CC serine and threonine rich region and a C-terminal segment of 20 amino  
 CC acid (aa's) rich in proline, and defines an SH3 binding domain. Nucleic  
 CC acids encoding native PSTPIP molecules can be used to isolate homologous  
 CC genes specifically expressed in tumour cells, which might provide more  
 CC specific targets for tumour therapy. The DNA is also useful for the  
 CC preparation of PSTPIP polypeptides by recombinant techniques and as  
 CC hybridisation probes for searching cDNA and genomic libraries for the  
 CC coding sequence of other PSTPIP polypeptide analogues in other species  
 SO  
 SQ Sequence 20 AA;  
 Query Match 28.1%; Score 32; DB 3; Length 20;  
 Best Local Similarity 62.5%; Pred. No. 1.2e+03;  
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 QY 8 RIGRPRGP 15  
 DB 5 RIGRPRGP 12  
 RESULT 54  
 AAB08487  
 ID AAB08487 standard; peptide; 20 AA.  
 XX  
 AC AAB08487;  
 XX  
 DT 20-DEC-2000 (first entry)  
 XX  
 DE Peptide derived from a protein tyrosine phosphatase.  
 XX  
 KW protein tyrosine phosphatase; PTP; phosphatase interacting protein;  
 KW PSTPIP; PEST family; protein tyrosine phosphatase; actin monomer;  
 KW tissue typing; tumour cell; tumour imaging.  
 XX  
 OS Synthetic.  
 XX  
 PN US611073-A.  
 XX  
 PD 29-AUG-2000.

XX 06-FEB-1998; 98US-00020222.  
 PF  
 XX 17-APR-1997; 97US-0104590P.  
 PR  
 XX (GETH ) GENENTECH INC.  
 XX  
 PI Lasky LA;  
 XX WPI; 2000-586378/55.  
 DR  
 PT Novel PST phosphatase interacting protein useful for inducing of PST  
 PT polymerization of actin monomers and for identifying homolog of PST  
 PT phosphatase interacting protein.  
 XX  
 PS Disclosure; Col 34; 48pp; English.  
 XX  
 CC AAB08487-90 represent peptides derived from protein tyrosine phosphatase  
 CC (PTP). They were used to identify interaction domains of a murine protein  
 CC tyrosine phosphatase (PTP) phosphatase interacting protein (PSTPIP).  
 CC PSTPIP polypeptides are bound by and dephosphorylated by the PEST family  
 CC of protein tyrosine phosphatases. PSTPIP associates with actin. PSTPIP is  
 CC useful for inducing the polymerisation of actin monomer in eukaryotic  
 CC cells by introducing the polypeptide into the cell. The polypeptide is  
 CC useful for identifying and isolating PSTPIP homologues in another  
 CC mammalian species, in screening assays to identify antagonists and  
 CC agonists of native PSTPIP polypeptide and as molecular weight markers on  
 CC protein gels. The PSTPIP nucleic acid is useful for tissue typing of  
 CC specific mammalian tissues, for preparing PSTPIP polypeptides by  
 CC recombinant techniques, as hybridisation probes for searching cDNA and  
 CC genomic libraries for the coding sequence of other PSTPIP analogues and  
 CC to isolate homologous genes specifically expressed in tumour cells.  
 CC Antagonists of PSTPIP peptide are useful for inhibiting biological  
 CC activity of the peptide. Antibodies of PSTPIP are useful to identify  
 CC rapidly dividing cells and are used to image tumours comprising such  
 CC rapidly dividing cells  
 XX  
 SQ Sequence 20 AA;  
 Query Match 28.1%; Score 32; DB 3; Length 20;  
 Best Local Similarity 62.5%; Pred. No. 1.2e+03;  
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 QY 8 RIGRPRGP 15  
 DB 5 RIGRPRGP 12  
 RESULT 55  
 ADJ90133  
 ID ADJ90133 standard; peptide; 20 AA.  
 XX  
 AC ADJ90133;  
 XX  
 DT 06-MAY-2004 (first entry)  
 XX  
 DE Human papillomavirus minor capsid protein L2 peptide #280.  
 XX  
 KW transporter peptide; UVV domain; Tag101; viral infection; HIV; AIDS;  
 KW hepatitis B virus infection; human herpesvirus 1 infection;  
 KW human herpesvirus 2 infection.  
 XX  
 OS Human papillomavirus type 6b.  
 XX  
 PN WO2003053332-A2.  
 XX  
 PD 03-JUL-2003.  
 XX  
 PF 20-AUG-2002; 2002WO-US026549.  
 XX  
 PR 20-AUG-2001; 2001US-0313695P.  
 XX  
 PA (MYRI-) MYRIAD GENETICS INC.

```
XX Morham S, Zavitz K, Hobden A;
XX MPI; 2003-586940/55.
DR Peptides and hybrid polypeptides associated with a transporter that
PT increases its uptake by a mammalian cell, useful for inhibiting viral
PT budding or propagation, especially for treating e.g. AIDS or hepatitis B
PT virus infection.
XX
XX Claim 35; SEQ ID NO 1601, 137pp; English.
XX
XX The invention comprises a composition which contains a peptide associated
XX with a transporter that is capable of increasing the uptake of the
XX peptide by a mammalian cell. The peptide of the invention contains the
XX amino acid motif Pro-Xaa-Xaa-Pro and is capable of binding the UBV domain
XX of Tsg101. The composition of the invention is useful in the manufacture
XX of a medicament for the treatment of viral infections, such as: HIV
XX infection (particularly AIDS), hepatitis B virus infection and human
XX herpesvirus 1/2 infection. The present amino acid sequence represents a
XX peptide of the invention.
XX
XX Sequence 20 AA;
SQ
XX
XX Query Match          28.1%; Score 32; DB 7; Length 20;
XX Best Local Similarity 31.2%; Pred. No. 1.2e+03;
XX Matches 5; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
QY 1 DYEPGSRIGNPKAPL 16
XX | : : | : : | : :
DB 3 DITFPTAPMGTPFSPV 18
XX
XX
XX RESULT 56
XX ID ADJ90135 standard; peptide; 20 AA.
XX
XX ADJ90135;
XX
XX 06-MAY-2004 (first entry)
XX
XX Human papillomavirus minor capsid protein L2 peptide #282.
XX
XX transporeter peptide; UBV domain; Tsg101; viral infection; HIV; AIDS;
XX hepatitis B virus infection; human herpesvirus 1 infection;
XX human herpesvirus 2 infection.
XX
XX Human papillomavirus type 6b.
XX
XX WO2003053332-A2.
XX
XX 03-JUL-2003.
XX
XX 20-AUG-2002; 2002WO-US026549.
XX
XX 20-AUG-2001; 2001US-0313695P.
XX
XX (MYRI-) MYRIAD GENETICS INC.
XX
XX Morham S, Zavitz K, Hobden A;
XX
XX MPI; 2003-586940/55.
XX
XX Peptides and hybrid polypeptides associated with a transporter that
XX increases its uptake by a mammalian cell, useful for inhibiting viral
XX budding or propagation, especially for treating e.g. AIDS or hepatitis B
XX virus infection.
XX
XX Claim 35; SEQ ID NO 1603, 137pp; English.
XX
XX The invention comprises a composition which contains a peptide associated
XX with a transporter that is capable of increasing the uptake of the
XX peptide by a mammalian cell. The peptide of the invention contains the
```

```
CC amino acid motif Pro-Xaa-Xaa-Pro and is capable of binding the UBV domain
CC of Tsg101. The composition of the invention is useful in the manufacture
CC of a medicament for the treatment of viral infections, such as: HIV
CC infection (particularly AIDS), hepatitis B virus infection and human
CC herpesvirus 1/2 infection. The present amino acid sequence represents a
CC peptide of the invention.
CC
CC Sequence 20 AA;
SQ
XX
XX Query Match          28.1%; Score 32; DB 7; Length 20;
XX Best Local Similarity 31.2%; Pred. No. 1.2e+03;
XX Matches 5; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
QY 1 DYEPGSRIGNPKAPL 16
XX | : : | : : | : :
DB 1 DITFPTAPMGTPFSPV 16
XX
XX
XX RESULT 57
XX ID ADJ90132 standard; peptide; 20 AA.
XX
XX ADJ90132;
XX
XX 06-MAY-2004 (first entry)
XX
XX Human papillomavirus minor capsid protein L2 peptide #279.
XX
XX transporeter peptide; UBV domain; Tsg101; viral infection; HIV; AIDS;
XX hepatitis B virus infection; human herpesvirus 1 infection;
XX human herpesvirus 2 infection.
XX
XX Human papillomavirus type 6b.
XX
XX WO2003053332-A2.
XX
XX 03-JUL-2003.
XX
XX 20-AUG-2002; 2002WO-US026549.
XX
XX 20-AUG-2001; 2001US-0313695P.
XX
XX (MYRI-) MYRIAD GENETICS INC.
XX
XX Morham S, Zavitz K, Hobden A;
XX
XX MPI; 2003-586940/55.
XX
XX Peptides and hybrid polypeptides associated with a transporter that
XX increases its uptake by a mammalian cell, useful for inhibiting viral
XX budding or propagation, especially for treating e.g. AIDS or hepatitis B
XX virus infection.
XX
XX Claim 35; SEQ ID NO 1600, 137pp; English.
XX
XX The invention comprises a composition which contains a peptide associated
XX with a transporter that is capable of increasing the uptake of the
XX peptide by a mammalian cell. The peptide of the invention contains the
XX amino acid motif Pro-Xaa-Xaa-Pro and is capable of binding the UBV domain
XX of Tsg101. The composition of the invention is useful in the manufacture
XX of a medicament for the treatment of viral infections, such as: HIV
XX infection (particularly AIDS), hepatitis B virus infection and human
XX herpesvirus 1/2 infection. The present amino acid sequence represents a
XX peptide of the invention.
XX
XX Sequence 20 AA;
SQ
XX
XX Query Match          28.1%; Score 32; DB 7; Length 20;
XX Best Local Similarity 31.2%; Pred. No. 1.2e+03;
XX Matches 5; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
QY 1 DYEPGSRIGNPKAPL 16
XX | : : | : : | : :
DB 1 DITFPTAPMGTPFSPV 16
XX
```

Db 4 DITFPTAPMGTPFSPV 19

RESULT 58  
AD700134

ADJ90134  
ID ADJ90134 standard; peptide; 20 AA.

AC ADJ90134 ;

DT 06-MAY-2004 (first entry)

DE Human papillomavirus minor capsid protein L2 peptide #281.

KW transporter peptide; UEV domain; Tsg101; viral infection; HIV; AIDS;

KW human herpesvirus 2 infection.

OS Human papillomavirus type 6b.

PN WO2003053332-A2.

PD 03-JUL-2003.

PF 20-AUG-2002; 2002WO-US026549.

PR 20-AUG-2001; 2001US-0313695P.

PA (MYRI-) MYRIAD GENETICS INC.

PI Morham S, Zavltz K, Hobder

DR WPI; 2003-586940/55.

PT Peptides and hybrid

PT budding or propagation, especially for treating e.g. AIDS or hepatitis B

**XX**

32

CC with a transporter that is capable of increasing the uptake of the

amino acid motif Pro-Xaa-Xaa-Pro and is c

CC of a medicament for the treatment of viral infections, such as: HIV

CC herpesvirus 1/2 infection. The present amino acid sequence represents a

3  
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:  
:

1. The first step is to identify the problem or question that needs to be answered. This involves understanding the context and the specific requirements of the task.

Best Local Similarity 31.28; Pred. No. 1.2e+03;

100

—	—
..	..
—	—
..	..
—	—
..	..
—	—
..	..
—	—
..	..

RESULT 59

ID	ADJ90131	standard; peptide; 20 AA.
.....		

AC ADJ90131;  
.....

DT 06-MAY-2004 (First entry)

DE Human papillomavirus minor capsid protein L2 peptide #278.

KW transporter peptide; UEV domain; Tsg101; viral infection; HIV; AIDS;

27

PI Boulikas T;  
 XX WPI; 2002-164295/21.  
 DR  
 XX  
 PT Encapsulation of plasmid DNA (lipogenes) and therapeutic agents with  
 PT nuclear localization signal/fusogenic peptide conjugates into targeted  
 PT liposome complexes.  
 XX  
 PS Claim 14; Page 62; 107pp; English.  
 CC The present invention describes a method for producing micelles with  
 CC entrapped therapeutic agents. The method comprises: (1) combining  
 CC negatively charged agent with a cationic lipid in a ratio where 30-90 %  
 CC of the negatively charged atoms are neutralised by positive charges on  
 CC lipid molecules to form an electrostatic micelle complex in 20-80 %  
 CC ethanol; and (2) combining the micelle complex of (a) with fusogenic-  
 CC karyophilic peptide conjugates in a 0.0-0.3 ratio, therefore producing  
 CC micelles with entrapped therapeutic agents. Also described is a method  
 CC for delivering a therapeutic agent in vivo, comprising the administration  
 CC of the micelle. ABB74256 to ABB74858 represent specifically claimed  
 CC nuclear localisation signal (NLS) peptides for use in the method as the  
 CC fusogenic-karyophilic peptides. The micelles produced can have cytostatic  
 CC and antitumour activities. The peptide-lipid-polynucleotide complexes  
 CC produced are useful for inhibiting the progression of neoplastic  
 CC diseases. The invention relates to the field of gene therapy and is  
 CC directed toward methods for producing peptide-lipid-polynucleotide  
 CC complexes suitable for delivery of polynucleotides. The encapsulated  
 CC molecules display therapeutic efficacy in eradicating solid tumours  
 CC including but not limited to breast carcinoma or prostate carcinoma.  
 CC ABB74235 to ABB74255 are used in the exemplification of the present  
 CC invention  
 CC  
 SQ Sequence 9 AA;  
 XX  
 Query Match 27.2%; Score 31; DB 5; Length 9;  
 Best Local Similarity 62.5%; Pred. No. 2e+06;  
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 QY 3 EYPSGRLG 10  
 : : | | | |  
 Db 2 KHPGKRLG 9  
 RESULT 61  
 ABB74355  
 ID ABB74355 standard; peptide; 9 AA.  
 XX  
 AC ABB74355;  
 XX  
 DT 18-APR-2002 (first entry)  
 XX  
 DE Karyophilic peptide SEQ ID NO:119.  
 XX  
 KW Fusogenic; nuclear localisation signal; NLS; encapsulation; lipogene;  
 KW liposome; micelle; karyophilic; cytosstatic; antitumour; solid tumour;  
 KW peptide-lipid-polynucleotide complex; neoplastic disease; gene therapy;  
 KW breast carcinoma; prostate carcinoma.  
 XX  
 OS Bos taurus.  
 OS Homo sapiens.  
 XX  
 PN WO200193836-A2.  
 XX  
 PD 13-DEC-2001.  
 XX  
 PF 08-JUN-2001; 2001WO-US018657.  
 XX  
 PR 09-JUN-2000; 2000US-0210925P.  
 XX  
 PA (BOUL/) BOULIKAS T.  
 XX  
 PI Boulikas T;  
 XX

DR WPI; 2002-164295/21.  
 XX  
 PT Encapsulation of plasmid DNA (lipogenes) and therapeutic agents with  
 PT nuclear localization signal/fusogenic peptide conjugates into targeted  
 PT liposome complexes.  
 XX  
 PS Claim 14; Page 62; 107pp; English.  
 CC The present invention describes a method for producing micelles with  
 CC entrapped therapeutic agents. The method comprises: (1) combining  
 CC negatively charged agent with a cationic lipid in a ratio where 30-90 %  
 CC of the negatively charged atoms are neutralised by positive charges on  
 CC lipid molecules to form an electrostatic micelle complex in 20-80 %  
 CC ethanol; and (2) combining the micelle complex of (a) with fusogenic-  
 CC karyophilic peptide conjugates in a 0.0-0.3 ratio, therefore producing  
 CC micelles with entrapped therapeutic agents. Also described is a method  
 CC for delivering a therapeutic agent in vivo, comprising the administration  
 CC of the micelle. ABB74256 to ABB74858 represent specifically claimed  
 CC nuclear localisation signal (NLS) peptides for use in the method as the  
 CC fusogenic-karyophilic peptides. The micelles produced can have cytostatic  
 CC and antitumour activities. The peptide-lipid-polynucleotide complexes  
 CC produced are useful for inhibiting the progression of neoplastic  
 CC diseases. The invention relates to the field of gene therapy and is  
 CC directed toward methods for producing peptide-lipid-polynucleotide  
 CC complexes suitable for delivery of polynucleotides. The encapsulated  
 CC molecules display therapeutic efficacy in eradicating solid tumours  
 CC including but not limited to breast carcinoma or prostate carcinoma.  
 CC ABB74235 to ABB74255 are used in the exemplification of the present  
 CC invention  
 CC  
 SQ Sequence 9 AA;  
 XX  
 Query Match 27.2%; Score 31; DB 5; Length 9;  
 Best Local Similarity 62.5%; Pred. No. 2e+06;  
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 QY 3 EYPSGRLG 10  
 : : | | | |  
 Db 2 KHPGKRLG 9  
 RESULT 62  
 ABB74364  
 ID ABB74364 standard; peptide; 9 AA.  
 XX  
 AC ABB74364;  
 XX  
 DT 18-APR-2002 (first entry)  
 XX  
 DE Karyophilic peptide SEQ ID NO:128.  
 XX  
 KW Fusogenic; nuclear localisation signal; NLS; encapsulation; lipogene;  
 KW liposome; micelle; karyophilic; cytosstatic; antitumour; solid tumour;  
 KW peptide-lipid-polynucleotide complex; neoplastic disease; gene therapy;  
 KW breast carcinoma; prostate carcinoma.  
 XX  
 OS Rattus sp.  
 XX  
 PN WO200193836-A2.  
 XX  
 PD 13-DEC-2001.  
 XX  
 PF 08-JUN-2001; 2001WO-US018657.  
 XX  
 PR 09-JUN-2000; 2000US-0210925P.  
 XX  
 PA (BOUL/) BOULIKAS T.  
 XX  
 PI Boulikas T;  
 XX  
 DR WPI; 2002-164295/21.  
 XX  
 PT Encapsulation of plasmid DNA (lipogenes) and therapeutic agents with



PT nuclear localization signal/fusogenic peptide conjugates into targeted  
XX liposome complexes.

PS Claim 14, Page 62, 107pp, English.

XX The present invention describes a method for producing micelles with  
CC entrapped therapeutic agents. The method comprises: (1) combining  
CC negatively charged agent with a cationic lipid in a ratio where 30-90 %  
CC of the negatively charged atoms are neutralised by positive charges on  
CC lipid molecules to form an electrostatic micelle complex in 20-80 %  
CC ethanol; and (2) combining the micelle complex of (a) with fusogenic-  
CC karyophilic peptide conjugates in a 0.0-0.3 ratio, therefore producing  
CC micelles with entrapped therapeutic agents. Also described is a method  
CC for delivering a therapeutic agent in vivo, comprising the administration  
CC of the micelle. ABB74256 to ABB74858 represent specifically claimed  
CC nuclear localization signal (NLS) peptides for use in the method as the  
CC fusogenic-karyophilic peptides. The micelles produced can have cytoskeletal  
CC and antitumour activities. The peptide-lipid-polynucleotide complexes  
CC produced are useful for inhibiting the progression of neoplastic  
CC diseases. The invention relates to the field of gene therapy and is  
CC directed toward methods for producing peptide-lipid-polynucleotide  
CC complexes suitable for delivery of polynucleotides. The encapsulated  
CC molecules display therapeutic efficacy in eradicating solid tumours  
CC including but not limited to breast carcinoma or prostate carcinoma.  
CC ABB74235 to ABB74255 are used in the exemplification of the present  
CC invention

XX Sequence 9 AA;

SO

Query Match 27.2%; Score 31; DB 5; Length 9;  
Best Local Similarity 62.5%; Pred. No. 2e+06;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 EYPGSRIG 10  
:::|||||  
DB 2 KHPGKRLG 9

RESULT 63  
AAB61173  
ID AAB61173 standard; peptide; 12 AA.

XX AAB61173;

AC 02-APR-2001 (first entry)

XX Anopheles albimanus anophelin peptide fragment #1.

DE Anopheles albimanus anophelin peptide fragment #1.

XX Anopheles albimanus; anophelin; anticoagulant; cardiac;  
KW cerebroprotective; thrombolytic; vulnerary; vasotropic;  
KW alpha-thrombin inhibitor; clot formation inhibitor; anticoagulant;  
KW thrombolysis; angina; arteriosclerosis.

XX Anopheles albimanus.

OS WO200100667-A2.

PN 04-JAN-2001.

XX 29-JUN-2000; 2000WO-US018078.

PF 29-JUN-1999; 99US-014123P.

XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.

PA Valenzuela JG, Ribetto J, Francischetti I;  
XX MPI, 2001-137934/14.

DR N-PSDB; AAF28388, AAF28389.

XX Antithrombin peptide, anophelin isolated from salivary glands of  
PT Anopheles albimanus, useful as anticoagulants to inhibit thrombin  
PT activity in subjects suffering from myocardial infarction or stroke.

XX Example 4; Page 19; 78pp, English.

PS

XX The present sequence is given in a specification relating to a purified  
CC or synthetic protein having anophelin biological activity. Compositions  
CC comprising this protein are useful for inhibiting thrombin activity in  
CC humans suffering from a condition such as myocardial infarction, stroke,  
CC pulmonary embolism, deep vein thrombosis, peripheral arterial occlusion,  
CC disseminated intravascular coagulation, cardiovascular and  
CC cerebrovascular thrombosis, thrombosis associated with post-operative  
CC trauma, obesity, pregnancy, side effects of oral contraceptives,  
CC prolonged immobilisation, and hypercoagulable states associated with  
CC haematologic, immunologic or rheumatologic disorders. The protein may  
CC also be useful for treating unstable angina, arteriosclerosis, redocking  
CC of vessels after angioplasty with a balloon catheter, or blood clotting  
CC in haemodialysis. It is also used as anticoagulant to inhibit thrombin  
CC activity by inhibiting platelet aggregation in extracorporeal blood

XX Sequence 12 AA;

SO

Query Match 27.2%; Score 31; DB 4; Length 12;  
Best Local Similarity 54.5%; Pred. No. 9.6e+02;  
Matches 6; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5 PGSRIGNPKAP 15  
||| |||  
DB 2 PGRRLGSGSKP 12

RESULT 64  
ADY62107  
ID ADY62107 standard; peptide; 12 AA.

XX ADY62107;

AC 19-MAY-2005 (first entry)

XX S\_marcescens chitinase A/ chitobiase proteins consensus peptide Seq 122.

DE S\_marcescens chitinase A/ chitobiase proteins consensus peptide Seq 122.

XX combinatorial library; DNA recombination; chitinase;  
KW beta-N-acetylhexosaminidase; chitobiase.

XX Serratia marcescens.

OS US2005053989-A1.

PN 10-MAR-2005.

XX 26-AUG-2004; 2004US-00926542.

PF 27-AUG-2003; 2003US-0497924P.

XX (SHAR/) SHARON G.  
PA (LABN/) LABAN A.

XX Sharon G, Laban A;  
PI MPI, 2005-221920/23.

XX Generating divergent libraries of chimeric proteins, comprises  
PT transfecting a host with a polynucleotide obtained by recombination  
PT between nucleotides encoding consensus amino acid sequences.

XX Disclosure; SEQ ID NO 122; 60pp; English.

PS

XX This invention relates to a novel method for generating divergent  
CC libraries of recombinant chimeric proteins. Specifically, it refers to a  
CC method that induces recombination between several distinct, uniform and  
CC predefined regions of overlapping polynucleotides encoding sequences with  
CC consensus polypeptides that correspond to sequences conserved in several  
CC related proteins. As such, this provides a route by which to produce  
CC chimeric polynucleotides, which can then be transfected into a host with  
CC the polynucleotides. The present invention describes using this method

CC for generating divergent libraries of several recombinant chimeric  
CC proteins to enable production of recombinant chimeric proteins in a less  
CC expensive, less labor-intensive and more efficient procedure. The  
CC shuffling between variable regions are essentially devoid of sequence  
CC homology, and it maintains the consensus backbone, increases the  
CC production of active enzymes while retaining high diversity and improved  
CC properties, thus, it is more favorable and generates important enzyme  
CC variants. In particular, it refers to the creation of a recombinant  
CC library of chimeric lipase proteins using four parental lipase genes from  
CC various *Candida* species that share little DNA homology but exhibit  
CC notable protein similarity. A second recombinant library refers to  
CC chimeric chitinase A/ chitinase proteins. This peptide sequence is  
CC identified as a conserved region between *Serratia marcescens* chitinase A  
CC and chitinase (beta-N-acetylhexosaminidase) proteins, given in figure 7  
CC of the invention.

XX Sequence 12 AA;

Query Match 27.2%; Score 31; DB 9; Length 12;  
Best Local Similarity 50.0%; Pred. No. 9.6e+02;  
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYEPGSR 8  
|:|:|:|:  
DB 5 DWEFGGK 12

RESULT 65

ID AD237873 standard; peptide; 13 AA.

XX AD237873;

XX 30-JUN-2005 (first entry)

XX Human kinase substrate peptide SEQ ID 803.

KW Kinase; substrate; drug delivery; cancer; restenosis; osteoporosis;  
KW rheumatoid arthritis; asthma; psoriasis; inflammatory bowel disease;  
KW systemic lupus erythematosus; multiple sclerosis; transplant rejection;  
KW neoplasm; cytostatic; vasotropic; cardiovascular disease; osteopathic;  
KW degeneration; endocrine disease; musculoskeletal disease;  
KW antiinflammatory; inflammation; autoimmune disease; immunosuppressive;  
KW immune disorder; antihypertensive; antirheumatic; antidiabetic;  
KW respiratory disease; antiproliferative; dermatological disease;  
KW gastrointestinal gen.; gastrointestinal disease; neuroprotective;  
KW gastrointestinal disease; dermatological; dermatological disease.

XX Homo sapiens.

XX MO2005035003-A2.

XX 21-APR-2005.

XX 22-SEP-2004; 2004WO-US031148.

XX 22-SEP-2003; 2003US-0505325P.

XX 04-MAY-2004; 2004US-0568340P.

XX 22-JUN-2004; 2004US-0581835P.

XX (DIHE-) DIHEDRON CORP.

XX Ballatore C, Castellino AJ, Desharnais J, Guo Z, Li Q, Newman MJ,  
PI Sun C,

XX WPI; 2005-315493/32.

PT New conjugate used for treating aberrant cellular activation, migration,  
PT proliferation or survival condition such as cancer, comprises drug and  
PT substrate for protein or lipid kinase linked to protein, optionally by  
PT non-releasable linker.

XX Disclosure; SEQ ID NO 803; 407bp; English.

XX The invention relates to a conjugate (I) comprising a drug and a  
CC substrate for a protein kinase or a lipid kinase non-releasably linked to  
CC it, optionally by a non-releasable linker. Also included are preparing  
CC a pacitaxel C10 carbamate of formula (8a) (which comprises reacting a  
CC pacitaxel compound of formula (5a) with a carbodimide compound and  
CC reacting the obtained compound of formula (6a) with an amine of formula  
CC X, all formulae given in the specification), a pharmaceutical composition  
CC (PCI) comprising (I) and a carrier, an article (comprising packaging  
CC material, (I) or its derivatives, for treatment/prevention/amelioration  
CC of one or more symptoms (associated with aberrant cellular activation,  
CC migration, proliferation or survival (ACMPs) and a label that indicates  
CC that (I) is used for treatment, prevention or amelioration of one or more  
CC symptoms associated with ACMPs), and a peptide comprising an ACMP  
CC substrate peptide. The conjugate has improved cytotoxic selectivity index  
CC as compared to an unconjugated drug. The conjugate is useful for treating  
CC conditions caused by ACMPs characterized by undesirable or aberrant  
CC activation, migration, proliferation or survival of tumor cells,  
CC endothelial cells, B cells, T cells, macrophages, neutrophils,  
CC eosinophils, basophils, monocytes, platelets, fibroblasts, other  
CC connective tissue cells, osteoblasts, osteoclasts and progenitors of  
CC these cell types. The ACMPs condition is a cancer, coronary restenosis,  
CC osteoporosis, chronic inflammation or autoimmunity disease. The  
CC autoimmune disease is rheumatoid arthritis, asthma, psoriasis,  
CC inflammatory bowel disease, systemic lupus erythematosus, systemic  
CC dermatomyositis, inflammatory optic neuropathy, autoimmune hematologic  
CC disorders, multiple sclerosis, vasculitis, idiopathic nephrotic syndrome,  
CC transplant rejection or graft versus host disease. The cancer is non-  
CC small cell lung cancer, head squamous cancer, neck squamous cancer,  
CC colorectal cancer, prostate cancer, breast cancer, acute lymphocytic  
CC leukemia, adult acute myeloid leukemia, adult non-Hodgkin's lymphoma,  
CC brain tumor, cervical cancer, childhood cancer, childhood sarcoma,  
CC chronic lymphocytic leukemia, chronic myeloid leukemia, esophageal  
CC cancer, hairy cell leukemia, kidney cancer, liver cancer, multiple  
CC myeloma, neuroblastoma, oral cancer, pancreatic cancer, primary central  
CC nervous system lymphoma, skin cancer or small-cell lung cancer. The  
CC cancer is brain stem glioma, cerebellar astrocytoma, cerebral  
CC astrocytoma, ependymoma, Ewing's sarcoma, germ cell tumor, Hodgkin's  
CC disease, acute myelogenous leukemia, acute lymphoblastic leukemia, liver  
CC cancer, medulloblastoma, neuroblastoma, non-Hodgkin's lymphoma,  
CC osteosarcoma, malignant fibrous histiocytoma of bone, retinoblastoma,  
CC rhabdomyosarcoma, soft tissue sarcoma, supratentorial primitive  
CC neuroectodermal and pineal tumors, visual pathway and hypothalamic  
CC glioma, Wilms' tumor or other childhood kidney tumor. The cancer is  
CC originated from or has metastasized to the bone, brain, breast, digestive  
CC and gastrointestinal system, endocrine system, blood, lung, respiratory  
CC system, thorax, musculoskeletal system, or skin. The cancer is selected  
CC from breast cancer, lung cancer, prostate cancer, ovarian cancer,  
CC esophageal cancer, bladder cancer, hepatoma, neuroblastoma, lymphoma,  
CC testicular cancer, renal cancer, leukemia, colorectal cancer and head and  
CC neck cancer. The conjugate is useful for identifying kinase substrates  
CC capable of selectively accumulating in a target system. The conjugate is  
CC useful for identifying conjugates capable of exhibiting selective  
CC toxicity against a target system. The conjugate is useful for enhancing  
CC drug efficiency. The present sequence is kinase substrate peptide useful  
CC in the conjugate of the invention.

XX Sequence 13 AA;

Query Match 27.2%; Score 31; DB 9; Length 13;  
Best Local Similarity 54.5%; Pred. No. 1e+03;  
Matches 6; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5 PGRSLGNRPKAP 15  
| | | | |  
DB 2 PGRSRRTPSLP 12

RESULT 66

ID ABP46490 standard; peptide; 14 AA.

XX ABP46490;

XX 19-AUG-2002 (first entry)  
 DT  
 XX Human Blys binding scFv VH CDR3 SEQ ID 2501.  
 DE  
 XX Blys/ B lymphocyte stimulator; TNF superfamily; human; cytostatic;  
 KW tumour necrosis factor; B cell proliferation; B cell differentiation;  
 KW immunosuppressive; immunomodulator; antirheumatic;  
 KW arthritis vaccine; cancer; immune; autoimmune disorder; immunodeficiency;  
 KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;  
 KW common variable immunodeficiency; acquired immunodeficiency syndrome.  
 OS  
 XX Homo sapiens.  
 PN WO200202641-A1.  
 XX  
 PD 10-JAN-2002.  
 XX  
 PF 15-JUN-2001; 2001MO-US019110.  
 XX  
 PR 16-JUN-2000; 2000US-0212210P.  
 PR 17-OCT-2000; 2000US-0240816P.  
 PR 16-MAR-2001; 2001US-0276248P.  
 PR 21-MAR-2001; 2001US-0277379P.  
 PR 25-MAY-2001; 2001US-0293499P.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 PA (CMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.  
 XX  
 PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;  
 PI WPI, 2002-114799/15.  
 XX  
 DR Antibodies against B lymphocyte stimulating polypeptides, useful for the  
 PT diagnosis and treatment of cancers and immune disorders.  
 XX  
 PS Claim 2, Page 3001, 3148pp; English.  
 XX  
 CC This invention describes novel antibodies that immunospecifically bind to  
 CC B lymphocyte stimulator (Blys) polypeptides. Blys is a member of the  
 CC tumour necrosis factor (TNF) super family and induces B cell  
 CC proliferation and differentiation. The antibodies of the invention have  
 CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,  
 CC antirheumatic and antiAIDS activity and can be used in vaccines to  
 CC inhibit the expression and activity of Blys. The antibodies bind to Blys  
 CC and so may be used to detect and quantitate the presence of Blys in  
 CC biological samples and may be used in this way to diagnose disease  
 CC associated with aberrant expression of Blys. They may also be  
 CC administered to treat diseases associated with aberrant Blys expression  
 CC and activity such as cancer, immune, and autoimmune disorders and  
 CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,  
 CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and  
 CC acquired immunodeficiency syndrome (AIDS)). ABP4390-ABP47228 represent  
 CC the antibodies and fragments of the antibodies described in the method of  
 CC the invention  
 CC  
 SO Sequence 14 AA;  
 Query Match 27.2%; Score 31; DB 5; Length 14;  
 Best Local Similarity 83.3%; Pred. No. 1.1e+03;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 12 PKAPLY 17  
 | : | | | |  
 Db 8 PRAPLY 13  
 RESULT 67  
 ID ADG97317 standard; peptide, 14 AA.  
 XX  
 AC ADG97317,  
 XX

DT 11-MAR-2004 (first entry)  
 XX  
 XX scFv VHCDR3 peptide that immunospecifically binds Blys SeqID 2501.  
 DE  
 XX antibody; B lymphocyte stimulator; Blys; tumour necrosis factor;  
 KW B cell proliferation; differentiation; scFv; myasthenia gravis;  
 KW multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukaemia;  
 KW carcinoma; lymphoma; antirheumatic; antiarthritic; neuroprotective;  
 KW antiinflammatory; antiasthmatic; antiallergic; cytostatic.  
 XX  
 OS Unidentified.  
 XX  
 PN WO2003055979-A2.  
 XX  
 PD 10-JUL-2003.  
 XX  
 PF 14-NOV-2002; 2002MO-US036496.  
 XX  
 PR 16-NOV-2001; 2001US-0331469P.  
 PR 19-DEC-2001; 2001US-0340817P.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;  
 PI WPI, 2003-505330/47.  
 XX  
 DR Novel antibody that immunospecifically binds to a B lymphocyte stimulator  
 PT (Blys), useful for detecting and treating diseases or disorders e.g.  
 PT rheumatoid arthritis, asthma and leukemia.  
 XX  
 PS Example 1; SEQ ID NO 2501; 394pp; English.  
 XX  
 CC This invention relates to novel antibodies that immunospecifically bind  
 CC to B lymphocyte stimulator (Blys). The Blys gene has been mapped to  
 CC chromosome 13q34 and encodes a protein that is a member of the tumour  
 CC necrosis factor superfamily and induces both in vivo and in vitro B cell  
 CC proliferation and differentiation. Specifically, it refers to single  
 CC chain antibody molecules (scFvs) derived, preferably, from the variable  
 CC heavy CDR3 region that immunospecifically bind to a polypeptide, or  
 CC fragment thereof, of either human, murine, rat or monkey Blys. The  
 CC present invention refers to the use of such antibodies in various methods  
 CC for the detection, diagnosis and prognosis of diseases related to the  
 CC aberrant expression or inappropriate function of Blys or its receptor. As  
 CC such, these compositions are useful for identifying immune disorders  
 CC including myasthenia gravis and multiple sclerosis, inflammatory  
 CC disorders e.g. asthma and rheumatoid arthritis, infectious diseases such  
 CC as AIDS and proliferative disorders including leukaemia, carcinoma and  
 CC lymphoma. Accordingly, they can be described as exhibiting various  
 CC activities such as antirheumatic, antiarthritic, neuroprotective,  
 CC antiinflammatory, antiasthmatic, antiallergic and cytostatic. This  
 CC peptide sequence is a single chain antibody variable heavy CDR3 peptide  
 CC that immunospecifically binds Blys of the invention.  
 CC  
 SO Sequence 14 AA;  
 Query Match 27.2%; Score 31; DB 7; Length 14;  
 Best Local Similarity 83.3%; Pred. No. 1.1e+03;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 12 PKAPLY 17  
 | : | | | |  
 Db 8 PRAPLY 13

RESULT 68  
 ID AAB86601 standard; peptide, 15 AA.  
 XX  
 AC AAB86601;  
 XX  
 DT 20-NOV-2001 (first entry)  
 XX

DE	Human cytomegalovirus strain AD169 IEI peptide fragment SEQ ID 58.
XX	
KW	Antigen-specific stimulation; T-lymphocyte; CD8 stimulation; pp65;
KM	CD4 stimulation; immuno-stimulation; IEI, lower matrix phosphoprotein.
XX	
OS	Human cytomegalovirus.
XX	
PN	WO200163286-A2.
XX	
PD	30-AUG-2001.
XX	
XX	
PF	17-FEB-2001; 2001MO-EP001773.
XX	
PR	22-FEB-2000; 2000DE-01009341.
XX	
PA	(KERN/) KERN F.
XX	
PI	Kern F, Volk H, Reinke P, Paulhaber N, Surel I, Khatazmas E;
XX	
DR	WPI, 2001-557718/62.
XX	
PT	Stimulating CD8 or CD4 T cells for the immuno-stimulation of mammals and
XX	
PT	the determination of the response to the antigen comprises using a
XX	
PT	synthetic peptide library of the specific antigen.
XX	
PS	Example; Fig 1; 85pp; German.
XX	
CC	This sequence represents a novel method for stimulating CD8 or CD4 T
XX	
CC	cells for the immuno-stimulation of mammals and the determination of the
XX	
CC	response to an antigen (I). The method comprises (i) dividing the amino
XX	
CC	acid sequence of the antigen into protein fragments (II) of at least 9
XX	
CC	amino acids, whereby adjacent or neighbouring fragments are in the whole
XX	
CC	antigen sequence; (ii) synthesizing a peptide library containing (ii);
XX	
CC	and (iii) incubating the CD8 and/or CD4 T lymphocytes in a suspension
XX	
CC	comprising (II) in a single culture vessel. The method is used to immuno-
XX	
CC	stimulate T cells of mammals, particularly humans, and is also useful for
XX	
CC	diagnostic purposes to determine if a mammal, especially human, has
XX	
CC	previously immunologically responded to a specific protein, and to
XX	
CC	determine strength of that response. The method is suitable for in vivo
XX	
CC	or in vitro immuno-stimulation of mammalian, more preferably human T
XX	
CC	lymphocytes, where the stimulation of T lymphocytes are expanded and can be
XX	
CC	transfused into a patient. AAB86544-AAB86803 represent fragments of the
XX	
CC	human cytomegalovirus IEI and pp65 lower matrix phosphoprotein which are
XX	
CC	used to illustrate the method of the invention
XX	
SQ	Sequence 15 AA;
Query Match	27.2%; Score 31; DB 4; Length 15;
Best Local Similarity	35.7%; Pred. No. 1.2e+03;
Matches	5; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
OY	5 PGSRLGNPKAPLYK 18  ::: :: :
Db	2 PSSKVPRPRTVPVK 15
RESULT 69	
ADJ90060	
ID	ADJ90060 standard; peptide; 15 AA.
XX	
AC	ADJ90060;
XX	
DT	06-MAY-2004 (first entry)
XX	
DE	Human papillomavirus minor capsid protein L2 peptide #207.
XX	
KW	transporter peptide; UEV domain; Tag101; viral infection; HIV; AIDS;
KM	hepatitis B virus infection; human herpesvirus 1 infection;
KX	human herpesvirus 2 infection.
XX	
OS	Human papillomavirus type 6b.
XX	
PN	WO2003053332-A2.

XX	03-JUL-2003.
PD	
XX	20-AUG-2002; 2002WO-US026549.
PF	
XX	20-AUG-2001; 2001US-0313695P.
PR	
XX	(MYRI-) MYRIAD GENETICS INC.
PA	
XX	Morham S, Zavitz K, Hobden A;
PI	
XX	WPI; 2003-586940/55.
DR	
XX	
PT	Peptides and hybrid polypeptides associated with a transporter that
PT	increases its uptake by a mammalian cell, useful for inhibiting viral
PT	budding or propagation, especially for treating e.g. AIDS or hepatitis B
XX	virus infection.
XX	
PS	Claim 35, SEQ ID NO 1528, 137pp; English.
XX	
CC	The invention comprises a composition which contains a peptide associated
CC	with a transporter that is capable of increasing the uptake of the
CC	peptide by a mammalian cell. The peptide of the invention contains the
CC	amino acid motif Pro-Xaa-Xaa-Pro and is capable of binding the UBV domain
CC	of Tsg101. The composition of the invention is useful in the manufacture
CC	of a medicament for the treatment of viral infections, such as: HIV
CC	infection (particularly AIDS), hepatitis B virus infection and human
CC	hepatitis 1/2 infection. The present amino acid sequence represents a
CC	peptide of the invention.
XX	
XX	Sequence 15 AA:
XX	
SO	
Query Match	27.2%; Score 31; DB 7; Length 15;
Best Local Similarity	33.3%; Pred. No. 1.2e+03;
Matches	5; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
OY	1 DYKYPGSRRLGNPKAP 15
	:   :   :   :
DB	1 DITEPTAPMGTPPSP 15
	:   :   :   :
RESULT 70	
ADV12192	
ID	ADV12192 standard; peptide; 15 AA.
XX	
AC	ADV12192;
XX	
DT	10-MAR-2005 (first entry)
XX	
DE	Human phosphorylated peptide from phosphoprotein #130.
XX	
KW	Alzheimers disease; neuroprotective; neurotropic; degeneration; tumor;
KW	neoplasm; neurological disease; phosphorylation; protein sequencing;
XX	phosphorylation.
XX	
OS	Homo sapiens.
XX	
PN	WO2004108948-A2.
XX	
PD	16-DEC-2004.
XX	
PF	04-JUN-2004; 2004WO-US017613.
XX	
PR	04-JUN-2003; 2003US-0476010P.
XX	
PA	(HARD ) HARVARD COLLEGE.
XX	
PI	Gygl SP;
XX	
DR	WPI; 2005-031720/03.
XX	
PT	Characterizing phosphorylated polypeptides in a sample comprises
PT	digesting the polypeptides with a protease thus generating test peptides,



XX 06-AUG-2004; 2004WO-EP008860.  
XX  
PR 08-AUG-2003; 2003US-0493599P.  
XX 08-AUG-2003; 2003US-0493836P.  
PR 08-AUG-2003; 2003US-0493867P.  
XX 08-AUG-2003; 2003US-0493985P.  
XX  
PA (XENO-) XENOVA LTD.  
PA (NOVS) NOVARTIS AG.  
PA (NOVS) NOVARTIS PHARMA GMBH.  
XX Argoud-Puy G, Beder N, Bougueleret L, Cusin I, Mahe E;  
PI Mkhnejad A, Refas S, Rose K, Saudrais C, Scherer A, Papoian R;  
XX WPI; 2005-195824/20.  
XX  
PT Screening and/or diagnosing cardiovascular disorder in subject involves  
PT detecting and/or quantifying level of polypeptide in biological sample  
PT from subject and comparing with control sample.  
XX  
PS Claim 1; SEQ ID NO 16; 349pp; English.  
XX  
XX The invention relates to a method of screening and/or diagnosing a  
CC cardiovascular disorder (CD) in a subject which comprises detecting  
CC and/or quantifying the level of a polypeptide in a biological sample from  
CC the subject and comparing the level to that of control sample. The method  
CC is useful for screening, diagnosing and treating coronary artery disease,  
CC biliary cirrhosis, gallstones, celliac disease, irritable bowel syndrome,  
CC diabetes, scleroderma, nausea, vomiting, constipation and diarrhea. The  
CC method is rapid and efficient. The present sequence represents a  
CC cardiovascular disorder plasma protein tryptic fragment.  
XX  
SQ Sequence 15 AA;

Query Match 27.2%; Score 31; DB 9; Length 15;  
Best Local Similarity 85.7%; Pred. No. 1.2e+03;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 GSRIGNP 12  
DB 6 GSPLGNP 12

RESULT 73  
AAW25403  
ID AAW25403 standard; peptide; 16 AA.  
XX  
AC AAW25403;  
XX  
DT 27-MAR-1998 (first entry)  
XX  
DE p53bp2 SH3 domain binding peptide SEQ ID NO:189.  
XX  
XX Cortactin; SH3 domain; binding peptide; Src homology region 3;  
KW tyrosine kinase; immune response; lymphokine; Interleukin 1; Nck; Abl;  
KW PLCgamma; p53bp2; Ctk; Yes; Grb2.  
XX  
OS Synthetic.  
OS Unidentified.  
XX  
PN WO9730074-A1.  
XX  
PD 21-AUG-1997.  
XX  
PF 14-FEB-1997; 97WO-US002298.  
XX  
PR 16-FEB-1996; 96US-00602999.  
XX  
PA (CYTO-) CYTOGEN CORP.  
PA (UYNC-) UNITIV NORTH CAROLINA.  
XX  
PI Sparks AB, Kay BK, Thorn JM, Quilliam LA, Der CJ, Fowlkes DM;

PI Rider JB;  
XX  
DR WPI; 1997-424972/39.  
XX  
PT Src homology region 3 binding peptide - used to activate Src tyrosine  
PT kinase(s) and to stimulate immune response by increasing production of  
PT certain lymphokine(s), e.g. interleukin-1.  
XX  
PS Claim 17; Page 99; 131pp; English.

XX The present sequence represents a Src homology region 3 (SH3) binding  
CC peptide. SH3 binding peptides are selected from: (a) peptides which bind  
CC the SH3 domain of Cortactin; (b) peptides which bind the middle SH3  
CC domain of Nck; (c) peptides which bind the SH3 domain of Abl; (d)  
CC peptides which bind the SH3 domain of Src; (e) peptides which bind the  
CC SH3 domain of PLC gamma; (f) peptides which bind the SH3 domain of p53bp2  
CC ; (g) peptides which bind the amino-terminal SH3 domain of Ctk; (h)  
CC peptides which bind the SH3 domain of Yes; and (i) peptides which bind  
CC the amino-terminal SH3 domain of Grb2. The purified binding peptides can  
CC be used in the method to identify inhibitors of their binding to their  
CC respective SH3 domains, which could be used to modulate the  
CC pharmacological activity of proteins or polypeptide containing the SH3  
CC domain. The peptides can also be used to activate Src or Src-related  
CC protein tyrosine kinases, to stimulate the immune response by increasing  
CC the production of certain lymphokines, e.g. tumour necrosis factor-alpha  
CC and interleukin-1, or to deliver a conjugated molecule to certain  
XX cellular compartments containing Src or Src related proteins

SQ Sequence 16 AA;  
Query Match 27.2%; Score 31; DB 2; Length 16;  
Best Local Similarity 60.0%; Pred. No. 1.3e+03;  
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 9 LGNPKAPLYK 18  
DB 4 LGRPETPRK 13

RESULT 74  
ADJ90072  
ID ADJ90072 standard; peptide; 16 AA.  
XX  
AC ADJ90072;  
XX  
DT 06-MAY-2004 (first entry)  
XX  
DE Human papillomavirus minor capsid protein I2 peptide #219.  
XX  
KW transporter peptide; UEV domain; Tsg101; viral infection; HIV; AIDS;  
KW hepatitis B virus infection; human herpesvirus 1 infection;  
KW human herpesvirus 2 infection.  
XX  
OS Human papillomavirus type 6b.  
OS  
PN WO2003053332-A2.  
XX  
PD 03-JUL-2003.  
XX  
PF 20-AUG-2002; 2002WO-US026549.  
XX  
PR 20-AUG-2001; 2001US-0313695P.  
XX  
PA (MYRI-) MYRIAD GENETICS INC.  
XX  
PI Morham S, Zavitz K, Hobden A;  
XX  
DR WPI; 2003-586940/55.  
XX  
PT Peptides and hybrid polypeptides associated with a transporter that  
PT increases its uptake by a mammalian cell, useful for inhibiting viral  
PT budding or propagation, especially for treating e.g. AIDS or hepatitis B  
PT virus infection.

XX Claim 35; SEQ ID NO 1540; 137bp; English.  
CC  
XX  
CC The invention comprises a composition which contains a peptide associated  
CC with a transporter that is capable of increasing the uptake of the  
CC peptide by a mammalian cell. The peptide of the invention contains the  
CC amino acid motif Pro-Xaa-Xaa-Pro and is capable of binding the UCV domain  
CC of Tsg101. The composition of the invention is useful in the manufacture  
CC of a medicament for the treatment of viral infections, such as: HIV  
CC infection (particularly AIDS), hepatitis B virus infection and human  
CC herpesvirus 1/2 infection. The present amino acid sequence represents a  
CC peptide of the invention.  
XX  
SQ Sequence 16 AA;  
XX  
Query Match 27.2%; Score 31; DB 7; Length 16;  
Best Local Similarity 33.3%; Pred. No. 1.3e+03;  
Matches 5; Conservative 4; Mismatches 6; Indels 0; Gaps 0;  
XX  
QY 1 DVEYPSGRLGNPKP 15  
DB 2 DTFPTAPMGTFFSP 16  
XX  
RESULT 75  
ADXS6200  
ID ADXS6200 standard; peptide; 16 AA.  
XX  
AC ADXS6200;  
XX  
XX 05-MAY-2005 (first entry)  
XX  
DE Cardiovascular disorder plasma protein tryptic fragment SEQ ID NO 17.  
XX  
XX coronary artery disease; primary biliary cirrhosis; gallstones;  
XX celiac disease; irritable bowel syndrome; diabetes; scleroderma; nausea;  
XX emesis; constipation; diarrhea; cardiovascular disease; immune disorder;  
XX endocrine disease; gastrointestinal disease; metabolic disorder;  
XX dermatological disease; musculoskeletal disease; Cardiant; Vasotropic;  
XX hepatotropic; litholytic; immunosuppressive; Gastrointestinal-Gen.;  
XX Antiinflammatory; Antidiabetic; Dermatological; Antileptic; Laxative;  
XX Antidiarrhetic; diagnosis.  
XX  
XX Homo sapiens.  
XX  
OS  
XX  
XX WO2005015206-A2.  
XX  
XX 17-FEB-2005.  
XX  
XX 06-AUG-2004; 2004WO-EP008860.  
XX  
XX 08-AUG-2003; 2003US-0493599P.  
XX PR 08-AUG-2003; 2003US-0493836P.  
XX PR 08-AUG-2003; 2003US-0493867P.  
XX PR 08-AUG-2003; 2003US-0493985P.  
XX  
XX (XENO-) XENOVA LTD.  
XX PA (NOVS ) NOVARTIS AG.  
XX PA (NOVS ) NOVARTIS PHARMA GMBH.  
XX  
XX Argoud-Puy G, Bederr N, Bougueleret L, Guin I, Mahe E;  
XX PI Niknejad A, Reifas S, Rose K, Saudrais C, Scherer A, Papoian R;  
XX PT Niknejad A, Reifas S, Rose K, Saudrais C, Scherer A, Papoian R;  
XX DR WPI, 2005-195824/20.  
XX  
XX Screening and/or diagnosing cardiovascular disorder in subject involves  
XX PT detecting and/or quantifying level of polypeptide in biological sample  
XX PT from subject and comparing with control sample.  
XX  
XX Claim 1; SEQ ID NO 17; 349pp; English.  
XX  
XX The invention relates to a method of screening and/or diagnosing a  
XX CC cardiovascular disorder (CD) in a subject which comprises detecting  
XX CC

CC and/or quantifying the level of a polypeptide in a biological sample from  
CC the subject and comparing the level to that of control sample. The method  
CC is useful for screening, diagnosing and treating coronary artery disease,  
CC biliary cirrhosis, gallstones, celiac disease, irritable bowel syndrome,  
CC diabetes, scleroderma, nausea, vomiting, constipation and diarrhea. The  
CC method is rapid and efficient. The present sequence represents a  
CC cardiovascular disorder plasma protein tryptic fragment.  
XX  
SQ Sequence 16 AA;  
XX  
Query Match 27.2%; Score 31; DB 9; Length 16;  
Best Local Similarity 85.7%; Pred. No. 1.3e+03;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
XX  
QY 6 GSRLLGNP 12  
DB 6 GSRLLGNP 12  
XX  
RESULT 76  
ADXS6207  
ID ADXS6207 standard; peptide; 16 AA.  
XX  
XX ADXS6207;  
XX  
XX 05-MAY-2005 (first entry)  
XX  
XX Cardiovascular disorder plasma protein tryptic fragment SEQ ID NO 24.  
XX  
XX coronary artery disease; primary biliary cirrhosis; gallstones;  
XX celiac disease; irritable bowel syndrome; diabetes; scleroderma; nausea;  
XX emesis; constipation; diarrhea; cardiovascular disease; immune disorder;  
XX endocrine disease; gastrointestinal disease; metabolic disorder;  
XX dermatological disease; musculoskeletal disease; Cardiant; Vasotropic;  
XX hepatotropic; litholytic; immunosuppressive; Gastrointestinal-Gen.;  
XX Antiinflammatory; Antidiabetic; Dermatological; Antileptic; Laxative;  
XX Antidiarrhetic; diagnosis.  
XX  
XX Homo sapiens.  
XX  
OS  
XX  
XX WO2005015206-A2.  
XX  
XX 17-FEB-2005.  
XX  
XX 06-AUG-2004; 2004WO-EP008860.  
XX  
XX 08-AUG-2003; 2003US-0493599P.  
XX PR 08-AUG-2003; 2003US-0493836P.  
XX PR 08-AUG-2003; 2003US-0493867P.  
XX PR 08-AUG-2003; 2003US-0493985P.  
XX  
XX (XENO-) XENOVA LTD.  
XX PA (NOVS ) NOVARTIS AG.  
XX PA (NOVS ) NOVARTIS PHARMA GMBH.  
XX  
XX Argoud-Puy G, Bederr N, Bougueleret L, Guin I, Mahe E;  
XX PI Niknejad A, Reifas S, Rose K, Saudrais C, Scherer A, Papoian R;  
XX PT Niknejad A, Reifas S, Rose K, Saudrais C, Scherer A, Papoian R;  
XX DR WPI, 2005-195824/20.  
XX  
XX Screening and/or diagnosing cardiovascular disorder in subject involves  
XX PT detecting and/or quantifying level of polypeptide in biological sample  
XX PT from subject and comparing with control sample.  
XX  
XX Claim 1; SEQ ID NO 24; 349pp; English.  
XX  
XX The invention relates to a method of screening and/or diagnosing a  
XX CC cardiovascular disorder (CD) in a subject which comprises detecting  
XX CC and/or quantifying the level of a polypeptide in a biological sample  
XX CC from the subject and comparing the level to that of control sample. The method  
XX CC is useful for screening, diagnosing and treating coronary artery disease,  
XX CC biliary cirrhosis, gallstones, celiac disease, irritable bowel syndrome,  
XX CC diabetes, scleroderma, nausea, vomiting, constipation and diarrhea. The







Db 7 GNPPEPLKK 15

## RESULT 79

ADP17331

ADP17331 standard; peptide; 17 AA.

AC ADP17331,

DT 12-FEB-2004 (first entry)

DE Nuclear targeting oligopeptide, SEQ ID No 374.

KM cell surface molecule; malignant cell line; cytotaxic; immunostimulant;  
KW vaccine; gene therapy; premalignant; cancer; nuclear targeting.

OS Unidentified.

PN WO200300928-A2.

XX 03-JUN-2003.

PF 19-JUN-2002; 2002WO-1B003534.

XX 25-JUN-2001; 2001DK-00000992.

PR 02-JUL-2001; 2001US-0301818P.

PA (ODIN-) ODIN MEDICAL AS.

PI Poulsen HS, Pedersen N, Mortensen S, Sorensen SB, Petersen MW,  
PI Elsenr HI;

DR WPI; 2003-247897/24.

PT Identifying cell surface molecules with differential expression in  
PT malignant cells, by comparing expression of mRNA in malignant cells and  
PT normal tissue, and selecting nucleic acid sequences encoding the  
PT molecules.

PS Disclosure; SEQ ID NO 374; 223pp; English.

XX The invention relates to a novel method for identifying cell surface  
XX molecules expressed at different levels in malignant cells. The method  
XX involves providing at least 3 malignant cell lines and 3 total RNA  
XX samples derived from normal tissue, comparing expression of mRNA in cell  
XX lines and normal tissue, identifying nucleic acid sequences for a  
XX difference in amount of mRNA expressed in cell lines and normal tissue,  
XX and selecting nucleic acid sequences encoding for the cell surface  
XX molecules. The cell surface molecule compositions have cytostatic and  
XX immunostimulant activities. The cell surface molecule proteins can be  
XX used to create a vaccine and their encoding nucleotides used in gene  
XX therapy. The specific binding partner, capable of associating with the  
XX cell surface molecules, is useful for the preparation of a targeting  
XX complex, comprising a binding partner capable of binding the cell surface  
XX molecules. The targeting complex is useful in the treatment of  
XX premalignant and/or malignant conditions in an individual. The condition  
XX includes cancer selected from melanoma, brain tumour (e.g. glioblastoma,  
XX neuroblastoma, astrocytoma, oligodendroglioma, meningioma,  
XX medulloblastoma, neuroma, ependymoma, craniopharyngioma, pineal tumour,  
XX germ cell tumour and schwannoma), breast cancer, lung cancer (e.g. small  
XX cell lung cancer (SCLC) and non-small cell lung cancer (NSCLC)), prostate  
XX cancer, cervix cancer, uterine cancer, ovarian cancer, leukaemia, colon  
XX cancer, rectum cancer and bladder cancer. The targeting complex is useful  
XX for the preparation of a premalignant and/or malignant conditions in an  
XX individual in need of it. This sequence represents a nuclear targeting  
XX peptide of the invention.

XX Sequence 17 AA;

Query Match 27.2%; Score 31; DB 7; Length 17;  
Best Local Similarity 66.7%; Pred. No. 1.4e+03;

Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 10 GNPAPLYK 18

Db 7 GNPPEPLKK 15

## RESULT 80

ADP86158

ID ADP86158 standard; peptide; 17 AA.

AC ADP86158;

DT 26-FEB-2004 (first entry)

DE Human NLS containing peptide (SeqID 58) derives antimicrobial peptides.

XX antimicrobial; nuclear localisation sequence; NLS; gram positive;

KM gram negative bacteria; human.

OS Homo sapiens.

PN WO2003091429-A1.

XX 06-NOV-2003.

PF 24-APR-2003; 2003WO-1P005225.

XX 25-APR-2002; 2002JP-00124830.

PA (TOAG ) TOA GOSEI KK.

PI Yoshida T, Kume M, Yamada Y, Matsuda Y, Kourai H;

DR WPI; 2003-854399/79.

PT Synthetic antimicrobial polypeptides for use as antimicrobials.

PS Disclosure; SEQ ID NO 58; 113pp; Japanese.

XX This invention relates to a novel method of synthesising artificial  
XX antimicrobial polypeptides. Specifically, these are peptides that each  
XX comprise at least one nuclear localisation sequence (NLS) or modified  
XX NLS. Furthermore, each NLS unit consists of at least 5 amino acids and  
XX makes up at least 30% of the total amino acids of the peptide. As such,  
XX the present invention describes the oligonucleotides encoding these  
XX antimicrobial peptides that are effective against a wide range of gram  
XX positive and gram negative bacteria including Klebsiella pneumoniae,  
XX Bacillus subtilis and Salmonella enteritidis. This peptide sequence  
XX represents a peptide from which the novel artificial antimicrobial  
XX peptides were derived in an exemplification of the invention.

XX Sequence 17 AA;

Query Match 27.2%; Score 31; DB 7; Length 17;  
Best Local Similarity 66.7%; Pred. No. 1.4e+03;  
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 10 GNPAPLYK 18

Db 7 GNPPEPLKK 15

## RESULT 81

ADJ90085

ID ADJ90085 standard; peptide; 17 AA.

AC ADJ90085;

DT 06-MAY-2004 (first entry)

DE Human papillomavirus minor capsid protein L2 peptide #232.

KM	transporter peptide; UB domain; Tsg101; viral infection; HIV; AIDS;
KM	hepatitis B virus infection; human herpesvirus 1 infection;
XX	human herpesvirus 2 infection.
XX	
OS	Human papillomavirus type 6b.
XX	
XX	MO2003053332-A2.
PN	
PD	03-JUL-2003.
XX	
XX	20-AUG-2002; 2002MO-US026549.
PF	
XX	20-AUG-2001; 2001US-0313695P.
PR	
XX	(MYRI-) MYRIAD GENETICS INC.
PA	
XX	Morham S, Zavitz K, Hobden A;
PI	
XX	WPI; 2003-586940/55.
DR	
XX	
XX	Peptides and hybrid polypeptides associated with a transporter that
PT	increases its uptake by a mammalian cell, useful for inhibiting viral
PT	budding or propagation, especially for treating e.g. AIDS or hepatitis B
PT	virus infection.
XX	
PS	Claim 35; SEQ ID NO 1553; 137pp; English.
XX	
CC	The invention comprises a composition which contains a peptide associated
CC	with a transporter that is capable of increasing the uptake of the
CC	peptide by a mammalian cell. The peptide of the invention contains the
CC	amino acid motif Pro-Xaa-Xaa-Pro and is capable of binding the UB domain
CC	of Tsg101. The composition of the invention is useful in the manufacture
CC	of a medicament for the treatment of viral infections, such as: HIV
CC	infection (particularly AIDS), hepatitis B virus infection and human
CC	herpesvirus 1/2 infection. The present amino acid sequence represents a
CC	peptide of the invention.
XX	
SQ	Sequence 17 AA;
Query Match	27.2%; Score 31; DB 7; Length 17;
Best Local Similarity	33.3%; Pred. No. 1.4e+03;
Matches	5; Conservative 4; Mismatches 6; Indels 0; Gaps 0
OY	1 DYEPGSRIGNPKAP 15
	:   :   :
Db	3 DITFPTAPMGTRPSP 17
RESULT 82	
AAW66652	
ID	AAW66652 standard; peptide; 18 AA.
XX	
AC	AAW66652;
XX	
DT	30-NOV-1998 (first entry)
XX	
DE	HSV-2 glycoprotein G partial sequence (residues 301-318).
XX	
KM	Herpes simplex virus type 2; HSV-2 antibody; detection; HSV-1;
XX	multiply displayed peptide structure.
OS	Synthetic.
OS	Herpes simplex virus 2.
XX	
PN	GB2323360-A.
XX	
PD	23-SEP-1998.
XX	
PF	14-JAN-1997; 97GB-00000660.
XX	
PR	14-JAN-1997; 97GB-00000660.
XX	
PA	(MEDI-) MEDICAL RES COUNCIL.

XX	Marsden HS;
P1	WPI, 1998-459516/40.
DR	New peptide compounds useful for detecting herpes simplex virus type 2 -
XX	can differentiate between herpes simplex virus type 1 and type 2.
PT	Example 1; Page 10; 25pp; English.
PS	The invention relates to a multiply displayed peptide structure of
CC	formula [(X1)p-A-(X2)q-Sp]-n-Core, X1, X2 = 1-6 non-interfering amino acid
CC	residues; A = Glu, Glu, Phe, Glu, Gly, Ala, Gly, Asp, Gly, Glu, Pro, Pro, Glu, Asp, Asp,
CC	Asp; Sp = spacer group extending outwardly from the core; n at least 4;
CC	and p, q = 0 or 1. The linkage between the core and the spacer may be
CC	chemical or physical. Peptides of this formula are used in the diagnosis
CC	of herpes simplex virus type 2 (HSV-2). The peptides can distinguish HSV-
CC	2 from HSV-1. A series of 67 peptides (AAW66524-W66690), mostly 18 amino
CC	acids long, that spanned amino acids 21-699 of the predicted open reading
CC	frame of HSV gG2 were synthesized. The peptides were made as multiply
CC	displayed peptide structures of the invention and were screened against
CC	sera from HSV-1, HSV-2 antibody-positive individuals and from individuals
CC	having no laboratory evidence of HSV infection. From the results, peptide
CC	55 (AAW66678) was considered a likely candidate for type specific
CC	serodiagnosis of HSV
XX	
SQ	Sequence 18 AA;
OY	Query Match 27.2%; Score 31; DB 2; Length 18;
DB	Best Local Similarity 43.8%; Pred. No. 1.5e+03;
	Matches 7; Conservative 1; Mismatches 8; Indels 0; Gaps 0
	5 FGSRLGNPKAPLYKKR 20
	2 PGALDDGPYPAPPPRP 17
ABP83560	RESULT 83
ID	ABP83560 standard; peptide; 18 AA.
AC	ABP83560;
XX	
DT	04-MAR-2003 (first entry)
DE	G protein-coupled receptor (GPCR) antigenic peptide SEQ ID NO:2233.
XX	
KM	G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
KM	G protein-coupled receptor modulator; antibody; immune-related disease;
KM	growth-related disease; cell regeneration-related disease; AIDS; cancer;
KM	immunological-related cell proliferative disease; autoimmune disease;
KM	Alzheimer's disease; arteriosclerosis; infection; osteoarthritis; allergy;
KM	osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
KM	grat versus host disease; Parkinson's disease; multiple sclerosis; pain;
KM	psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
KM	mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
KM	hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
XX	ulcer.
OS	Homo sapiens.
PN	WO200261087-A2.
PD	08-AUG-2002.
PF	19-DEC-2001; 2001WO-US050107.
PR	19-DEC-2000; 2000US-0257144P.
PA	(LIFE-) LIFESPAN BIOSCIENCES INC.
PI	Burner GC, Roush CL, Brown JP;
XX	

DR	WPI, 2003-046718/04.
XX	
PT	New isolated antigenic peptides e.g., for G protein-coupled receptors
PT	(GPCR), useful for diagnosing and designing drugs for treating conditions
PT	in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
PT	autoimmune diseases.
XX	
PS	Claim 1, Fig 2, 523pp; English.
XX	
CC	The present invention describes antigenic peptides (1) comprising: (a)
CC	any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
CC	acids. Also described: (1) an assay for the detection of a particular G
CC	protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
CC	and (2) an isolated antibody having high specificity and high affinity or
CC	avidity for a particular GPCR. (1) can be used as GPCR modulators and in
CC	gene therapy. The antigenic peptides for GPCRs are useful in detecting an
CC	antibody against a particular GPCR, and in the production of specific
CC	antibodies. The peptides and antibodies are also useful for detecting the
CC	presence or absence of corresponding GPCRs. The antigenic peptides for
CC	GPCRs and antibodies are useful for diagnosing and designing drugs for
CC	creating immune-related diseases, growth-related diseases, cell
CC	regeneration-related disease, immunological-related cell proliferative
CC	diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
CC	atherosclerosis, bacterial, fungal, protozoan or viral infections,
CC	osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
CC	inflammation, allergies, Crohn's disease, diabetes, graft versus host
CC	disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
CC	anxiety, depression, schizophrenia, dementia, mental retardation, memory
CC	loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,
CC	hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
CC	any other disorder in which GPCRs are involved. The antibodies may be
CC	used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode
CC	GPCR proteins given in ABP81675 to ABP82018, which are used in the
CC	exemplification of the present invention
XX	
SQ	Sequence 18 AA,
XX	
OY	1 DYEPGGS 7
D6	3 DYGPXS 9
XX	
RESULT 84	
ADJ90099	
ID	ADJ90099 standard; peptide; 18 AA.
XX	
AC	ADJ90099;
XX	
DT	06-MAY-2004 (first entry)
XX	
DE	Human papillomavirus minor capsid protein I2 peptide #246.
XX	
KV	transporter peptide; UEV domain; Tsg101; viral infection; HIV; AIDS;
KV	hepatitis B virus infection; human herpesvirus 1 infection;
XX	human herpesvirus 2 infection.
XX	
OS	Human papillomavirus type 6b.
XX	
PN	WO2003053332-A2.
PD	03-JUL-2003.
XX	
PF	20-AUG-2002; 2002MO-USO26549.
XX	
PR	20-AUG-2001; 2001US-031695P.
XX	
PA	(MYRI-) MYRIAD GENETICS INC.
XX	
PI	Morham S, Zavitz K, Hobden A,

XX	WP1; 2003-586940/55.
DR	
PT	Peptides and hybrid polypeptides associated with a transporter that
PT	increases its uptake by a mammalian cell, useful for inhibiting viral
PT	budding or propagation, especially for treating e.g. AIDS or hepatitis B
PT	virus infection.
XX	
PS	Claim 35; SEQ ID NO 1567; 137pp; English.
XX	
CC	The invention comprises a composition which contains a peptide associated
CC	with a transporter that is capable of increasing the uptake of the
CC	peptide by a mammalian cell. The peptide of the invention contains the
CC	amino acid motif Pro-Xaa-Xaa-Pro and is capable of binding the URV domain
CC	of Tsg101. The composition of the invention is useful in the manufacture
CC	of a medicament for the treatment of viral infections, such as: HIV
CC	infection (particularly AIDS), hepatitis B virus infection and human
CC	hepatitis 1/2 infection. The present amino acid sequence represents a
CC	peptide of the invention.
XX	
SQ	Sequence 18 AA;
Query Match	27.2%; Score 31; DB 7; Length 18;
Best Local Similarity	33.3%; Pred. No. 1.5e+03;
Matches	5; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
Oy	1 DYEPYGSRLGNPKAP 15   :   :   :   :   Db 4 DTFPTAPMGTPPSP 18
RESULT 85	
ID ADK50419	
ID ADK50419	standard; peptide; 18 AA.
AC ADK50419;	
XX 04-NOV-2004	(first entry)
DE Human carcinoma-related C35 epitope / gp100 Pme117 polypeptide peptide 1310.	
KW C35 epitope; cytosstatic; vaccine; tumour; breast; bladder carcinoma;	
XX human; polypeptide; gp100 Pme117.	
OS Homo sapiens.	
OS Unidentified.	
XX WO2003104428-A2.	
PN	
XX 18-DEC-2003.	
PD	
PP 10-JUN-2003; 2003WO-US018252.	
XX	
XX 10-JUN-2002; 2002US-0386738P.	
PR 11-DEC-2002; 2002US-0432241P.	
PR 23-APR-2003; 2003US-0464650P.	
XX	
PA (VACC-) VACCINEX INC.	
PA (UTRP ) UNITV ROCHESTER.	
XX	
P1 Zauderer M, Evans BE, Borrello MA;	
XX	
DR WP1; 2004-062349/06.	
XX	
PT Novel C35 polypeptide useful for formulation of immunogenic composition	
PT to induce antibodies and cell-mediated immunity against tumor cells.	
XX	
PS Disclosure; Page 176; 626pp; English.	
XX	
CC The invention relates to a novel isolated polypeptide comprising or	
CC consisting of two or more C35 peptide epitopes. The polypeptide of the	
CC invention demonstrates cytostatic activity and may be useful for the	
CC formulation of an immunogenic composition, such as a vaccine, to induce	

CC antibodies and cell-mediated immunity against target cells such as tumour  
 CC cells. Furthermore, the polypeptide and its analogues may be useful as  
 CC prognostic markers for carcinoma, such as human breast or bladder  
 CC carcinoma. The current sequence is that of human breast/bladder carcinoma  
 CC C35 polypeptide polypeptide of the invention.

XX Sequence 18 AA;

Query Match 27.2%; Score 31; DB 8; Length 18;  
 Best Local Similarity 38.5%; Pred. No. 1.5e+03;  
 Matches 5; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 8 RLGNPKAPLYKRP 20  
 ::|||::|  
 Db 1 KITNSRPPLYLKP 13

RESULT 86  
 AAP81357  
 ID AAP81357 standard; protein; 19 AA.  
 XX  
 AC AAP81357;

XX 25-MAR-2003 (revised)  
 DT 19-SEP-1990 (first entry)

XX Sequence of immunogenic synthetic peptide containing AAs 64 to 77 of  
 DE herpes simplex virus type 1 (HSV1) glycoprotein B (GB).

KW Herpes simplex virus type 1 glycoprotein B; vaccines;  
 XX immunogenic synthetic peptide.

OS Herpes simplex virus type 1.

PH Key Location/Qualifiers

FT Misc-difference 1 /label= Tyr, Lys

FT Misc-difference 1 /note= "or may be absent"

FT /label= OTHER

FT /note= "X-amino, amino-p-benzoylbenzoyl, N-acetyl or  
 carboxyl"

FT Misc-difference 2 /label= Nle

FT /note= "or absent"

FT Misc-difference 17 /label= Thr, Cys, Nle

FT /note= "or absent"

FT Misc-difference 18 /label= Pro

FT /note= "or absent"

FT Misc-difference 19 /label= OTHER

FT /note= "P-amino or carboxyl, or a pharmaceutically-  
 acceptable salt thereof"

FT Misc-difference 19 /label= Pro

FT /note= "or absent"

XX US4761470-A.

XX 02-AUG-1988.

XX 10-APR-1987; 87US-00036651.

XX 16-DEC-1985; 85US-00809452.

XX (MERI ) MERCK & CO INC.  
 XX Emint EA, Larson VM, Boger JS;  
 PI WPI; 1988-234840/33.  
 XX

PT New synthetic oligopeptide immunogens and their conjugates - used for  
 PT inducing prodn. of antibodies against herpes simplex virus type 1.

XX Claim 1; Page 10; 6pp; English.

XX Immunogenic synthetic peptides of this formula and their salts are new.  
 CC Also new are conjugates of the peptides covalently bonded to a carrier  
 CC protein or synthetic polymer. The peptides are immunogens for inducing  
 CC prodn. of HSV1 neutralising antibodies and so are useful in vaccines.  
 CC (Updated on 25-MAR-2003 to correct PD field.)

XX Sequence 19 AA;

Query Match 27.2%; Score 31; DB 1; Length 19;  
 Best Local Similarity 50.0%; Pred. No. 1.6e+03;  
 Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 9 LGNPKAPLYKRP 20  
 ||::|||::|  
 Db 2 LGDPKPKKKKKP 13

RESULT 87  
 AAW17416  
 ID AAW17416 standard; peptide; 19 AA.  
 XX  
 AC AAW17416;

XX 17-OCT-2003 (revised)  
 DT 18-JUN-1997 (first entry)

XX Chicken anaemia virus immunogenic peptide #16.

DE Immunogenic polypeptide; CAV; serum; antibody; diagnosis;  
 XX chicken anaemia virus; vaccine.

OS Chicken anaemia virus.

PN JP09071599-A.

XX 18-MAR-1997.

XX 06-SEP-1995; 95JP-00229004.

XX 06-SEP-1995; 95JP-00229004.

XX (NISK ) NIPPON SEIBUTSU KAGAKU KENKYUSHO ZH.

XX WPI; 1997-231187/21.

XX Polypeptide(s) highly reactive to chick anaemia virus-infected chicken  
 PT serum - are used for antibody and vaccine production for protection  
 PT against chicken anaemia virus.

XX Claim 1; Page 14; 26pp; English.

XX The sequences given in AAW17401-17 are immunogenic polypeptides which  
 CC have a high reactivity to CAV-infected chicken serum. These peptides and  
 CC antibodies against them can be used for the diagnosis of chicken anaemia  
 CC virus (CAV) infection or in vaccines for preventing CAV infection. The  
 CC polypeptides have a high reactivity to CAV-infected chicken serum.  
 CC (Updated on 17-OCT-2003 to standardise OS field)

XX Sequence 19 AA;

Query Match 27.2%; Score 31; DB 2; Length 19;  
 Best Local Similarity 46.7%; Pred. No. 1.6e+03;  
 Matches 7; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 5 POSRLGNPKAPLYKR 19  
 |||::|||::|  
 Db 2 PDLRTDQPKPKKKR 16

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RESULT 88
AAW32884
ID AAW32884 standard; peptide; 19 AA.
XX
AC AAW32884;
XX
DT 25-MAR-2003 (revised)
DT 16-JAN-1998 (first entry)
XX
DE Peptide K fragment of OA-519.
XX
KM OA-519; cross-reaction; haptoglobin related; hpr; antibody; epitope;
KM haptoglobin 1; haptoglobin 2; cancer; breast cancer; prognosis assay;
KM peptide K.
XX
OS Homo sapiens.
XX
PN US5665874-A.
XX
PD 09-SEP-1997.
XX
PF 05-JUN-1995; 95US-00469005.
XX
PR 17-JAN-1989; 89US-00297722.
PR 04-DEC-1990; 90US-00622407.
PR 26-JUL-1991; 91US-00735522.
PR 24-JUL-1992; 92US-00917716.
PR 26-JUL-1993; 93US-00096908.
PR 24-JAN-1994; 94US-00188426.
XX
PA (UYJO ) UNIV JOHNS HOPKINS.
XX
PI Kuhajda FP, Pasternack GR;
XX
DR WPI; 1997-469516/43.
XX
PT DNA encoding protein cross-reactive with hpr gene product - useful to
PT raise antibodies reactive with epitope(s) found on hpr gene product,
PT useful in cancer, especially breast cancer, prognosis assays.
XX
PS Example 12; Col 39-40; 68bp; English.
XX
CC The present sequence is a peptide fragment of a protein (OA-519) cross-
CC reactive with the haptoglobin related (hpr) gene product. OA-519 can be
CC used to raise antibodies reactive with epitopes found on the hpr gene
CC product, but not on haptoglobin 1 or 2, useful in cancer, especially
CC breast cancer, prognosis assays. (Updated on 25-MAR-2003 to correct PF
CC field.)
XX
SQ Sequence 19 AA;

Query Match          27.2%; Score 31; DB 2; Length 19;
Best Local Similarity 42.9%; Pred. No. 1.6e+03;
Matches 6; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 4 YPGSRIGNPKAPLY 17
   :| | | | |
   :| | | | |
Db 1 HPESPPTNPPTBPLF 14

RESULT 89
AAW57227
ID AAW57227 standard; peptide; 19 AA.
XX
AC AAW57227;
XX
DT 25-MAR-2003 (revised)
DT 04-AUG-1998 (first entry)
XX
DE OA-519 peptide fragment SEQ ID NO:3.
XX
KM Human; hpr gene; haptoglobin; solid tumour; cancer; metastasis; breast;

```

```

KM screening; prognosis; prostatic adenocarcinoma.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN US5759791-A.
XX
PD 02-JUN-1998.
XX
PF 24-JAN-1994; 94US-00188426.
XX
PR 17-JAN-1989; 89US-00297722.
PR 04-DEC-1990; 90US-00622407.
PR 26-JUL-1991; 91US-00735522.
PR 24-JUL-1992; 92US-00917716.
PR 26-JUL-1993; 93US-00096908.
XX
PA (UYJO ) UNIV JOHNS HOPKINS.
XX
PI Pasternack GR, Kuhajda FP;
XX
DR WPI; 1998-332128/29.
XX
PT Prognosis of solid tumours e.g. breast carcinoma - based on detection of
PT OA-519 protein or mRNA in histological sections and biological fluids.
XX
PS Example 12; Col 39; 50pp; English.
XX
CC The present sequence represents an OA-519 peptide fragment from an
CC example of the present invention. The present invention describes a
CC method and a kit for screening human samples to aid in determining the
CC prognosis of breast carcinoma. The kit comprises in one or more
CC containers: an antibody which specifically binds to one or more epitopes
CC found on the sequence: Leu Tyr Ser Gly Asn Asp Val Thr Asp Ile Ser Asp
CC Asp Arg Phe Pro Lys Pro Glu Ile Ala Asn Gly Tyr Val Glu Lys Leu Phe
CC Arg Tyr Glu Cys but not found on haptoglobin 1 or 2; and a reagent for
CC detecting the antibody. The method comprises providing a histologic
CC section from the tumour, and contacting the section with an antibody (as
CC described above), and determining whether the antibody specifically binds
CC to the section in cytoplasmic cellular regions, where the presence of the
CC antibody binding correlates with a worsened prognosis of the solid
CC tumour. The method is useful for the prognosis of solid tumours,
CC especially breast carcinomas and prostatic adenocarcinomas. (Updated on
CC 25-MAR-2003 to correct PF field.)
XX
SQ Sequence 19 AA;

Query Match          27.2%; Score 31; DB 2; Length 19;
Best Local Similarity 42.9%; Pred. No. 1.6e+03;
Matches 6; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 4 YPGSRIGNPKAPLY 17
   :| | | | |
   :| | | | |
Db 1 HPESPPTNPPTBPLF 14

RESULT 90
AAW71597
ID AAW71597 standard; peptide; 19 AA.
XX
AC AAW71597;
XX
DT 24-NOV-1998 (first entry)
XX
DE Protein tyrosine phosphatase peptide PTP PEP.
XX
KM Mouse; tyrosine phosphorylated cleavage furrow-associated protein;
KM PSTPIP; PST family; protein tyrosine phosphatase; murine;
KM polymerisation; actin monomer; eukaryotic cell; identification;
XX
XX antagonist.
XX
OS Synthetic.
OS Mus sp.

```

XX WO9835037-A1.  
 XX 13-AUG-1998.  
 PD  
 XX 30-JAN-1998; 98WO-US001774.  
 PF  
 XX 07-FEB-1997; 97US-00798419.  
 PR  
 XX 29-SEP-1997; 97US-00938829.  
 PR  
 XX (GETH ) GENENTECH INC.  
 PA  
 XX Lasky LA, Dowbenko DJ;  
 PI  
 XX WPI; 1998-447234/38.  
 DR  
 XX  
 XX  
 PT New PE8T-type protein tyrosine phosphatase interacting polypeptide -  
 PT nucleic acids and vectors; for inducing the polymerisation of actin  
 PT monomers in eukaryotic cells and identifying antagonists.  
 CC  
 XX  
 PS Disclosure; Page 37; 111pp; English.  
 CC  
 XX The present sequence represents a peptide from the present invention  
 CC which describes murine tyrosine phosphorylated cleavage furrow-  
 CC associated protein (PSTRIP), which is a PE8T-type protein tyrosine  
 CC phosphatase (PTP)-interacting polypeptide. PSTRIP induces the  
 CC polymerisation of actin monomers in a eukaryotic cell, by introducing a  
 CC vector containing the nucleic acid sequence encoding PSTRIP into the  
 CC cell. Assays for identifying (ant)agonists of PSTRIP comprise contacting  
 CC PSTRIP with the agent and monitoring the ability of PSTRIP to induce  
 CC actin polymerisation  
 CC  
 XX  
 SQ Sequence 19 AA;

Query Match 27.2%; Score 31; DB 2; Length 19;  
 Best Local Similarity 50.0%; Pred. No. 1.6e+03;  
 Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 6 GSRLGNPKAP 15  
 DB 3 GNRFSKPKGP 12

RESULT 91  
 AAW96751  
 ID AAW96751 standard; peptide; 19 AA.

XX AAW96751;  
 AC  
 XX  
 XX  
 DT 14-APR-1999 (first entry)  
 XX

DE Peptide fragment derived from protein OA-519.  
 XX  
 KW Monoclonal antibody; OA-519; haptoglobin 1; Hg1, Hg2;  
 KW haptoglobin related protein; hpr; diagnostic marker; human solid tumour;  
 KW tumour invasion; early metastasis; breast cancer.  
 XX

OS Homo sapiens.  
 XX  
 PN US5872217-A.  
 XX  
 PD 16-FEB-1999.  
 XX  
 XX  
 PF 05-JUN-1995; 95US-00469007.  
 XX  
 XX  
 PR 17-JAN-1989; 89US-00297722.  
 PR 04-DEC-1990; 90US-00622407.  
 PR 26-JUL-1991; 91US-00735522.  
 PR 24-JUL-1992; 92US-00917716.  
 PR 26-JUL-1993; 93US-00069908.  
 PR 24-JAN-1994; 94US-00188426.  
 XX  
 XX (UYJO ) UNIV JOHNS HOPKINS.

XX KuhaJda FP, Pasternack GR;  
 PI  
 XX WPI; 1999-166717/14.  
 DR  
 XX  
 PT New anti-OA-519 antibodies - useful as diagnostic and prognostic markers  
 PT for human solid tumours, particularly breast cancers.  
 CC  
 XX  
 PS Example 12; Col 25; 51pp; English.  
 CC  
 XX

CC Peptides AAW96750-53 are derived from the OA-519 protein. The  
 CC specification describes monoclonal antibodies which specifically bind an  
 CC epitope found on OA-519 but not on haptoglobin 1 (Hg1) or Hg2 or,  
 CC optionally haptoglobin related protein (hpr) gene product. The antibodies  
 CC can be used to detect OA-519 which is useful as a diagnostic marker in  
 CC human solid tumours and for predicting the propensity for tumour invasion  
 CC and early metastasis, particularly with breast cancer. They can detect  
 CC aggressive tumour cells which result in decreased survival, increased  
 CC metastasis, increased rates of clinical recurrence and overall worsened  
 CC prognosis. The antibodies can also be used to purify haptoglobin related  
 CC (hpr) proteins  
 CC  
 XX

SQ Sequence 19 AA;  
 Query Match 27.2%; Score 31; DB 2; Length 19;  
 Best Local Similarity 42.9%; Pred. No. 1.6e+03;  
 Matches 6; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 4 YPSRLGNPKAPLY 17  
 DB 1 HPSEPTPNTEPLP 14

RESULT 92  
 AAW84378  
 ID AAW84378 standard; peptide; 19 AA.

XX AAW84378;  
 AC  
 XX  
 XX  
 DT 26-MAR-1999 (first entry)  
 XX

DE Peptide K from a protein cross-reactive with the hpr gene product.  
 XX  
 KW Haptoglobin related gene; hpr gene; haptoglobin 1; haptoglobin 2;  
 KW antibody; breast carcinoma; diagnostic marker; human solid tumour.  
 XX

OS Synthetic.  
 OS Homo sapiens.  
 OS  
 XX  
 PN US5864011-A.  
 XX  
 PD 26-JAN-1999.  
 XX  
 XX  
 PF 05-JUN-1995; 95US-00469009.  
 XX  
 XX  
 PR 17-JAN-1989; 89US-00297722.  
 PR 04-DEC-1990; 90US-00622407.  
 PR 26-JUL-1991; 91US-00735522.  
 PR 24-JUL-1992; 92US-00917716.  
 PR 26-JUL-1993; 93US-00069908.  
 PR 24-JAN-1994; 94US-00188426.  
 XX  
 XX (UYJO ) UNIV JOHNS HOPKINS.

XX KuhaJda FP, Pasternack GR;  
 PI  
 XX WPI; 1999-131358/11.  
 DR  
 XX  
 PT Polypeptide comprising epitope of hpr gene product - useful for producing  
 PT antibodies for cancer prognosis.  
 CC  
 XX  
 PS Example 12; Col 25; 51pp; English.  
 XX

CC The present sequence represents a peptide derived from a protein that is  
 CC immunologically cross-reactive with the haptoglobin related (hpr) gene  
 CC product from breast cancer cells. The specificfication also describes a  
 CC peptide that is immunologically cross-reactive with polyclonal antibodies  
 CC that specifically bind the hpr gene product. The peptide can be used to  
 CC raise antibodies specific for a protein that is immunologically cross-  
 CC reactive with the hpr gene product but not with haptoglobin 1 or  
 CC haptoglobin 2. The peptide is found in the cytoplasm of breast carcinoma  
 CC cells and is a useful diagnostic marker in human solid tumours for  
 CC predicting the propensity for tumour invasion and early metastasis  
 CC  
 XX Sequence 19 AA;  
 SQ

Query Match 27.2%; Score 31; DB 2; Length 19;  
 Best Local Similarity 42.9%; Pred. No. 1.6e+03;  
 Matches 6; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 4 YPGSRIGNPKAPLY 17  
 Db 1 HPBSPPTNPTEPPLF 14

RESULT 93  
 AAY81931  
 ID AAY81931 standard; protein; 19 AA.

AC AAY81931;

DT 27-JUN-2000 (first entry)

DE Peptide fragment of PXXF-HSCF.

KM PST phosphatase interacting protein; PSTPIP; tumour therapy;  
 KM protein tyrosine phosphatase; PTP.

OS Unidentified.

PN US6040437-A.

PD 21-MAR-2000.

PF 29-SEP-1997; 97US-00938830.

PR 17-APR-1997; 97US-0104590P.

XX (GETH ) GENENTECH INC.

PI Dowbenko DJ, Lasky LA;

DR WPI; 2000-282393/24.

PT Novel genes encoding protein tyrosine phosphatase binding proteins useful  
 PT for isolating homologous genes, e.g. in tumor cells, which provide more  
 PT specific targets for tumor therapy.

PS Disclosure; Col 35; 65pp; English.

XX This sequence represents a fragment of a protein tyrosine phosphatase  
 CC (PTP). It was used to isolate the PST phosphatase interacting protein  
 CC (PSTPIP) sequence of the invention. The protein is a protein tyrosine  
 CC phosphatase that possesses a non-catalytic domain comprising a proline,  
 CC serine and threonine rich region and a C-terminal segment of 20 amino  
 CC acid (aa 8) rich in proline, and defines an SH3 binding domain. Nucleic  
 CC acids encoding native PSTPIP molecules can be used to isolate homologous  
 CC genes specifically expressed in tumour cells, which might provide more  
 CC specific targets for tumour therapy. The DNA is also useful for the  
 CC preparation of PSTPIP polypeptides by recombinant techniques and as  
 CC hybridisation probes for searching cDNA and genomic libraries for the  
 CC coding sequence of other PSTPIP polypeptide analogues in other species  
 CC  
 XX Sequence 19 AA;  
 SQ

Query Match 27.2%; Score 31; DB 3; Length 19;

Best Local Similarity 50.0%; Pred. No. 1.6e+03;  
 Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 6 GSRIGNPKAP 15  
 Db 3 GNRFSKPKGP 12

RESULT 94  
 AAB08488  
 ID AAB08488 standard; peptide; 19 AA.

AC AAB08488;

DT 20-DEC-2000 (first entry)

DE Peptide derived from a protein tyrosine phosphatase.

KM protein tyrosine phosphatase; PTP; phosphatase interacting protein;  
 KM PSTPIP; PST family; protein tyrosine phosphatase; actin monomer;  
 KM tissue typing; tumour cell; tumour imaging.

OS Synthetic.

PN US611073-A.

PD 29-AUG-2000.

PF 06-FEB-1998; 98US-00020222.

PR 17-APR-1997; 97US-0104590P.

XX (GETH ) GENENTECH INC.

PI Lasky LA;

DR WPI; 2000-586378/55.

PT Novel PST phosphatase interacting protein useful for inducing  
 PT polymerization of actin monomers and for identifying homolog of PST  
 PT phosphatase interacting protein.

PS Disclosure; Col 34; 48pp; English.

XX AAB08487-90 represent peptides derived from protein tyrosine phosphatase  
 CC (PTP). They were used to identify interaction domains of a murine protein  
 CC tyrosine phosphatase (PTP) phosphatase interacting protein (PSTPIP).  
 CC PSTPIP polypeptides are bound by and dephosphorylated by the PST family  
 CC of protein tyrosine phosphatases. PSTPIP associates with actin. PSTPIP is  
 CC useful for inducing the polymerisation of actin monomer in eukaryotic  
 CC cells by introducing the polypeptide into the cell. The polypeptide is  
 CC useful for identifying and isolating PSTPIP homologues in another  
 CC mammalian species, in screening assays to identify antagonists and  
 CC agonists of native PSTPIP polypeptide and as molecular weight markers on  
 CC protein gels. The PSTPIP nucleic acid is useful for tissue typing of  
 CC specific mammalian tissues, for preparing PSTPIP polypeptides by  
 CC recombinant techniques, as hybridisation probes for searching cDNA and  
 CC genomic libraries for the coding sequence of other PSTPIP analogues and  
 CC to isolate homologous genes specifically expressed in tumour cells.  
 CC Antagonists of PSTPIP peptide are useful for inhibiting biological  
 CC activity of the peptide. Antibodies of PSTPIP are useful to identify  
 CC rapidly dividing cells and are used to image tumours comprising such  
 CC rapidly dividing cells  
 CC  
 XX Sequence 19 AA;  
 SQ

Query Match 27.2%; Score 31; DB 3; Length 19;  
 Best Local Similarity 50.0%; Pred. No. 1.6e+03;  
 Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 6 GSRIGNPKAP 15  
 Db 3 GNRFSKPKGP 12

```

RESULT 95
AD90114
ID ADJ90114 standard; peptide; 19 AA.
XX
AC ADJ90114;
XX
DT 06-MAY-2004 (first entry)
XX
DE Human papillomavirus minor capsid protein L2 peptide #261.
XX
KW transporter peptide; UEV domain; Tag101; viral infection; HIV; AIDS;
KW hepatitis B virus infection; human herpesvirus 1 infection;
KW human herpesvirus 2 infection.
XX
OS Human papillomavirus type 6b.
XX
PN MO200305332-A2.
XX
PD 03-JUL-2003.
XX
PF 20-AUG-2002; 2002MO-US026549.
XX
PR 20-AUG-2001; 2001US-0313695P.
XX
PA (MYRI-) MYRIAD GENETICS INC.
XX
PI Morham S, Zavitz K, Hobden A,
XX
DR WPI; 2003-586940/55.
XX
PT Peptides and hybrid polypeptides associated with a transporter that
PT increases its uptake by a mammalian cell, useful for inhibiting viral
PT budding or propagation, especially for treating e.g. AIDS or hepatitis B
PT virus infection.
XX
PS Claim 35; SEQ ID NO 1582; 137pp; English.
XX
CC The invention comprises a composition which contains a peptide associated
CC with a transporter that is capable of increasing the uptake of the
CC peptide by a mammalian cell. The peptide of the invention contains the
CC amino acid motif Pro-Xaa-Xaa-Pro and is capable of binding the UEV domain
CC of Tag101. The composition of the invention is useful in the manufacture
CC of a medicament for the treatment of viral infections, such as: HIV
CC infection (particularly AIDS), hepatitis B virus infection and human
CC herpesvirus 1/2 infection. The present amino acid sequence represents a
CC peptide of the invention.
XX
SQ Sequence 19 AA;
XX
Query Match 27.2%; Score 31; DB 7; Length 19;
Best Local Similarity 33.3%; Pred. No. 1.6e+03;
Matches 5; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
QY 1 DYEYPSRLGNPKAP 15
DB 5 DITFPYRWKTPSP 19
XX
RESULT 96
ADV13539
ID ADV13539 standard; peptide; 19 AA.
XX
AC ADV13539;
XX
DT 10-MAR-2005 (first entry)
XX
DE Human phosphorylated peptide from phosphoprotein #1477.
XX
KW Alzheimer's disease; neuroprotective; nootropic; degeneration; tumor;
KW neoplasm; neurological disease; phosphorylation; protein sequencing;
KW phosphoprotein.

```

```

XX
OS Homo sapiens.
XX
PN WO2004108948-A2.
XX
PD 16-DEC-2004.
XX
PF 04-JUN-2004; 2004MO-US017613.
XX
PR 04-JUN-2003; 2003US-0476010P.
XX
PA (HARD ) HARVARD COLLEGE.
XX
PI Gylt SP;
XX
DR WPI; 2005-031720/03.
XX
PT Characterizing phosphorylated polypeptides in a sample comprises
PT digesting the polypeptides with a protease thus generating test peptides,
PT and collecting a fraction of test peptides that enriched for positively
PT charged peptides.
XX
PS Claim 16; Page 87; 123pp; English.
XX
CC The invention relates to characterizing phosphorylated polypeptides in a
CC sample comprising digesting the polypeptides with a protease thus
CC generating test peptides, and collecting a fraction of test peptides that
CC enriched for positively charged peptides. Also included are a method
CC (comprising determining the presence, absence or level of one ore more
CC phosphorylated peptides as identified above in cells having a cell state
CC and determining the degree of correlation between the presence, absence
CC or level of phosphorylated polypeptide with the cell state), an isolated
CC peptide of 5-50 amino acids comprising an amino acid sequence that is a
CC subsequence of any of the protein sequences given in the specification
CC (and which comprise a phosphorylation site within the subsequence), an
CC isolated polypeptide selected from any of the polypeptides listed in the
CC specification and is modified at a modification site, an isolated peptide
CC comprising a mass spectral peak signatures, a method for identifying a
CC treatment that modulates phosphorylation of an amino acid in a target
CC polypeptide, a method for generating a peptide standard, a pair of
CC peptide standards comprising the peptide obtained (where the peptide is
CC phosphorylated and a corresponding peptide comprising an identical amino
CC acid sequence but which is not phosphorylated), a system (comprising a
CC computer memory comprising data files storing information relating to the
CC identifying characteristics of positively charged peptides, and a data
CC analysis module capable of executing instructions for organizing and/or
CC searching the data files), a computer program product (comprising data
CC relating to the identifying characteristics of positively charged
CC peptides and comprising instructions for organizing and/or searching the
CC data), and a method for identifying N-terminal peptides in a sample. The
CC method is useful for characterizing phosphorylated polypeptides in a
CC sample. The present sequence is a peptide from a human phosphoprotein,
CC containing a phosphorylation site, identified by the method of the
CC invention.
XX
SQ Sequence 19 AA;
XX
Query Match 27.2%; Score 31; DB 9; Length 19;
Best Local Similarity 50.0%; Pred. No. 1.6e+03;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 11 NPKAPLYKRP 20
DB 1 NPKMPQYSSP 10
XX
RESULT 97
ADE15767
ID ADE15767 standard; peptide; 20 AA.
XX
AC ADE15767;
XX
DT 29-JAN-2004 (first entry)

```





PR 31-AUG-2001; 2001US-031680SP.  
 XX (STRD ) UNIV STANFORD.  
 PA (ELIL ) LILLY & CO ELI.  
 XX  
 XX Glenn JS, Myers TM, Glass JI,  
 DR WPI; 2003-201229/19.  
 XX  
 XX Identifying a compound for treating Hepatitis C virus (HCV) infection by  
 PT assessing the ability of a compound to interfere the binding of an  
 PT amphipathic helix of an HCV nonstructural protein with cytoplasmic  
 PT membranes of eukaryotic cell.  
 XX  
 PS Claim 44; Page 17; 43pp; English.  
 XX  
 CC The invention relates to a novel method for identifying a compound useful  
 CC for treating Hepatitis C virus (HCV) infection. The method comprises  
 CC assessing the ability of a candidate compound to interfere with the  
 CC binding of an amphipathic helix present in the N-terminal region of an  
 CC HCV non-structural protein with cytoplasmic membranes of a eukaryotic  
 CC cell, where a compound that interferes with the binding is useful for  
 CC treating the infection. The compounds of the invention have virucide, and  
 CC hepatotropic activity. The peptides may have a use in gene therapy. The  
 CC methods and compounds are useful for treating Hepatitis C virus (HCV)  
 CC infection. The composition is useful for eliciting an immunological  
 CC response against HCV. The peptides are useful for the preparation of a  
 CC medicament for the prevention or treatment of HCV infection in a human.  
 CC The sequences shown in ABR00747-ABR00754 represent ligands of the  
 CC amphipathic helix of the HCV nonstructural protein NS5A  
 XX  
 SQ Sequence 13 AA;

Query Match 26.8%; Score 30.5; DB 6; Length 13;  
 Best Local Similarity 64.3%; Pred. No. 1.3e+03;  
 Matches 9; Conservative 1; Mismatches 1; Indels 3; Gaps 2;

OY 4 YPGSRIGN--PKAP 15  
 |||:|||||  
 DB 1 YP-SKPGNTPPKAP 13

RESULT 100  
 ADU70749  
 ID ADU70749 standard; peptide; 9 AA.  
 XX  
 AC ADU70749;  
 XX  
 DT 10-FEB-2005 (first entry)  
 XX  
 DE Human heparanase peptide SEQ ID NO:434.  
 XX  
 KM enzyme; heparinase; vaccine; human leukocyte antigen; HLA;  
 KW immunostimulant; cytostatic; immune disorder; metastasis.  
 XX  
 OS Homo sapiens.  
 XX  
 XX EPI479764-A1.  
 PN  
 XX 24-NOV-2004.  
 PD  
 XX 19-MAY-2003; 2003BP-00011038.  
 PF  
 XX 19-MAY-2003; 2003BP-00011038.  
 PR  
 XX (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.  
 PA (UYH-) UNIV HEIDELBERG RUPRECHT-KARLS.  
 XX  
 PI Schlirmacher V, Beckhove P, Sommerfeldt N;  
 XX WPI; 2005-014847/02.  
 DR  
 XX New heparanase nonapeptide that binds to a human leukocyte antigen (HLA)  
 PT

PT molecule or its functional derivative, useful for preparing a medicament  
 PT for inducing an immune response or for treating metastatic tumors.  
 XX  
 XX  
 PS Claim 3; SEQ ID NO 434; 269pp; English.  
 XX

CC The invention relates to a novel heparanase peptide that binds to a human  
 CC leukocyte antigen (HLA) molecule, where the peptide is a nonapeptide, or  
 CC its functional derivative. A peptide of the invention has immunostimulant  
 CC and cytostatic activity, and is used in a vaccine. The heparinase peptide  
 CC is useful for preparing a medicament which induces an immune response or  
 CC for treating metastatic tumors. The present sequence represents a  
 CC heparinase peptide of the invention.  
 XX

SQ Sequence 9 AA;

Query Match 26.3%; Score 30; DB 9; Length 9;  
 Best Local Similarity 75.0%; Pred. No. 2e+06;  
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 5 PGRSLGNP 12  
 |||:|||||  
 DB 2 PGSSIGLP 9

Search completed: January 20, 2006, 19:05:10  
 Job time : 79.5769 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 20, 2006, 18:58:05 ; Search time 20.9615 seconds

(without alignments)  
78.883 Million cell updates/sec

Title: US-09-662-293-2

Perfect score: 114

Sequence: 1 DYEPGSRIGNPKAPLYKRP 20

Scoring table: BLOSUM62

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 223517

Minimum DB seq length: 0

Maximum DB seq length: 20

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/prodata/1/aa/5\_COMB.pep:\*  
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3: /cgn2\_6/prodata/1/aa/H\_COMB.pep:\*  
4: /cgn2\_6/prodata/1/aa/PCPUS\_COMB.pep:\*  
5: /cgn2\_6/prodata/1/aa/RB\_COMB.pep:\*  
6: /cgn2\_6/prodata/1/aa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	36	31.6	16	1	US-08-179-557-37
3	36	31.6	16	2	US-08-981-601-12
4	36	31.6	20	2	US-08-938-830-22
5	36	31.6	20	2	US-09-020-222-22
6	36	31.6	20	2	US-09-068-377-22
7	34.5	30.3	18	1	US-07-972-032-8
8	34.5	30.3	18	1	US-08-642-255-8
9	34	29.8	14	1	US-07-955-905A-3
10	33	28.9	18	1	US-09-025-706-6
11	33	28.9	18	2	US-09-025-622-6
12	33	28.9	19	2	US-10-394-980-17
13	32	28.1	13	1	US-08-233-203-4
14	32	28.1	15	1	US-08-625-691-15
15	32	28.1	17	1	US-08-729-152-43
16	32	28.1	17	2	US-08-630-915A-226
17	32	28.1	17	2	US-08-469-260A-251
18	32	28.1	17	2	US-08-488-446-251
19	32	28.1	17	2	US-08-467-344A-251
20	32	28.1	17	2	US-09-879-957-226
21	32	28.1	17	2	US-08-424-550B-251
22	32	28.1	20	2	US-08-938-830-20
23	32	28.1	20	2	US-09-020-222-20
24	31	27.2	20	2	US-09-068-377-20
25	31	27.2	14	1	US-08-211-070A-1
26	31	27.2	14	1	US-08-859-183-8
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29	31	27.2	16	2	US-08-602-999A-189	Sequence 189, App
30	31	27.2	16	2	US-09-500-124-189	Sequence 189, App
31	31	27.2	18	1	US-09-017-205-29	Sequence 29, App1
32	31	27.2	19	1	US-08-469-005A-3	Sequence 3, App1
33	31	27.2	19	1	US-08-188-426-3	Sequence 3, App1
34	31	27.2	19	1	US-08-469-009-3	Sequence 3, App1
35	31	27.2	19	1	US-08-469-007-3	Sequence 3, App1
36	31	27.2	19	2	US-08-938-830-21	Sequence 21, App1
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48	30	26.3	18	2	US-09-402-181B-163	Sequence 163, App
49	30	26.3	18	2	US-09-721-456-163	Sequence 163, App
50	30	26.3	18	2	US-09-623-548A-1140	Sequence 1140, App
51	30	26.3	18	2	US-10-131-346-8	Sequence 8, App1
52	30	26.3	18	2	US-09-657-276-1140	Sequence 1140, App
53	30	26.3	18	2	US-10-131-543-8	Sequence 8, App1
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60	30	26.3	19	2	US-08-394-748A-9	Sequence 9, App1
61	30	26.3	19	2	US-08-564-315-1	Sequence 1, App1
62	30	26.3	19	2	US-08-505-318-12	Sequence 12, App1
63	30	26.3	19	2	US-08-505-318-22	Sequence 22, App1
64	30	26.3	19	2	US-09-675-922-13	Sequence 13, App1
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72	30	26.3	20	1	US-08-462-784-2	Sequence 2, App1
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82	29	25.4	10	2	US-08-292-694A-36	Sequence 36, App1
83	29	25.4	12	2	US-09-177-249-108	Sequence 108, App
84	29	25.4	12	2	US-09-812-283-108	Sequence 108, App
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86	29	25.4	16	2	US-10-210-428-21	Sequence 21, App1
87	29	25.4	19	1	US-08-436-420-24	Sequence 24, App1
88	29	25.4	19	1	US-08-129-722A-8	Sequence 8, App1
89	29	25.4	19	2	US-09-674-674D-42	Sequence 42, App1
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93	29	25.4	20	2	US-09-991-433-34	Sequence 34, App1
94	29	25.4	20	2	US-10-017-75A-184A	Sequence 184, App
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96	28	24.6	7	1	US-08-331-394-43	Sequence 43, App1
97	28	24.6	7	1	US-08-250-858-43	Sequence 43, App1
98	28	24.6	7	1	US-08-446-915-43	Sequence 43, App1
99	28	24.6	7	1	US-08-744-139-43	Sequence 43, App1
100	28	24.6	7	2	US-08-779-599-43	Sequence 43, App1

## ALIGNMENTS

```
RESULT 1
US-09-293-225-2
; Sequence 2, Application US/09292225
; Patent No. 6455686
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine A.
; APPLICANT: Hunter, Shirley Wu
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: AL-2-C3
; CURRENT APPLICATION NUMBER: US/09/292,225
; EARLIER FILING DATE: 1999-04-15
; EARLIER APPLICATION NUMBER: 60/098,909
; EARLIER FILING DATE: 1998-09-02
; EARLIER APPLICATION NUMBER: 60/085,295
; EARLIER FILING DATE: 1998-05-13
; EARLIER APPLICATION NUMBER: 60/098,565
; EARLIER FILING DATE: 1998-04-17
; EARLIER APPLICATION NUMBER: 09/062,013
; EARLIER FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 2
; LENGTH: 20
; TYPE: PR1
; ORGANISM: Dermatophagoides farinae
US-09-292-225-2

Query Match      100.0%; Score 114; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 1,5e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DYEYPSRLGNPKAPLYKRP 20
DB      1 DYEYPSRLGNPKAPLYKRP 20

RESULT 2
US-08-179-557-37
; Sequence 37, Application US/08179557
; Patent No. 5837509
; GENERAL INFORMATION:
; APPLICANT: ISRAELSEN, Hans
; APPLICANT: BECH HANSEN, Egon
; APPLICANT: MADSEN, Soeren Michael
; APPLICANT: JOHANSEN, Eric
; APPLICANT: NILSSON, Dan
; APPLICANT: VRANG, Astrid
; TITLE OF INVENTION: Recombinant Lactic Acid Bacterium
; TITLE OF INVENTION: Containing an Inserted Promoter and Method of Constructing
; TITLE OF INVENTION: Same
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESSES:
; ADDRESSES: Foley & Lardner
; STREET: 3000 K Street, N.W.
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/179,557
; FILING DATE: 07-JAN-1994
; CLASSIFICATION: 435
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DK 1579/92
; FILING DATE: 30-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DK 0988/93
; FILING DATE: 01-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/DK94/00004
; FILING DATE: 03-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/036,681
; FILING DATE: 25-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30307/140/PLVI
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202 672 5300
; TELEFAX: 202 672 5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-179-557-37

Query Match      31.6%; Score 36; DB 1; Length 16;
Best Local Similarity 70.0%; Pred. No. 59;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 DYEYPSRLG 10
DB      7 DLQDPGSLG 16

RESULT 3
US-08-981-601-12
; Sequence 12, Application US/08981601
; Patent No. 6133023
; GENERAL INFORMATION:
; APPLICANT: MADSEN, Soeren Michael
; APPLICANT: VRANG, Astrid
; APPLICANT: ARNAU, Jose
; APPLICANT: RAVN, Peter
; APPLICANT: GROENVALD JOHNSEN, Mads
; APPLICANT: ISRAELSEN, Hans
; TITLE OF INVENTION: A LACTIC ACID BACTERIAL REGULATABLE
; TITLE OF INVENTION: EXPRESSION SYSTEM
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESSES:
; ADDRESSES: FOLEY & LARDNER
; STREET: 3000 K Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/981,601
; FILING DATE: 29-DEC-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/DK97/00341
; FILING DATE: 22-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/711,434
; FILING DATE: 06-SEP-1996
; ATTORNEY/AGENT INFORMATION:
```

NAME: Bent, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 030307/0158  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 672-5300  
TELEFAX: (202) 672-5399  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-981-601-12

Query Match 31.6%; Score 36; DB 2; Length 16;  
Best Local Similarity 70.0%; Pred. No. 59;  
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DYEPGSRIG 10  
DB 7 DLDPGSRIG 16

## RESULT 4

US-08-938-830-22  
Sequence 22, Application US/08938830  
Patent No. 6040437  
GENERAL INFORMATION:  
APPLICANT: Laeky, Laurence A.  
APPLICANT: Dowbenko, Donald J.  
TITLE OF INVENTION: Tyrosine Phosphorylated Cleavage  
TITLE OF INVENTION: Furrow-Associated Proteins (PSTPIPs)  
NUMBER OF SEQUENCES: 73  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Winpatin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/938,830  
FILING DATE:  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/798419  
FILING DATE: 07-FEB-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Dregler, Ginger R.  
REGISTRATION NUMBER: 33,055  
REFERENCE/DOCKET NUMBER: P1066P1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-3216  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: Amino Acid  
TOPOLOGY: linear  
US-08-938-830-22

Query Match 31.6%; Score 36; DB 2; Length 20;  
Best Local Similarity 60.0%; Pred. No. 75;  
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 GSRIGPKAP 15  
DB 6 GSRIGPKAP 15

DB 3 GNRGKPKP 12

## RESULT 5

US-09-020-222-22  
Sequence 22, Application US/09020222  
Patent No. 611073  
GENERAL INFORMATION:  
APPLICANT: Laeky, Laurence A.  
TITLE OF INVENTION: Tyrosine Phosphorylated Cleavage  
TITLE OF INVENTION: Furrow-Associated Proteins (PSTPIPs)  
NUMBER OF SEQUENCES: 27  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Winpatin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/020,222  
FILING DATE: 06-Feb-1998  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/798419  
FILING DATE: 02/07/1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Dregler, Ginger R.  
REGISTRATION NUMBER: 33,055  
REFERENCE/DOCKET NUMBER: P1066P1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-3216  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: Amino Acid  
TOPOLOGY: linear  
US-09-020-222-22

Query Match 31.6%; Score 36; DB 2; Length 20;  
Best Local Similarity 60.0%; Pred. No. 75;  
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 GSRIGPKAP 15  
DB 3 GNRGKPKP 12

## RESULT 6

US-09-068-377-22  
Sequence 22, Application US/09068377  
Patent No. 688705  
GENERAL INFORMATION:  
APPLICANT: Laeky, Laurence A.  
APPLICANT: Dowbenko, Donald J.  
TITLE OF INVENTION: Tyrosine Phosphorylated Cleavage Furrow-Associated  
TITLE OF INVENTION: Proteins (PSTPIPs)  
FILE REFERENCE: P1066P2  
CURRENT APPLICATION NUMBER: US/09/068,377  
CURRENT FILING DATE: 1999-05-08  
EARLIER APPLICATION NUMBER: US 08/938,300  
EARLIER FILING DATE: 1997-09-29  
EARLIER APPLICATION NUMBER: US 08/798,419  
EARLIER FILING DATE: 1997-02-07  
NUMBER OF SEQ ID NOS: 73  
SEQ ID NO 22  
LENGTH: 20

TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
NAME/KEY: Artificial Sequence  
LOCATION: 1-20  
OTHER INFORMATION: Synthetic oligopeptide  
US-09-068-377-22

Query Match 31.6%; Score 36; DB 2; Length 20;  
Best Local Similarity 60.0%; Pred. No. 75;  
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 6 GSRLGNPKAP 15  
Db 3 GNRCKPKGP 12

RESULT 7  
US-07-972-032-8  
Sequence 8, Application US/07972032  
Patent No. 5496712  
GENERAL INFORMATION:  
APPLICANT: Cappello, Joseph  
APPLICANT: Ferrari, Franco A.  
TITLE OF INVENTION: HIGH MOLECULAR WEIGHT COLLAGEN-LIKE  
TITLE OF INVENTION: PROTEIN POLYMERS  
NUMBER OF SEQUENCES: 85  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Bertam I. Rowland  
STREET: 4 Embarcadero Center, Suite 3400  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: CA 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/972,032  
FILING DATE: 19921105  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/791,960  
FILING DATE: 12-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Rowland, Bertam I.  
REGISTRATION NUMBER: 20,015  
REFERENCE/DOCKET NUMBER: A-55556-1/BIR,PROP-08-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 781-1983  
TELEFAX: (415) 398-3249  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-07-972-032-8

Query Match 30.3%; Score 34.5; DB 1; Length 18;  
Best Local Similarity 72.7%; Pred. No. 1.1e+02;  
Matches 8; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

Qy 5 PGSRLGNPKAP 15  
Db 6 PGSR-GDPGAP 15

RESULT 8  
US-08-642-255-8  
Sequence 8, Application US/08642255

Patent No. 5773249  
GENERAL INFORMATION:  
APPLICANT: CAPPELLO, Joseph  
APPLICANT: FERRARI, Franco A.  
TITLE OF INVENTION: High Molecular Weight Collagen-Like  
TITLE OF INVENTION: Protein Polymers  
NUMBER OF SEQUENCES: 135  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT  
STREET: 4 Embarcadero Center, Suite 3400  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-4187  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/642,255  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: ROWLAND, Bertam I.  
REGISTRATION NUMBER: 20,015  
REFERENCE/DOCKET NUMBER: A55556-3/BIR  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 494-8700  
TELEFAX: (415) 494-8771  
TELEX: 910 277299 FHT UR  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-642-255-8

Query Match 30.3%; Score 34.5; DB 1; Length 18;  
Best Local Similarity 72.7%; Pred. No. 1.1e+02;  
Matches 8; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

Qy 5 PGSRLGNPKAP 15  
Db 6 PGSR-GDPGAP 15

RESULT 9  
US-07-955-905A-3  
Sequence 3, Application US/07955905A  
Patent No. 5770453  
GENERAL INFORMATION:  
APPLICANT:  
TITLE OF INVENTION: RECOMBINANT 47 AND 31 KD COCOA PROTEINS AND  
TITLE OF INVENTION: PRECURSOR  
NUMBER OF SEQUENCES: 28  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/955,905A  
FILING DATE: 21-JAN-1993  
CLASSIFICATION: 435  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein

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; ORIGINAL SOURCE:
; ORGANISM: Theobroma cacao
; FEATURE:
; NAME/KEY: Region
; LOCATION: 1..14
; OTHER INFORMATION: /note="Tentative N-terminal
; OTHER INFORMATION: sequence of 47kD mature protein"
US-07-955-905A-3

Query Match      29.8%; Score 34; DB 1; Length 14;
Best Local Similarity 60.0%; Pred. NO. 1e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      3 EYPSGRUGNP 12
DB      1 EEPGSGPAMP 10

RESULT 10
US-09-025-706-6
; Sequence 6, Application US/09025706
; Patent No. 5958874
; GENERAL INFORMATION:
; APPLICANT: Clark, Richard A
; APPLICANT: Gelling, Doris
; APPLICANT: Gailit, James
; TITLE OF INVENTION: RECOMBINANT FIBRONECTIN-BASED
; TITLE OF INVENTION: EXTRACELLULAR MATRIX FOR WOUND HEALING
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Jaackle Fleischmann & Mugel, LLP
; STREET: 39 State Street
; CITY: Rochester
; STATE: New York
; COUNTRY: USA
; ZIP: 14614-1310
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,706
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Braham, Susan J
; REGISTRATION NUMBER: 34,103
; REFERENCE/DOCKET NUMBER: 87653.97R263
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 716-262-3640
; TELEFAX: 716-262-4133
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-025-706-6

Query Match      28.9%; Score 33; DB 1; Length 18;
Best Local Similarity 42.1%; Pred. NO. 1.9e+02;
Matches 8; Conservative 2; Mismatches 5; Indels 4; Gaps 1;

QY      2 YEYPSGRUGNP 20
DB      1 YEKPGS----PREVPRP 15

RESULT 11
US-09-025-622-6
; Sequence 6, Application US/09025622
```

```

; Patent No. 6194378
; GENERAL INFORMATION:
; APPLICANT: Clark, Richard A
; APPLICANT: Gelling, Doris
; APPLICANT: Gailit, James
; TITLE OF INVENTION: FIBRONECTIN PEPTIDES-BASED EXTRACELLULAR
; TITLE OF INVENTION: MATRIX FOR WOUND HEALING
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Jaackle Fleischmann & Mugel, LLP
; STREET: 39 State Street
; CITY: Rochester
; STATE: New York
; COUNTRY: USA
; ZIP: 14614-1310
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,622
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Braham, Susan J
; REGISTRATION NUMBER: 34,103
; REFERENCE/DOCKET NUMBER: 87653.97R270
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 716-262-3640
; TELEFAX: 716-262-4133
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-025-622-6

Query Match      28.9%; Score 33; DB 2; Length 18;
Best Local Similarity 42.1%; Pred. NO. 1.9e+02;
Matches 8; Conservative 2; Mismatches 5; Indels 4; Gaps 1;

QY      2 YEYPSGRUGNP 20
DB      1 YEKPGS----PREVPRP 15

RESULT 12
US-10-394-980-17
; Sequence 17, Application US/10394980
; Patent No. 6908740
; GENERAL INFORMATION:
; APPLICANT: Vandekerckhove, Joel
; APPLICANT: Gevaert, Kris
; TITLE OF INVENTION: METHODS AND APPARATUS FOR GEL-FREE QUALITATIVE AND
; FILE REFERENCES: VBV-001
; CURRENT APPLICATION NUMBER: US/10/394,980
; CURRENT FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: PCT/EP02/03368
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: US60/278,171
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: US60/318,749
; PRIOR FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US60/323,999
; PRIOR FILING DATE: 2001-09-20
; NUMBER OF SEQ ID NOS: 473
; SOFTWARE: Patent In version 3.1
; SEQ ID NO 17
; LENGTH: 19
; TYPE: PRT
```

ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: MISC FEATURE  
OTHER INFORMATION: part of HBB\_HUMAN ((P02023) hemoglobin beta chain)  
US-10-394-980-17

Query Match 28.9%; Score 33; DB 2; Length 19;  
Best Local Similarity 46.2%; Pred. No. 2e+02;  
Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 DYEPGSRGNPK 13  
| : |||||  
DB 7 DLSTPDVAVGNPK 19

RESULT 13  
US-08-233-203-4  
Sequence 4, Application US/08233203  
Patent No. 5409898  
GENERAL INFORMATION:  
APPLICANT: Darveau, Richard P.  
APPLICANT: Blake, James J.  
TITLE OF INVENTION: COBAND, Wesley L.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING  
TITLE OF INVENTION: INFECTIONS CAUSED BY ORGANISM SENSITIVE TO BETA-LACTAM  
TITLE OF INVENTION: ANTIBIOTICS  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Bristol-Myers Squibb Company, Patent  
ADDRESSEE: Department  
STREET: 3005 First Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98121  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/233,203  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/655,321  
FILING DATE: 19-FEB-1991  
APPLICATION NUMBER: US 07/484,020  
FILING DATE: 23-FEB-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Poor, Brian W.  
REGISTRATION NUMBER: 32,928  
REFERENCE/DOCKET NUMBER: ON0063A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206/728-4800  
TELEFAX: 206/448-4775  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 13 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: YES  
US-08-233-203-4

Query Match 28.1%; Score 32; DB 1; Length 13;  
Best Local Similarity 83.3%; Pred. No. 1.9e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 15 PLYKKP 20  
| : |||||  
DB 1 PLYKKP 6

RESULT 14  
US-08-625-691-15  
Sequence 15, Application US/08625691  
Patent No. 5763574  
GENERAL INFORMATION:  
APPLICANT: Conley, Anthony J.  
APPLICANT: Boots, Lynn J.  
APPLICANT: Arnold, Beth A.  
APPLICANT: Keller, Paul M.  
TITLE OF INVENTION: HIV-SPECIFIC SYNTHETIC ANTIGENS AND  
TITLE OF INVENTION: THEIR USE  
NUMBER OF SEQUENCES: 33  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Joanne M. Glesser  
STREET: 126 E. Lincoln Avenue, P.O. Box 2000  
CITY: Rahway  
STATE: NJ  
COUNTRY: USA  
ZIP: 07065

COMPUTER READABLE FORM:  
MEDIUM TYPE: Tape  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/625,691  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Glesser, Joanne M.  
REGISTRATION NUMBER: 32,838  
REFERENCE/DOCKET NUMBER: 19270  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (908) 594-3046  
TELEFAX: (908) 594-4720  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: internal  
US-08-625-691-15

Query Match 28.1%; Score 32; DB 1; Length 15;  
Best Local Similarity 71.4%; Pred. No. 2.2e+02;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 YEYPSGR 8  
| : |||||  
DB 9 YHYPSGR 15

RESULT 15  
US-08-729-152-43  
Sequence 43, Application US/08729152  
Patent No. 5871739  
GENERAL INFORMATION:  
APPLICANT: Inoue, Brl  
TITLE OF INVENTION: Pharmaceutical Composition  
NUMBER OF SEQUENCES: 47  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wenderoth, Land & Ponack  
STREET: Southern Building, Suite 700, 805 Fifteenth  
CITY: Street, N.W.  
STATE: D.C.  
COUNTRY: USA



ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Mb storage  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE:  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/729,152  
FILING DATE: 11-OCT-1996  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 291993/1995  
FILING DATE: 13-OCT-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek, Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8850  
TELEFAX:  
TELEX:  
INFORMATION FOR SEQ ID NO: 43:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE:  
DESCRIPTION: peptide  
US-08-729-152-43

Query Match 28.1%; Score 32; DB 1; Length 17;  
Best Local Similarity 71.4%; Pred. No. 2.5e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 2 YEPYGR 8  
DB 10 YQYGR 16

RESULT 16  
US-08-630-915A-226  
Sequence 226, Application US/08630915A  
Patent No. 6309820  
GENERAL INFORMATION:  
APPLICANT: SPARKS, Andrew B.  
APPLICANT: HOFFMAN, No. 6309820h  
APPLICANT: KAY, Brian K.  
APPLICANT: FOWLES, Dana M.  
APPLICANT: MCCONNELL, Stephen J.  
TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL  
TITLE OF INVENTION: DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND  
NUMBER OF SEQUENCES: 227  
CORRESPONDENCE ADDRESSES:  
ADDRESSER: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/630,915A  
FILING DATE: 03-APR-1996  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Mastrook, S. Leslie  
REGISTRATION NUMBER: 18,872

REFERENCE/DOCKET NUMBER: 1101-174  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-5090  
TELEFAX: (212) 869-8864/9741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 226:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHEICAL: NO  
ANTI-SENSE: NO  
US-08-630-915A-226

Query Match 28.1%; Score 32; DB 2; Length 17;  
Best Local Similarity 63.6%; Pred. No. 2.5e+02;  
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 6 GSRLGNPKAPL 16  
DB 2 GSGIAPPKPL 12

RESULT 17  
US-08-469-260A-251  
Sequence 251, Application US/08469260A  
Patent No. 6451578  
GENERAL INFORMATION:  
APPLICANT: JOHN N. SIMONS  
APPLICANT: TAMI J. PILOT-MARTIAS  
APPLICANT: GEORGE J. DAWSON  
APPLICANT: GEORGE G. SCHLAUDER  
APPLICANT: SURESH M. DESAI  
APPLICANT: THOMAS P. LEARY  
APPLICANT: ANTHONY SCOTT MUEHRHOF  
APPLICANT: JAMES C. ERKER  
APPLICANT: SHERI L. BUTIK  
APPLICANT: ISA K. MUSHAWAR  
TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS  
TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE  
NUMBER OF SEQUENCES: 716  
CORRESPONDENCE ADDRESSES:  
ADDRESSER: ABBOTT LABORATORIES D377/AP6D  
STREET: 100 ABBOTT PARK ROAD  
CITY: ABBOTT PARK  
STATE: IL  
COUNTRY: USA  
ZIP: 60064-3500  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/469,260A  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/424,550  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: POREMSKI, PRISCILLA B.  
REGISTRATION NUMBER: 33,207  
REFERENCE/DOCKET NUMBER: 5527.PC.01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 708-938-2623  
TELEFAX: 708-937-6365  
INFORMATION FOR SEQ ID NO: 251:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 amino acids  
TYPE: amino acid

TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-469-260A-251

Query Match 28.1%; Score 32; DB 2; Length 17;  
Best Local Similarity 41.7%; Pred. No. 2.5e+02;  
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 5 PGSRLGNPKAPL 16  
DB 1 PSERFSSPKLPV 12

RESULT 18  
US-08-488-446-251

Sequence 251, Application US/08488446  
Patent No. 6558898

GENERAL INFORMATION:  
APPLICANT: JOHN N. SIMONS  
APPLICANT: TAMU J. PILOT-MATIAS  
APPLICANT: GEORGE J. DAWSON  
APPLICANT: SURESH M. DESAI  
APPLICANT: THOMAS P. LEARY  
APPLICANT: ANTHONY SCOTT MUEHRHOFF  
APPLICANT: JAMES C. ERKER  
APPLICANT: SHERI L. BUIJK  
APPLICANT: ISA K. MUSHAMMAR  
TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS  
TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE  
NUMBER OF SEQUENCES: 716  
CORRESPONDENCE ADDRESS:  
ADDRESS: ABBOTT LABORATORIES D377/AP6D  
STREET: 100 ABBOTT PARK ROAD  
CITY: ABBOTT PARK  
STATE: IL  
COUNTRY: USA  
ZIP: 60064-3500

COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/488,446

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/424,550

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: POREMSKI, PRISCILLA E.

REGISTRATION NUMBER: 33,207

REFERENCE/DOCKET NUMBER: 5527.PC.01

TELECOMMUNICATION INFORMATION:

TELEPHONE: 708-937-6365

TELEFAX: 708-938-2623

INFORMATION FOR SEQ ID NO: 251:

SEQUENCE CHARACTERISTICS:

LENGTH: 17 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-488-446-251

Query Match 28.1%; Score 32; DB 2; Length 17;  
Best Local Similarity 41.7%; Pred. No. 2.5e+02;  
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 5 PGSRLGNPKAPL 16  
DB 1 PSERFSSPKLPV 12

RESULT 19  
US-08-467-344A-251

Sequence 251, Application US/08467344A  
Patent No. 6586568

GENERAL INFORMATION:  
APPLICANT: JOHN N. SIMONS  
APPLICANT: TAMU J. PILOT-MATIAS  
APPLICANT: GEORGE J. DAWSON  
APPLICANT: SURESH M. DESAI  
APPLICANT: THOMAS P. LEARY  
APPLICANT: ANTHONY SCOTT MUEHRHOFF  
APPLICANT: JAMES C. ERKER  
APPLICANT: SHERI L. BUIJK  
APPLICANT: ISA K. MUSHAMMAR  
TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS  
TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE  
NUMBER OF SEQUENCES: 716  
CORRESPONDENCE ADDRESS:  
ADDRESS: ABBOTT LABORATORIES D377/AP6D  
STREET: 100 ABBOTT PARK ROAD  
CITY: ABBOTT PARK  
STATE: IL  
COUNTRY: USA  
ZIP: 60064-3500

COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/467,344A  
FILING DATE: 07-Jun-1995  
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/424,550

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: POREMSKI, PRISCILLA E.

REGISTRATION NUMBER: 33,207

REFERENCE/DOCKET NUMBER: 5527.PC.01

TELECOMMUNICATION INFORMATION:

TELEPHONE: 708-937-6365

TELEFAX: 708-938-2623

INFORMATION FOR SEQ ID NO: 251:

SEQUENCE CHARACTERISTICS:

LENGTH: 17 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 251:

US-08-467-344A-251

Query Match 28.1%; Score 32; DB 2; Length 17;  
Best Local Similarity 41.7%; Pred. No. 2.5e+02;  
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 5 PGSRLGNPKAPL 16  
DB 1 PSERFSSPKLPV 12

RESULT 20  
US-09-879-957-226

Sequence 226, Application US/09879957  
Patent No. 6709821

GENERAL INFORMATION:  
APPLICANT: SPARKS, Andrew B.  
APPLICANT: HOFFMAN, No. 6709821h  
APPLICANT: KAY, Brian K.  
APPLICANT: FOWLES, Dana M.  
APPLICANT: MCCONNELL, Stephen J.

TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL  
DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND  
USING SAME  
NUMBER OF SEQUENCES: 227  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/879,957  
FILING DATE: 13-Jun-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/630,915  
FILING DATE: 03-APR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Mastrock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 1101-174  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-8864/9741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 226:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHEICAL: NO  
ANTI-SENSE: NO  
SEQUENCE DESCRIPTION: SEQ ID NO: 226:  
US-09-879-957-226  
Query Match 28.1%; Score 32; DB 2; Length 17;  
Best Local Similarity 63.6%; Pred. No. 2.5e+02;  
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 6 GSRGNGPKAPL 16  
DB 2 GSGIAPKPP 12  
RESULT 21  
US-08-424-550B-251  
Sequence 251, Application US/08424550B  
Patent No. 6720166  
GENERAL INFORMATION:  
APPLICANT: JOHN N. SIMONS  
APPLICANT: TAM J. PILOT-MATIAS  
APPLICANT: GEORGE J. DAWSON  
APPLICANT: GEORGE G. SCHLAUDER  
APPLICANT: SURESH M. DESAI  
APPLICANT: THOMAS P. LEARY  
APPLICANT: ANTHONY SCOTT MUEHRHOFF  
APPLICANT: JAMES C. BRKER  
APPLICANT: SHERI L. BUTIK  
APPLICANT: ISA K. MUSHAWAR  
TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS  
TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE  
NUMBER OF SEQUENCES: 716  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: ABBOTT LABORATORIES D377/APed  
STREET: 100 ABBOTT PARK ROAD

CITY: ABBOTT PARK  
STATE: IL  
COUNTRY: USA  
ZIP: 60064-3500  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/424,550B  
FILING DATE:  
CLASSIFICATION: 435435  
ATTORNEY/AGENT INFORMATION:  
NAME: FOREMSKI, PRISCILLA E.  
REGISTRATION NUMBER: 33,207  
REFERENCE/DOCKET NUMBER: 5527.PC.01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 708-937-6365  
TELEFAX: 708-938-2623  
INFORMATION FOR SEQ ID NO: 251:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-424-550B-251  
Query Match 28.1%; Score 32; DB 2; Length 17;  
Best Local Similarity 41.7%; Pred. No. 2.5e+02;  
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;  
QY 5 PSRRFSSPKLPV 12  
DB 1 PSRRFSSPKLPV 12  
RESULT 22  
US-08-938-830-20  
Sequence 20, Application US/08938830  
Patent No. 6040437  
GENERAL INFORMATION:  
APPLICANT: Laeky, Laurence A.  
APPLICANT: Dowbenko, Donald J.  
TITLE OF INVENTION: Tyrosine Phosphorylated Cleavage  
TITLE OF INVENTION: Furrow-Associated Proteins (PstPfs)  
NUMBER OF SEQUENCES: 73  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 Inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/938,830  
FILING DATE:  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/798419  
FILING DATE: 07-FEB-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Dreyer, Ginger R.  
REGISTRATION NUMBER: 33,055  
REFERENCE/DOCKET NUMBER: P1066P1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-3216  
TELEFAX: 650/952-9881

; INFORMATION FOR SEQ ID NO: 20:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 20 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
US-08-938-830-20

Query Match 28.1%; Score 32; DB 2; Length 20;  
Best Local Similarity 62.5%; Pred. No. 3e+02;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 8 RLGNPKAP 15  
|:|:|:|:  
Db 5 RIGRPKGP 12

RESULT 23  
US-09-020-222-20  
; Sequence 20, Application US/09020222  
; Patent No. 611073  
; GENERAL INFORMATION:

; APPLICANT: Laeky, Laurence A.  
; TITLE OF INVENTION: Tyrosine Phosphorylated Cleavage  
; TITLE OF INVENTION: Furrow-Associated Proteins (PSYPIPS)  
; NUMBER OF SEQUENCES: 27  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSER: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/020,222  
; FILING DATE: 06-Feb-1998  
; CLASSIFICATION:

; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/798419  
; FILING DATE: 02/07/1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Dreyer, Ginger R.  
; REGISTRATION NUMBER: 33,055  
; REFERENCE/DOCKET NUMBER: P1066r1

; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/952-3216  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 20:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 20 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
US-09-020-222-20

Query Match 28.1%; Score 32; DB 2; Length 20;  
Best Local Similarity 62.5%; Pred. No. 3e+02;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 8 RLGNPKAP 15  
|:|:|:|:  
Db 5 RIGRPKGP 12

RESULT 24  
US-09-068-377-20  
; Sequence 20, Application US/09068377  
; Patent No. 6887705  
; GENERAL INFORMATION:  
; APPLICANT: Laeky, Laurence A.

; APPLICANT: Dowbenko, Donald J.  
; TITLE OF INVENTION: Tyrosine Phosphorylated Cleavage Furrow-Associated  
; TITLE OF INVENTION: Proteins (PSYPIPS)  
; FILE REFERENCE: P1066r2  
; CURRENT APPLICATION NUMBER: US/09/068,377  
; CURRENT FILING DATE: 1999-05-08  
; EARLIER APPLICATION NUMBER: US 08/938,300  
; EARLIER FILING DATE: 1997-09-29  
; EARLIER APPLICATION NUMBER: US 08/798,419  
; EARLIER FILING DATE: 1997-02-07  
; NUMBER OF SEQ ID NOS: 73  
; SEQ ID NO 20  
; LENGTH: 20  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: Artificial Sequence  
; LOCATION: 1-20  
; OTHER INFORMATION: Synthetic oligopeptide  
US-09-068-377-20

Query Match 28.1%; Score 32; DB 2; Length 20;  
Best Local Similarity 62.5%; Pred. No. 3e+02;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 8 RLGNPKAP 15  
|:|:|:|:  
Db 5 RIGRPKGP 12

RESULT 25  
US-08-211-070A-1  
; Sequence 1, Application US/08211070A  
; Patent No. 5585350  
; GENERAL INFORMATION:

; APPLICANT: Friedrich, Thomas  
; APPLICANT: Koewer, Wolfgang  
; APPLICANT: Kroegeer, Burkhard  
; APPLICANT: Bialojan, Siegfried  
; TITLE OF INVENTION: No. 5585350e1 thrombin-inhibitory protein from ticks.  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSER: Keil & Weinkauff  
; STREET: 1101 Connecticut Avenue  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20036

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb storage  
; COMPUTER: IBM AT-compatible, 80486 processor  
; OPERATING SYSTEM: MS-DOS version 6.0  
; SOFTWARE: Wordperfect version 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/211,070A  
; FILING DATE: 18-MAR-1994  
; CLASSIFICATION: 435  
; CLASSIFICATION: C12P 21/02  
; CLASSIFICATION: A61K 37/64  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/EP92/02198  
; FILING DATE: 23-SEP-1992  
; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:  
; LENGTH: 14 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
US-08-211-070A-1

Query Match 27.2%; Score 31; DB 1; Length 14;  
Best Local Similarity 41.7%; Pred. No. 2.9e+02;  
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

OY 1 DYEPGSRGPNP 12  
|||:|:|  
Db 2 DYEPGPKKCRP 13

## RESULT 26

US-08-859-183-8  
Sequence 8, Application US/08859183  
Patent No. 5827731  
GENERAL INFORMATION:  
APPLICANT: Friedrich, Thomas  
APPLICANT: Bialojan, Siegfried  
APPLICANT: Bollschweiler, Claus  
APPLICANT: Kueneast, Christoph  
TITLE OF INVENTION: No. 5827731el thrombin-inhibitory protein  
TITLE OF INVENTION: from ticks  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Kell & Weinkauff  
STREET: 1101 Connecticut Avenue  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 1.2 Mb storage  
COMPUTER: IBM AT-compatible, 80486 processor  
OPERATING SYSTEM: MS-DOS version 6.0  
SOFTWARE: WordPerfect version 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/859,183  
FILING DATE: 20-MAY-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/415,999  
FILING DATE: 04-APR-1995  
APPLICATION NUMBER: PCT/EP92/02179  
FILING DATE: 21-SEP-1992  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-859-183-8

Query Match 27.2%; Score 31; DB 1; Length 14;  
Best Local Similarity 41.7%; Pred. No. 2.9e+02;  
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

OY 1 DYEPGSRGPNP 12  
|||:|:|  
Db 2 DYEPGPKKCRP 13

## RESULT 27

US-08-374-652C-12  
Sequence 12, Application US/08374652C  
Patent No. 5834286  
GENERAL INFORMATION:  
APPLICANT: NEVALAINEN, HELENA K.M.  
APPLICANT: PALOHEIMO, MARJA T.  
APPLICANT: PAGERSTROM, RICHARD B.  
APPLICANT: MERTINEN-OINONEN, ARJA S.  
APPLICANT: TURUNEN, MARJA K.  
APPLICANT: RAMBOSER, JOHN A.  
APPLICANT: PIDDINGTON, CHRISTOPHER S.  
APPLICANT: HOUSTON, CHRISTINE S.  
APPLICANT: CANTRELL, MICHAEL A.  
TITLE OF INVENTION: RECOMBINANT CELLS, DNA CONSTRUCTS,  
TITLE OF INVENTION: VECTORS AND METHODS FOR EXPRESSING PHYTATE DEGRADING  
TITLE OF INVENTION: ENZYMES IN DESIRED RATIOS  
NUMBER OF SEQUENCES: 94  
CORRESPONDENCE ADDRESS:

ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
STREET: 1100 NEW YORK AVENUE, SUITE 600  
CITY: WASHINGTON  
STATE: DC  
COUNTRY: USA  
ZIP: 20005

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/374,652C  
FILING DATE: 24-MAY-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/07058  
FILING DATE: 27-JUL-1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/925,401  
FILING DATE: 31-JUL-1992  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: REED, GRANT R.  
REGISTRATION NUMBER: 41,264  
REFERENCE/DOCKET NUMBER: 1050.071001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-2600  
TELEFAX: 202-371-2540  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: not relevant  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Modified-Site  
LOCATION: 4  
OTHER INFORMATION: /NOTE= "Can be His or Leu"  
US-08-374-652C-12

Query Match 27.2%; Score 31; DB 1; Length 14;  
Best Local Similarity 50.0%; Pred. No. 2.9e+02;  
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 4 YPGSRGPNKAP 15  
|||:|:|  
Db 1 YPGXGAGNPGP 12

## RESULT 28

US-09-012-097A-19  
Sequence 19, Application US/09012097A  
Patent No. 6187757  
GENERAL INFORMATION:  
APPLICANT: Clackson, Timothy  
APPLICANT: Gilman, Michael  
APPLICANT: Holt, Dennis  
APPLICANT: Keenan, Terence  
APPLICANT: Rozamus, Leonard  
APPLICANT: Yang, Wu  
TITLE OF INVENTION: Regulation of Biological Events Using  
TITLE OF INVENTION: No. 6187757el Compounds  
NUMBER OF SEQUENCES: 66  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: ARIAD Pharmaceuticals, Inc.  
STREET: 26 Landsdowne Street  
CITY: Cambridge  
STATE: MA  
COUNTRY: USA  
ZIP: 02139

COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/012,097A  
FILING DATE: 22-JAN-1998  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Berstein Esq., David L.  
REGISTRATION NUMBER: 31,235  
REFERENCE/DOCKET NUMBER: 374 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-494-0400  
TELEFAX: 617-494-0208  
INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: internal  
US-09-012-097A-19

Query Match 27.2%; Score 31; DB 2; Length 15;  
Best Local Similarity 54.5%; Pred. No. 3.1e+02;  
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 9 LGNPKAPLYKR 19  
DB 4 LGGSSSPKCKR 14

RESULT 29  
US-08-602-999A-189  
Sequence 189, Application US/08602999A  
Patent No. 6184205  
GENERAL INFORMATION:  
APPLICANT: SPARKS, Andrew B.  
APPLICANT: KAY, Brian K.  
APPLICANT: THORN, Judith M.  
APPLICANT: QUILIAM, Lawrence A.  
APPLICANT: DER, Channing J.  
APPLICANT: FOWLKES, Dana M.  
APPLICANT: RIDER, James E.  
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
TITLE OF INVENTION: ISOLATING AND USING SAME  
NUMBER OF SEQUENCES: 467  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/602,999A  
FILING DATE: 16-FEB-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Mistrock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 1101-202  
TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 189:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-602-999A-189

Query Match 27.2%; Score 31; DB 2; Length 16;  
Best Local Similarity 60.0%; Pred. No. 3.3e+02;  
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 9 LGNPKAPLYK 18  
DB 4 LGRPERIPLYK 13

RESULT 30  
US-09-500-124-189  
Sequence 189, Application US/09500124  
Patent No. 6432920  
GENERAL INFORMATION:  
APPLICANT: SPARKS, Andrew B.  
APPLICANT: KAY, Brian K.  
APPLICANT: THORN, Judith M.  
APPLICANT: QUILIAM, Lawrence A.  
APPLICANT: DER, Channing J.  
APPLICANT: FOWLKES, Dana M.  
APPLICANT: RIDER, James E.  
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
TITLE OF INVENTION: ISOLATING AND USING SAME  
NUMBER OF SEQUENCES: 467  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/500,124  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/602,999  
FILING DATE: 16-FEB-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Mistrock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 1101-202  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 189:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-09-500-124-189

Query Match 27.2%; Score 31; DB 2; Length 16;  
Best Local Similarity 60.0%; Pred. No. 3.3e+02;  
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 9 LGNPKAPLYK 18  
|||:||||  
Db 4 LGRPEIPLRK 13

## RESULT 31

US-09-017-205-29  
Sequence 29, Application US/09017205  
Patent No. 5965357  
GENERAL INFORMATION:  
APPLICANT: Marden, Howard S  
TITLE OF INVENTION: PEPTIDE STRUCTURES AND THEIR USE IN  
NUMBER OF INVENTIONS: DIAGNOSIS OF HERPES SIMPLEX VIRUS TYPE 2  
NUMBER OF SEQUENCES: 86  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Nixon & Vanderhye PC  
STREET: 8th Floor, 1100 No. 5965357th Glee Road  
CITY: Arlington  
STATE: Virginia  
COUNTRY: USA  
ZIP: 22201-4714  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/017,205  
FILING DATE: 02-FEB-1998  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Mitchard, Leonard C  
REGISTRATION NUMBER: 29,009  
REFERENCE/DOCKET NUMBER: 604-436  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703)816-4000  
TELEFAX: (703)816-4100  
INFORMATION FOR SEQ ID NO: 29:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide from HSV-2 glycoprotein G  
FRAGMENT TYPE: internal  
US-09-017-205-29

Query Match 27.2%; Score 31; DB 1; Length 18;  
Best Local Similarity 43.8%; Pred. No. 3.8e+02;  
Matches 7; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

Qy 5 PGRRLGNPKAPLYKRP 20  
|||:|||||  
Db 2 PGRLLDGPYAPPPRP 17

## RESULT 32

US-08-469-005A-3  
Sequence 3, Application US/08469005A  
Patent No. 565874  
GENERAL INFORMATION:  
APPLICANT: KUHAJDA, FRANCIS P.  
TITLE OF INVENTION: CANCER RELATED ANTIGEN  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BAKER & BOTS, L.L.P.  
STREET: 1299 Pennsylvania Avenue, N.W.  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20004-2400  
COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/469,005A  
FILING DATE: 05-JUN-1995  
CLASSIFICATION: 536

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/188,426  
FILING DATE: 24-JAN-1994

APPLICATION NUMBER: 08/096,908  
FILING DATE: 26-JUL-1993  
APPLICATION NUMBER: 07/917,716  
FILING DATE: 24-JUL-1992

ATTORNEY/AGENT INFORMATION:  
NAME: Posorske, Laurence H  
REGISTRATION NUMBER: 34,698

REFERENCE/DOCKET NUMBER: 062482-0113  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-639-7700  
TELEFAX: 202-639-7890

TELEX:  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:

LENGTH: 19 amino acids  
TYPE: amino acid  
STRANDEDNESS: single

TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO

ANTI-SENSE: NO  
FRAGMENT TYPE: N-terminal  
ORIGINAL SOURCE:  
US-08-469-005A-3

Query Match 27.2%; Score 31; DB 1; Length 19;  
Best Local Similarity 42.9%; Pred. No. 4e+02;  
Matches 6; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 4 YPGRRLGNPKAPLY 17  
|||:|||||  
Db 1 HPESPPTNPTRPLP 14

## RESULT 33

US-08-188-426-3  
Sequence 3, Application US/08188426  
Patent No. 5759791  
GENERAL INFORMATION:  
APPLICANT: KUHAJDA, FRANCIS P.  
TITLE OF INVENTION: CANCER RELATED ANTIGEN  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Banner, Birch, McKie & Beckett  
STREET: 1001 G Street, N.W. -- 11th Floor  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20001  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/188,426  
FILING DATE: 24-JAN-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Posorske, Laurence H.  
REGISTRATION NUMBER: 34,698

REFERENCE/DOCKET NUMBER: 1107.45253  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202 508-9100  
TELEFAX: 202 508-9299  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
US-08-188-426-3

Query Match 27.2%; Score 31; DB 1; Length 19;  
Best Local Similarity 42.9%; Pred. No. 4e+02;  
Matches 6; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 4 YPGSRIGNPKAPLY 17  
DB 1 HPSPTNPTEPLF 14

RESULT 34  
US-08-469-009-3  
Sequence 3, Application US/08469009  
Patent No. 5864011  
GENERAL INFORMATION:  
APPLICANT: Kuhajda, Francis P.  
APPLICANT: Pasternack, Gary R.  
TITLE OF INVENTION: CANCER RELATED ANTIGEN  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESSES:  
ADDRESSES: Banner, Birch, McKie & Beckett  
STREET: 1001 G Street, N.W. -- 11th Floor  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20001  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/469,009  
FILING DATE: 05-JUN-1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/188,426  
FILING DATE: 24-JAN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Poborske, Laurence H.  
REGISTRATION NUMBER: 34,698  
REFERENCE/DOCKET NUMBER: 1107.45253  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202 508-9100  
TELEFAX: 202 508-9299  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
US-08-469-009-3

Query Match 27.2%; Score 31; DB 1; Length 19;  
Best Local Similarity 42.9%; Pred. No. 4e+02;  
Matches 6; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 4 YPGSRIGNPKAPLY 17  
DB 1 HPSPTNPTEPLF 14

RESULT 35  
US-08-469-007-3  
Sequence 3, Application US/08469007  
Patent No. 5872217  
GENERAL INFORMATION:  
APPLICANT: Kuhajda, Francis P.  
APPLICANT: Pasternack, Gary R.  
TITLE OF INVENTION: CANCER RELATED ANTIGEN  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESSES:  
ADDRESSES: Banner, Birch, McKie & Beckett  
STREET: 1001 G Street, N.W. -- 11th Floor  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20001  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/469,007  
FILING DATE: 05-JUN-1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/188,426  
FILING DATE: 24-JAN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Poborske, Laurence H.  
REGISTRATION NUMBER: 34,698  
REFERENCE/DOCKET NUMBER: 1107.45253  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202 508-9100  
TELEFAX: 202 508-9299  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
US-08-469-007-3

Query Match 27.2%; Score 31; DB 1; Length 19;  
Best Local Similarity 42.9%; Pred. No. 4e+02;  
Matches 6; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 4 YPGSRIGNPKAPLY 17  
DB 1 HPSPTNPTEPLF 14

RESULT 36  
US-08-938-830-21  
Sequence 21, Application US/08938830  
Patent No. 6040437  
GENERAL INFORMATION:  
APPLICANT: Laskey, Laurence A.  
APPLICANT: Dowbenko, Donald J.  
TITLE OF INVENTION: Tyrosine Phosphorylated Cleavage  
NUMBER OF SEQUENCES: 73  
CORRESPONDENCE ADDRESSES:  
ADDRESSES: Genentech, Inc.



STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: MinipacIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/938,830  
FILING DATE:  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/798419  
FILING DATE: 07-FEB-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Dreger, Ginger R.  
REGISTRATION NUMBER: 33,055  
REFERENCE/DOCKET NUMBER: P1066P1  
TELEPHONE: 650/225-3216  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 21:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-08-938-830-21

Query Match 27.2%; Score 31; DB 2; Length 19;  
Best Local Similarity 50.0%; Pred. No. 4e+02;  
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
QY 6 GSRLGNPKAP 15  
|:|:|:|:  
Db 3 GNRFSKPKGP 12

RESULT 37  
US-09-020-222-21  
Sequence 21, Application US/09020222  
Patent No. 6111073  
GENERAL INFORMATION:  
APPLICANT: Laeky, Laurence A.  
TITLE OF INVENTION: Tyrosine phosphorylated Cleavage  
NUMBER OF SEQUENCES: 27  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: MinipacIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/020,222  
FILING DATE: 06-FEB-1998  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/798419  
FILING DATE: 02/07/1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Dreger, Ginger R.  
REGISTRATION NUMBER: 33,055  
REFERENCE/DOCKET NUMBER: P1066P1  
TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-3216  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 21:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-09-020-222-21

Query Match 27.2%; Score 31; DB 2; Length 19;  
Best Local Similarity 50.0%; Pred. No. 4e+02;  
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
QY 6 GSRLGNPKAP 15  
|:|:|:|:  
Db 3 GNRFSKPKGP 12

RESULT 38  
US-08-821-278A-22  
Sequence 22, Application US/08821278A  
Patent No. 6238902  
GENERAL INFORMATION:  
APPLICANT: Cheng, Jili  
TITLE OF INVENTION: Protein Tyrosine Phosphatases  
FILE REFERENCE: P1010R1  
CURRENT APPLICATION NUMBER: US/08/821,278A  
CURRENT FILING DATE: 1997-03-20  
NUMBER OF SEQ ID NOS: 23  
SEQ ID NO 22  
LENGTH: 19  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic oligonucleotide probe  
US-08-821-278A-22

Query Match 27.2%; Score 31; DB 2; Length 19;  
Best Local Similarity 50.0%; Pred. No. 4e+02;  
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
QY 6 GSRLGNPKAP 15  
|:|:|:|:  
Db 3 GNRFSKPKGP 12

RESULT 39  
US-09-068-377-21  
Sequence 21, Application US/09068377  
Patent No. 6887705  
GENERAL INFORMATION:  
APPLICANT: Laeky, Laurence A.  
APPLICANT: Dowbenko, Donald J.  
TITLE OF INVENTION: Tyrosine phosphorylated Cleavage Furrow-Associated  
FILE REFERENCE: P1066P2  
CURRENT APPLICATION NUMBER: US/09/068,377  
CURRENT FILING DATE: 1999-05-08  
EARLIER APPLICATION NUMBER: US 08/938,300  
EARLIER FILING DATE: 1997-09-29  
EARLIER APPLICATION NUMBER: US 08/798,419  
EARLIER FILING DATE: 1997-02-07  
NUMBER OF SEQ ID NOS: 73  
SEQ ID NO 21  
LENGTH: 19  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
NAME/KEY: Artificial Sequence  
LOCATION: 1-19  
OTHER INFORMATION: Synthetic oligopeptide  
US-09-068-377-21

Query Match 27.2%; Score 31; DB 2; Length 19;  
Best Local Similarity 50.0%; Pred. No. 4e+02;  
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 6 GSRLEGNPKAP 15  
| | | | |  
DB 3 GNRFSKPKP 12

RESULT 40  
US-08-461-005-6  
; Sequence 6, Application US/08461005  
; Patent No. 5734035  
; GENERAL INFORMATION:  
; APPLICANT: Sharp, Phillip J  
; APPLICANT: Magland, Barry M  
; TITLE OF INVENTION: Nematode Vaccine  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley and Lardner  
; STREET: Suite 500, 1800 Diagonal Road  
; CITY: Alexandria  
; STATE: Virginia  
; COUNTRY: United States of America  
; ZIP: 22313-0299  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/461,005  
; FILING DATE: 05-JUN-1995  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/930,685  
; FILING DATE: 06-OCT-1992  
; CLASSIFICATION: 536  
; APPLICATION NUMBER: AT PK4487  
; FILING DATE: 06-FEB-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/AU92/00041  
; FILING DATE: 06-FEB-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Bent, Stephen A  
; REGISTRATION NUMBER: 29,768  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 836-9300  
; TELEFAX: (703) 683-4109  
; TELEX: 999149  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 14 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; ORIGINAL SOURCE:  
; ORGANISM: Haemonchus contortus  
; FEATURE:  
; NAME/KEY: Modified-site  
; LOCATION: 9  
; OTHER INFORMATION: /note= "May be Gln or Tyr"  
; FEATURE:  
; NAME/KEY: Modified-site  
; LOCATION: 14  
; OTHER INFORMATION: /note= "May be Gly or Ser"  
US-08-461-005-6  
Query Match 26.3%; Score 30; DB 1; Length 14;  
Best Local Similarity 75.0%; Pred. No. 4.1e+02;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 9 LGNPKAPL 16  
| | | | |  
DB 6 LGNPKAPL 13

RESULT 41  
US-08-374-652C-13  
; Sequence 13, Application US/08374652C  
; Patent No. 5834286  
; GENERAL INFORMATION:  
; APPLICANT: NEVALAINEN, HELENA K.M.  
; APPLICANT: PALOHIMO, MARJA T.  
; APPLICANT: FAGERSTROM, RICHARD B.  
; APPLICANT: MIETTINEN-OINONEN, ARJA S.  
; APPLICANT: RAMBOSER, JOHN A.  
; APPLICANT: PIDDINGTON, CHRISTOPHER S.  
; APPLICANT: HOUSTON, CHRISTINE S.  
; APPLICANT: CANTRELL, MICHAEL A.  
; TITLE OF INVENTION: RECOMBINANT CELLS, DNA CONSTRUCTS,  
; TITLE OF INVENTION: VECTORS AND METHODS FOR EXPRESSING PHYTATE DEGRADING  
; ENZYMES IN DESIRED RATIOS  
; NUMBER OF SEQUENCES: 94  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
; STREET: 1100 NEW YORK AVENUE, SUITE 600  
; CITY: WASHINGTON  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/374,652C  
; FILING DATE: 24-MAY-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US93/07058  
; FILING DATE: 27-JUL-1993  
; CLASSIFICATION: 435  
; APPLICATION NUMBER: US 07/925,401  
; FILING DATE: 31-JUL-1992  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: REED, GRANT E.  
; REGISTRATION NUMBER: 41,264  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-2600  
; TELEFAX: 202-371-2540  
; INFORMATION FOR SEQ ID NO: 13:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 14 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: not relevant  
; MOLECULE TYPE: peptide  
US-08-374-652C-13  
Query Match 26.3%; Score 30; DB 1; Length 14;  
Best Local Similarity 50.0%; Pred. No. 4.1e+02;  
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
QY 4 YPSRLGNPKAP 15  
| | | | |  
DB 1 YRGHAGNPLGP 12  
RESULT 42

US-07-930-685-6  
Sequence 6, Application US/07930685  
Patent No. 5871738  
GENERAL INFORMATION:  
APPLICANT: Sharp, Phillip J  
APPLICANT: Magland, Barry M  
TITLE OF INVENTION: Nemacode Vaccine  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley and Lardner  
STREET: Suite 500, 1800 Diagonal Road  
CITY: Alexandria  
STATE: Virginia  
COUNTRY: United States of America  
ZIP: 22313-0299  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/930.685  
FILING DATE: 19921006  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: AU PK4487  
FILING DATE: 06-FEB-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/AU92/00041  
FILING DATE: 06-FEB-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Bent, Stephen A  
REGISTRATION NUMBER: 29,768  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 836-9300  
TELEFAX: (703) 683-4109  
TELEX: 899149  
INFORMATION FOR SEQ. ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
ORGANISM: Haemophilus contortus  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 9  
OTHER INFORMATION: /note= "May be Gln or Tyr"  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 14  
OTHER INFORMATION: /note= "May be Gly or Ser"  
US-07-930-685-6  
Query Match 26.3%; Score 30; DB 1; Length 14;  
Best Local Similarity 75.0%; Pred. No. 4.1e+02;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 9 LGNKPAPL 16  
DB 6 LGNKPAPL 13  
RESULT 43  
US-08-505-318-27  
Sequence 27, Application US/08505318  
Patent No. 6107459  
GENERAL INFORMATION:  
APPLICANT: Dean, Richard T  
TITLE OF INVENTION: Technetium-99m Labeled Peptides for  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Banner & Allegretti, Ltd.  
STREET: 10 South Wacker Drive, Suite 3000  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/290.853  
FILING DATE: 11-OCT-1994  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 5989519nan, Kevin E  
REGISTRATION NUMBER: 35,303  
REFERENCE/DOCKET NUMBER: 92,112-H  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-715-1000

CORRESPONDENCE ADDRESS:  
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff  
STREET: 300 South Wacker Drive, Seventh Floor  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/505.318  
FILING DATE: 07-DEC-1995  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 6107459nan, Kevin E  
REGISTRATION NUMBER: 35,303  
REFERENCE/DOCKET NUMBER: 90,1104-FP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-913-0001  
TELEFAX: 312-913-0002  
TELEX:  
INFORMATION FOR SEQ. ID NO: 27:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-505-318-27  
Query Match 26.3%; Score 30; DB 2; Length 15;  
Best Local Similarity 71.4%; Pred. No. 4.4e+02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 13 KAPLYKR 19  
DB 1 QAPLYKR 7  
RESULT 44  
US-08-290-853-37  
Sequence 37, Application US/08290853  
Patent No. 5989519  
GENERAL INFORMATION:  
APPLICANT: Dean, Richard T  
TITLE OF INVENTION: Technetium-99m Labeled Peptides for  
NUMBER OF SEQUENCES: 37  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Banner & Allegretti, Ltd.  
STREET: 10 South Wacker Drive, Suite 3000  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/290.853  
FILING DATE: 11-OCT-1994  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 5989519nan, Kevin E  
REGISTRATION NUMBER: 35,303  
REFERENCE/DOCKET NUMBER: 92,112-H  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-715-1000

TELEFAX: 312-715-1234  
TELEX: 910-221-5317  
INFORMATION FOR SEQ ID NO: 37:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 1..3  
OTHER INFORMATION: /label= Modified-Cys  
OTHER INFORMATION: /note= "The thiol group of each cysteine is  
OTHER INFORMATION: protected with an acetamidomethyl group."  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 1..3  
OTHER INFORMATION: /label= acetyl-Cys  
OTHER INFORMATION: /note= "The amino terminal residue is  
OTHER INFORMATION: linked to an acetyl group."  
US-08-290-853-37

Query Match 26.3%; Score 30; DB 1; Length 18;  
Best Local Similarity 71.4%; Pred. No. 5.3e+02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 13 KAPLYKR 19  
:|||||:  
DB 4 QAPLYKK 10

RESULT 45  
US-08-505-318-21  
Sequence 21, Application US/08505318  
Patent No. 6107459  
GENERAL INFORMATION:  
APPLICANT: Dean, Richard T  
TITLE OF INVENTION: Technetium-99m Labeled Peptides for  
TITLE OF INVENTION: Diagnostic Imaging  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff  
STREET: 300 South Wacker Drive, Seventh Floor  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/505,318  
FILING DATE: 07-DEC-1995  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: NO. 6107459nan, Kevin E  
REGISTRATION NUMBER: 35,303  
REFERENCE/DOCKET NUMBER: 90,1104-FP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-913-0001  
TELEFAX: 312-913-0002  
TELEX:  
INFORMATION FOR SEQ ID NO: 21:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-505-318-21

Query Match 26.3%; Score 30; DB 2; Length 18;

Best Local Similarity 71.4%; Pred. No. 5.3e+02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 13 KAPLYKR 19  
:|||||:  
DB 4 QAPLYKK 10

RESULT 46  
US-08-505-318-23  
Sequence 23, Application US/08505318  
Patent No. 6107459  
GENERAL INFORMATION:  
APPLICANT: Dean, Richard T  
TITLE OF INVENTION: Technetium-99m Labeled Peptides for  
TITLE OF INVENTION: Diagnostic Imaging  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff  
STREET: 300 South Wacker Drive, Seventh Floor  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/505,318  
FILING DATE: 07-DEC-1995  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: NO. 6107459nan, Kevin E  
REGISTRATION NUMBER: 35,303  
REFERENCE/DOCKET NUMBER: 90,1104-FP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-913-0001  
TELEFAX: 312-913-0002  
TELEX:  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 1..3  
OTHER INFORMATION: /label= Tc-99m-chelator  
OTHER INFORMATION: /note= "The N-terminal amino group is acetylated,  
OTHER INFORMATION: and the sidechain sulfur atoms of both Cys  
OTHER INFORMATION: residues are each protected by an acetamidomethyl  
OTHER INFORMATION: group"  
US-08-505-318-23

Query Match 26.3%; Score 30; DB 2; Length 18;  
Best Local Similarity 71.4%; Pred. No. 5.3e+02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 13 KAPLYKR 19  
:|||||:  
DB 4 QAPLYKK 10

RESULT 47  
US-08-974-549A-163  
Sequence 163, Application US/08974549A  
Patent No. 6166178  
GENERAL INFORMATION:  
APPLICANT: Cech, Thomas R.  
APPLICANT: Langner, Joachim

APPLICANT: Nakamura, Toru  
APPLICANT: Chapman, Karen B.  
APPLICANT: Morin, Gregg B.  
APPLICANT: Harley, Calvin B.  
APPLICANT: Andrews, William H.  
TITLE OF INVENTION: Human Telomerase Catalytic Subunit  
NUMBER OF SEQUENCES: 727  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/974,549A  
FILING DATE: 19-NOV-1997  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/724,643  
FILING DATE: 01-OCT-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/844,419  
FILING DATE: 18-APR-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/846,017  
FILING DATE: 25-APR-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/851,843  
FILING DATE: 06-MAY-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/854,050  
FILING DATE: 09-MAY-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/911,312  
FILING DATE: 14-AUG-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/912,951  
FILING DATE: 14-AUG-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/915,503  
FILING DATE: 14-AUG-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US97/17618  
FILING DATE: 01-OCT-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US97/17885  
FILING DATE: 01-OCT-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Apple, Randolph Ted  
REGISTRATION NUMBER: 36,429  
REFERENCE/DOCKET NUMBER: 015389-002610US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 163:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULAR TYPE: peptide  
US-08-974-549A-163

Query Match 26.3%; Score 30; DB 2; Length 18;  
Best Local Similarity 62.5%; Pred. No. 5.3e+02;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Oy 11 NPKAPLYK 18  
Db 5 NPKTPICK 12

RESULT 48  
US-09-402-181B-163  
Sequence 163, Application US/09402181B  
Patent No. 6610839  
GENERAL INFORMATION:  
APPLICANT: Cech, Thomas R.  
Lingner, Joachim  
Nakamura, Toru  
Chapman, Karen B.  
Morin, Gregg B.  
Harley, Calvin B.  
Andrews, William H.  
TITLE OF INVENTION: Human Telomerase Catalytic Subunit  
NUMBER OF SEQUENCES: 633  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/402,181B  
FILING DATE: 29-Sep-1997  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/724,643  
FILING DATE: 01-OCT-1996  
APPLICATION NUMBER: US 08/844,419  
FILING DATE: 18-APR-1997  
APPLICATION NUMBER: US 08/846,017  
FILING DATE: 25-APR-1997  
APPLICATION NUMBER: US 08/851,843  
FILING DATE: 06-MAY-1997  
APPLICATION NUMBER: US 08/854,050  
FILING DATE: 09-MAY-1997  
APPLICATION NUMBER: US 08/911,312  
FILING DATE: 14-AUG-1997  
APPLICATION NUMBER: US 08/912,951  
FILING DATE: 14-AUG-1997  
APPLICATION NUMBER: US 08/915,503  
FILING DATE: 14-AUG-1997  
APPLICATION NUMBER: WO PCT/US97/17885  
FILING DATE: 01-OCT-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Ausubius, Scott L.  
REGISTRATION NUMBER: 42,271  
REFERENCE/DOCKET NUMBER: 015389-002620US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 163:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear  
MOLECULAR TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 163:  
US-09-402-181B-163

Query Match 26.3%; Score 30; DB 2; Length 18;  
Best Local Similarity 62.5%; Pred. No. 5.3e+02;

Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
Qy 11 NPKAPLYK 18  
Db 5 NPKTPIKK 12

RESULT 49  
US-09-721-456-163  
; Sequence 163, Application US/09721456  
; Patent No. 6617110  
; GENERAL INFORMATION:  
; APPLICANT: Cech, Thomas R.  
; Lingner, Joachim  
; Nakamura, Toru  
; Chapman, Karen B.  
; Morin, Gregg B.  
; Harley, Calvin B.  
; Andrews, William H.  
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit  
; NUMBER OF SEQUENCES: 727  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/721,456  
; FILING DATE: 22-No. 6617110-2000  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/974,549A  
; FILING DATE: 19-NOV-1997  
; APPLICATION NUMBER: US 08/724,643  
; FILING DATE: 01-OCT-1996  
; APPLICATION NUMBER: US 08/844,419  
; FILING DATE: 18-APR-1997  
; APPLICATION NUMBER: US 08/846,017  
; FILING DATE: 25-APR-1997  
; APPLICATION NUMBER: US 08/851,843  
; FILING DATE: 06-MAY-1997  
; APPLICATION NUMBER: US 08/854,050  
; FILING DATE: 09-MAY-1997  
; APPLICATION NUMBER: US 08/911,312  
; FILING DATE: 14-AUG-1997  
; APPLICATION NUMBER: US 08/912,951  
; FILING DATE: 14-AUG-1997  
; APPLICATION NUMBER: US 08/915,503  
; FILING DATE: 14-AUG-1997  
; APPLICATION NUMBER: WO PCT/US97/17618  
; FILING DATE: 01-OCT-1997  
; APPLICATION NUMBER: WO PCT/US97/17865  
; FILING DATE: 01-OCT-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Apple, Randolph Ted  
; REGISTRATION NUMBER: 36,429  
; REFERENCE/DOCKET NUMBER: 015389-002610US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 163:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: <Unknown>  
; TOPOLOGY: linear

MOLECULE TYPE: Peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 163:  
US-09-721-456-163

Query Match 26.3%; Score 30; DB 2; Length 18;  
Best Local Similarity 62.5%; Pred. No. 5.3e+02;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
Qy 11 NPKAPLYK 18  
Db 5 NPKTPIKK 12

RESULT 50  
US-09-623-548A-1140  
; Sequence 1140, Application US/09623548A  
; Patent No. 6849714  
; GENERAL INFORMATION:  
; APPLICANT: Conjughem, Inc.  
; APPLICANT: Bridon, Dominique  
; APPLICANT: Ezrin, Alan  
; APPLICANT: Milner, Peter  
; APPLICANT: Holmes, Darren  
; APPLICANT: Thibodeau, Karen  
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM  
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD  
; FILE REFERENCE: 2110  
; CURRENT APPLICATION NUMBER: US/09/623,548A  
; CURRENT FILING DATE: 2000-09-05  
; PRIOR APPLICATION NUMBER: 60/134,406  
; PRIOR FILING DATE: 1999-05-17  
; PRIOR APPLICATION NUMBER: 60/153,406  
; PRIOR FILING DATE: 1999-09-10  
; PRIOR APPLICATION NUMBER: 60/159,783  
; PRIOR FILING DATE: 1999-10-18  
; NUMBER OF SEQ ID NOS: 1617  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 1140  
; LENGTH: 18  
; TYPE: PPT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: Peptide  
US-09-623-548A-1140

Query Match 26.3%; Score 30; DB 2; Length 18;  
Best Local Similarity 42.1%; Pred. No. 5.3e+02;  
Matches 8; Conservative 1; Mismatches 6; Indels 4; Gaps 1;  
Qy 2 YEPGSRILNPKAPLYKRP 20  
Db 1 YEKPGS---PPRRVPRP 15

RESULT 51  
US-10-131-346-8  
; Sequence 8, Application US/10131346  
; Patent No. 6881396  
; GENERAL INFORMATION:  
; APPLICANT: Cyr, John B.  
; TITLE OF INVENTION: STABILIZATION OF RADIOPHARMACEUTICAL COMPOSITIONS  
; TITLE OF INVENTION: USING HYDROPHILIC 6-HYDROXY CHROMANS  
; FILE REFERENCE: 09744-017001  
; CURRENT APPLICATION NUMBER: US/10/131,346  
; CURRENT FILING DATE: 2002-04-24  
; PRIOR APPLICATION NUMBER: US 09/695,360  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR APPLICATION NUMBER: PCT/US01/50423  
; PRIOR FILING DATE: 2001-10-24  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 8  
LENGTH: 18  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURES:  
OTHER INFORMATION: Synthetic construct  
US-10-131-346-8

Query Match 26.3%; Score 30; DB 2; Length 18;  
Best Local Similarity 71.4%; Pred. No. 5.3e+02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 13 KAPLYKR 19  
Db 4 QAPLYKK 10

RESULT 52  
US-09-657-276-1140  
Sequence 1140, Application US/09657276  
Patent No. 6887470  
GENERAL INFORMATION:  
APPLICANT: Conjuchem, Inc.  
APPLICANT: Bridon, Dominique  
APPLICANT: Ezrin, Alan  
APPLICANT: Milner, Peter  
APPLICANT: Holmes, Darren  
APPLICANT: Thibaudau, Karen  
TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM  
TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD  
FILE REFERENCE: 2110  
CURRENT APPLICATION NUMBER: US/09/657,276  
CURRENT FILING DATE: 2000-09-07  
PRIOR APPLICATION NUMBER: 60/134,406  
PRIOR FILING DATE: 1999-05-17  
PRIOR APPLICATION NUMBER: 60/153,406  
PRIOR FILING DATE: 1999-09-10  
PRIOR APPLICATION NUMBER: 60/159,783  
PRIOR FILING DATE: 1999-10-18  
NUMBER OF SEQ ID NOS: 1617  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 1140  
LENGTH: 18  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURES:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-657-276-1140

Query Match 26.3%; Score 30; DB 2; Length 18;  
Best Local Similarity 42.1%; Pred. No. 5.3e+02;  
Matches 8; Conservative 1; Mismatches 6; Indels 4; Gaps 1;

Qy 2 YETPGSLGNPKAPLYKR 20  
Db 1 YERKGS---PPEVVRP 15

RESULT 53  
US-10-131-543-8  
Sequence 8, Application US/10131543  
Patent No. 6902718  
GENERAL INFORMATION:  
APPLICANT: Cyr, John E.  
APPLICANT: Pearson, Daniel A.  
TITLE OF INVENTION: STABILIZATION OF RADIOPHARMACEUTICAL COMPOSITIONS  
TITLE OF INVENTION: USING HYDROPHILIC THIOETHERS  
FILE REFERENCE: 09744-016001  
CURRENT APPLICATION NUMBER: US/10/131,543  
CURRENT FILING DATE: 2002-04-24  
PRIOR APPLICATION NUMBER: US 09/694,992

PRIOR FILING DATE: 2000-10-24  
PRIOR APPLICATION NUMBER: PCT/US01/50423  
PRIOR FILING DATE: 2001-10-24  
NUMBER OF SEQ ID NOS: 29  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 8  
LENGTH: 18  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURES:  
OTHER INFORMATION: Synthetic construct  
US-10-131-543-8

Query Match 26.3%; Score 30; DB 2; Length 18;  
Best Local Similarity 71.4%; Pred. No. 5.3e+02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 13 KAPLYKR 19  
Db 4 QAPLYKK 10

RESULT 54  
US-07-805-437-4  
Sequence 4, Application US/07805437  
Patent No. 5364757  
GENERAL INFORMATION:  
APPLICANT: Garry, R.F. et al.  
TITLE OF INVENTION: Association Between A Human  
TITLE OF INVENTION: Immunodeficiency Virus-Related Retrovirus And Autoimmune  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESSES:  
ADDRESSER: Pennie & Edmonds  
STREET: 1155 Avenue of Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/805,437  
FILING DATE: 19911211  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Mastrock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 5113-024  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212 790-9080  
TELEFAX: 212 8698864/9741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19 amino acids  
TYPE: AMINO ACID  
STRANDEDNESS: single  
TOPOLOGY: unknown  
MOLECULAR TYPE: peptide  
US-07-805-437-4

Query Match 26.3%; Score 30; DB 1; Length 19;  
Best Local Similarity 71.4%; Pred. No. 5.6e+02;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 12 PKAPLYK 18  
Db 5 PKPPFYK 11

RESULT 55  
US-08-291-349A-1  
; Sequence 1, Application US/08291349A  
; Patent No. 5545620  
; GENERAL INFORMATION:  
; APPLICANT: Wahl, Sharon M.  
; APPLICANT: McCarthy, James B.  
; APPLICANT: Furcht, Leo T.  
; TITLE OF INVENTION: Synthetic Fibronectin Fragments As  
; TITLE OF INVENTION: Inhibitors of Retroviral Infection  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSES: Allegretti & Witcoff  
; STREET: 10 S. Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: IBM PC compatible  
; SOFTWARE: Patent Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/291,349A  
; FILING DATE: 16 AUG 1994  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/006,121  
; FILING DATE: 19 JAN 1993  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: McDonnell, John J.  
; REGISTRATION NUMBER: 26,949  
; REFERENCE/DOCKET NUMBER: 92,673-B  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312-715-1000  
; TELEFAX: 312-715-1234  
; TELETYPE: 910-221-5317  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 19 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FEATURE:  
; NAME/KEY: Peptide  
; LOCATION: 1..19  
; OTHER INFORMATION: /note="FNI (1906-1924)  
; OTHER INFORMATION: fibronectin fragment : FN-C/H-I"  
US-08-291-349A-1  
Query Match 26.3%; Score 30; DB 1; Length 19;  
Best Local Similarity 42.1%; Pred. No. 5.6e+02;  
Matches 8; Conservative 1; Mismatches 6; Indels 4; Gaps 1;  
QY 2 YEYPSRLGNPKAPLYKRP 20  
DB 1 YEKPGS----PPREVVRP 15  
RESULT 56  
US-07-990-296-1  
; Sequence 1, Application US/07990296  
; Patent No. 5591719  
; GENERAL INFORMATION:  
; APPLICANT: Furcht, Leo T.  
; APPLICANT: Allen, Janice B.  
; APPLICANT: Wahl, Sharon M.  
; APPLICANT: McCarthy, James B.  
; TITLE OF INVENTION: Method for Treating Acute and

; TITLE OF INVENTION: Chronic Inflammatory Disorders Using Polypeptides  
; TITLE OF INVENTION: with Fibronectin Activity  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSES: Merchant & Gould  
; STREET: 3100 No. 5591719west Center  
; CITY: Minneapolis  
; STATE: MN  
; COUNTRY: USA  
; ZIP: 55402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: IBM PC compatible  
; SOFTWARE: WordPerfect 5.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/990,296  
; FILING DATE: 19921210  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kowalczyk, Alan W.  
; REGISTRATION NUMBER: 31,535  
; REFERENCE/DOCKET NUMBER: 600,252-US-01  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 612-332-5300  
; TELEFAX: 612-332-9081  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 19 amino acid residues  
; TYPE: AMINO ACID  
; TOPOLOGY: linear  
; MOLECULE TYPE: Peptide  
; FRAGMENT TYPE: Internal Fragment  
; ORIGINAL SOURCE: Synthetically Derived  
; FEATURE:  
; NAME/KEY: Fragment of the 33 KD carboxy  
; NAME/KEY: terminal heparin-binding fragment of the A  
; NAME/KEY: chain of fibronectin  
; LOCATION: Represents isolated fibronectin  
; LOCATION: residues 1906-1924 from all plasma isoforms  
; LOCATION: of fibronectin  
US-07-990-296-1  
Query Match 26.3%; Score 30; DB 1; Length 19;  
Best Local Similarity 42.1%; Pred. No. 5.6e+02;  
Matches 8; Conservative 1; Mismatches 6; Indels 4; Gaps 1;  
QY 2 YEYPSRLGNPKAPLYKRP 20  
DB 1 YEKPGS----PPREVVRP 15  
RESULT 57  
US-08-462-784-1  
; Sequence 1, Application US/08462784  
; Patent No. 5714313  
; GENERAL INFORMATION:  
; APPLICANT: Dean, Richard T.  
; APPLICANT: Moyer, Brian  
; TITLE OF INVENTION: Technetium-99m Labeled Peptides for  
; TITLE OF INVENTION: Imaging Inflammation  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSES: McDonnell Boehnen Hulbert & Berghoff  
; STREET: 300 South Wacker Drive Seventh Floor  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS



SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/462,784  
FILING DATE: 05-JUN-1995  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 571433nan, Kevin B  
REGISTRATION NUMBER: 35,303  
REFERENCE/DOCKET NUMBER: 90,1104-X  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312 913 0001  
TELEFAX: 312 913 0002  
TELEX:  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 1..4  
OTHER INFORMATION: /label= MODIFIED-CYS  
OTHER INFORMATION: /note= "The thiol group of each cysteine is  
OTHER INFORMATION: protected by an acetamidomethyl group; the amino  
OTHER INFORMATION: terminal amine is acetylated."  
US-08-462-784-1

Query Match 26.3%; Score 30; DB 1; Length 19;  
Best Local Similarity 71.4%; Pred. No. 5.6e+02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 13 KAPLYRK 19  
:|||||:  
DB 5 QAPLYRK 11

RESULT 58  
US-08-202-989-2  
Sequence 2, Application US/08202989  
Patent No. 5795860  
GENERAL INFORMATION:  
APPLICANT: MITT, DAVID P.  
APPLICANT: HERLIHY, WALTER C.  
TITLE OF INVENTION: ANALOGS FOR SPECIFIC OLIGOSACCHARIDE  
TITLE OF INVENTION: -PROTEIN INTERACTIONS AND USES THEREFOR  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ &  
ADDRESSEE: THIBEAULT  
STREET: 53 STATE STREET  
CITY: BOSTON  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/202,989  
FILING DATE:  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/024,558  
FILING DATE: 01-MAR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: KELLEY, ROBIN D.  
REGISTRATION NUMBER: 34,637  
REFERENCE/DOCKET NUMBER: GLY-003  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-248-7000

TELEFAX: 617-248-7100  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FEATURE:  
NAME/KEY: Protein  
LOCATION: 1..19  
OTHER INFORMATION: /label= PR4  
OTHER INFORMATION: /note= "OPENHEIM ET AL. (1991) ANN. REV. IMMUNOL.  
OTHER INFORMATION: 9:617-648"  
US-08-202-989-2

Query Match 26.3%; Score 30; DB 1; Length 19;  
Best Local Similarity 71.4%; Pred. No. 5.6e+02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 13 KAPLYRK 19  
:|||||:  
DB 5 QAPLYRK 11

RESULT 59  
US-08-480-133A-1  
Sequence 1, Application US/08480133A  
Patent No. 5840691  
GENERAL INFORMATION:  
APPLICANT: Furcht, Leo T.  
APPLICANT: McCarthy, James B.  
APPLICANT: Wahl, Sharon M.  
APPLICANT: Allen, Janice B.  
APPLICANT: Billups, Kevin L.  
APPLICANT: Everett, Jeffrey E.  
TITLE OF INVENTION: Method for Treating Inflammatory  
TITLE OF INVENTION: Diseases Using Polypeptides with Fibronectin Activity  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Merchant & Gould  
STREET: 90 South 7th Street, 3100 No. 5840691west Center  
CITY: Minneapolis  
STATE: MN  
COUNTRY: USA  
ZIP: 55402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/480,133A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/139,903  
FILING DATE: 21-OCT-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/990,296  
FILING DATE: 10-DEC-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Carter, Charles G.  
REGISTRATION NUMBER: 35,093  
REFERENCE/DOCKET NUMBER: 600-308US01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 612-332-5300  
TELEFAX: 612-332-9081  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19 amino acids  
TYPE: amino acid  
STRANDEDNESS:

TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-480-133A-1

Query Match 26.3%; Score 30; DB 1; Length 19;  
Best Local Similarity 42.1%; Pred. No. 5.6e+02;  
Matches 8; Conservative 1; Mismatches 6; Indels 4; Gaps 1;

QY 2 YEYPSRLGNPKAPLYKRP 20  
DB 1 YEKPSG---PPREVVRP 15

## RESULT 60

US-08-394-748A-9  
Sequence 9, Application US/08394748A  
Patent No. 6013628  
GENERAL INFORMATION:  
APPLICANT: Skubitz, Amy P.N.  
APPLICANT: Furcht Leo T.  
APPLICANT: Balles, Mark  
APPLICANT: Gegeron, Dale S.  
APPLICANT: Agarwal, Anita  
APPLICANT: Wright, Martha M.  
APPLICANT: Murali, Shobana  
TITLE OF INVENTION: Method for Treating Conditions of the Eye  
TITLE OF INVENTION: Using Polypeptides  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Merchant & Gould  
STREET: 3100 No. 6013628west Center  
CITY: Minneapolis  
STATE: MN  
COUNTRY: USA  
ZIP: 55402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/394,748A  
FILING DATE: 27-FEB-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/203,458  
FILING DATE: 28-FEB-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Carter, Charles G.  
REGISTRATION NUMBER: 35,093  
REFERENCE/DOCKET NUMBER: 600.307US01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 612-332-5300  
TELEFAX: 612-332-9081  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
ORIGINAL SOURCE:  
STRAIN: FN-C/H-1  
US-08-394-748A-9

Query Match 26.3%; Score 30; DB 2; Length 19;  
Best Local Similarity 42.1%; Pred. No. 5.6e+02;  
Matches 8; Conservative 1; Mismatches 6; Indels 4; Gaps 1;

QY 2 YEYPSRLGNPKAPLYKRP 20  
DB 1 YEKPSG---PPREVVRP 15

## RESULT 61

US-08-564-315-1  
Sequence 1, Application US/08564315  
Patent No. 601958  
GENERAL INFORMATION:  
APPLICANT: Dean, Richard T.  
APPLICANT: Moyer, Brian  
TITLE OF INVENTION: Technetium-99m Labeled Peptides for  
TITLE OF INVENTION: Imaging Inflammation  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff  
STREET: 300 South Wacker Drive Seventh Floor  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/564,315  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/462,784  
FILING DATE: 05-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 601958nan, Kevin E  
REGISTRATION NUMBER: 35,303  
REFERENCE/DOCKET NUMBER: 90,1104-X  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312 913 0001  
TELEFAX: 312 913 0002  
TELEX:  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 1..4  
OTHER INFORMATION: /label= MODIFIED-CYS  
OTHER INFORMATION: /notes="The thiol group of each cysteine is  
OTHER INFORMATION: protected by an acetamidomethyl group; the amino  
OTHER INFORMATION: terminal amine is acetylated."  
US-08-564-315-1

Query Match 26.3%; Score 30; DB 2; Length 19;  
Best Local Similarity 71.4%; Pred. No. 5.6e+02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 13 KAPLYK 19  
DB 5 QAPLYK 11

## RESULT 62

US-08-505-318-12  
Sequence 12, Application US/08505318  
Patent No. 6107459  
GENERAL INFORMATION:  
APPLICANT: Dean, Richard T.  
TITLE OF INVENTION: Technetium-99m Labeled Peptides for  
TITLE OF INVENTION: Diagnostic Imaging  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff  
STREET: 300 South Wacker Drive, Seventh Floor

CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/505,318  
FILING DATE: 07-DEC-1995  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 6107459nan, Kevin E  
REGISTRATION NUMBER: 35,303  
REFERENCE/DOCKET NUMBER: 90,1104-FP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-913-0001  
TELEFAX: 312-913-0002  
TELEX:  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 1..4  
OTHER INFORMATION: /label=Tc-99m-chelator  
OTHER INFORMATION: /note="The N-terminal amino group is acetylated,  
OTHER INFORMATION: and the sidechain sulfur atoms of both Cys  
OTHER INFORMATION: residues are each protected by an acetamidomethyl  
US-08-505-318-12

Query Match 26.3%; Score 30; DB 2; Length 19;  
Best Local Similarity 71.4%; Pred. No. 5.6e+02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 13 KAPLYKR 19  
:|||||:  
Db 5 QAPLYKK 11

RESULT 63  
US-08-505-318-22  
Sequence 22, Application US/08505318  
Patent No. 6107459  
GENERAL INFORMATION:  
APPLICANT: Dean, Richard T  
TITLE OF INVENTION: Technetium-99m Labeled Peptides for  
TITLE OF INVENTION: Diagnostic Imaging  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESS:  
ADDRESSES: McDonnell Boehnen Hulbert & Berghoff  
STREET: 300 South Wacker Drive, Seventh Floor  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/505,318  
FILING DATE: 07-DEC-1995  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 6107459nan, Kevin E

REGISTRATION NUMBER: 35,303  
REFERENCE/DOCKET NUMBER: 90,1104-FP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-913-0001  
TELEFAX: 312-913-0002  
TELEX:  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 1..4  
OTHER INFORMATION: /label=Tc-99m-chelator  
OTHER INFORMATION: /note="The N-terminal amino group is acetylated,  
OTHER INFORMATION: and the sidechain sulfur atoms of both Cys  
OTHER INFORMATION: residues are each protected by an acetamidomethyl  
US-08-505-318-22

Query Match 26.3%; Score 30; DB 2; Length 19;  
Best Local Similarity 71.4%; Pred. No. 5.6e+02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 13 KAPLYKR 19  
:|||||:  
Db 5 QAPLYKK 11

RESULT 64  
US-09-675-922-13  
Sequence 13, Application US/09675922  
Patent No. 6468731  
GENERAL INFORMATION:  
APPLICANT: Hubbell A., Jeffrey  
APPLICANT: Schense C., Jason  
APPLICANT: Sakiyama E., Shelley  
TITLE OF INVENTION: Enzyme-Mediated Modification of Fibrin for Tissue  
TITLE OF INVENTION: Engineering: Incorporation of Proteins  
FILE REFERENCE: ETH 107 DIV  
CURRENT APPLICATION NUMBER: US/09/675,922  
CURRENT FILING DATE: 2000-09-29  
NUMBER OF SEQ ID NOS: 28  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 13  
LENGTH: 19  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:  
OTHER INFORMATION: heparin-binding sequence  
US-09-675-922-13

Query Match 26.3%; Score 30; DB 2; Length 19;  
Best Local Similarity 42.1%; Pred. No. 5.6e+02;  
Matches 8; Conservative 1; Mismatches 6; Indels 4; Gaps 1;

QY 2 YEYPSRLGNPKRKLKRP 20  
:|||||:  
Db 1 YEKPSG---PPREVVRP 15

RESULT 65  
US-09-600-502A-15  
Sequence 15, Application US/09600502A  
Patent No. 6855329  
GENERAL INFORMATION:  
APPLICANT: Shakesheff, Kevin  
APPLICANT: Nikin, Patal  
APPLICANT: Camlizzaro, Scott M  
APPLICANT: Langer, Robert S.

```
/ TITLE OF INVENTION: Surface Coating in Spatially Controlled Patterns
/ FILE REFERENCE: MIT 7896 UK
/ CURRENT APPLICATION NUMBER: US/09/600,502A
/ CURRENT FILING DATE: 2000-10-17
/ NUMBER OF SEQ ID NOS: 19
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO: 15
/ LENGTH: 19
/ TYPE: prt
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: proteoglycan
US-09-600-502A-15

Query Match          26.3%; Score 30; DB 2; Length 19;
Best Local Similarity 42.1%; Pred. No. 5.6e+02;
Matches 8; Conservative 1; Mismatches 6; Indels 4; Gaps 1;

QY 2 YEYPSRLGNPKAPLYKRP 20
   ||||| | : |||
Db 1 YEKPGS-----PPREVVRP 15

RESULT 66
US-09-563-760A-13
/ Sequence 13, Application US/09563760A
/ Patent No. 6894022
/ GENERAL INFORMATION:
/ APPLICANT: Hubbell, Jeffrey A
/ APPLICANT: Schense, Jason C
/ APPLICANT: Sakiyama-Bibert, Shelly B
/ TITLE OF INVENTION: Growth Factor Modified Protein Matrices for Tissue
/ FILE REFERENCE: ETH 107 CIP
/ CURRENT APPLICATION NUMBER: US/09/563,760A
/ CURRENT FILING DATE: 2000-05-01
/ PRIOR APPLICATION NUMBER: 09/141,153
/ PRIOR FILING DATE: 1998-08-27
/ NUMBER OF SEQ ID NOS: 37
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO: 13
/ LENGTH: 19
/ TYPE: prt
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence:
US-09-563-760A-13

Query Match          26.3%; Score 30; DB 2; Length 19;
Best Local Similarity 42.1%; Pred. No. 5.6e+02;
Matches 8; Conservative 1; Mismatches 6; Indels 4; Gaps 1;

QY 2 YEYPSRLGNPKAPLYKRP 20
   ||||| | : |||
Db 1 YEKPGS-----PPREVVRP 15

RESULT 67
US-09-586-937-52
/ Sequence 52, Application US/09586937
/ Patent No. 6958212
/ GENERAL INFORMATION:
/ APPLICANT: Hubbell, Jeffrey A.
/ APPLICANT: Bibert, Donald
/ APPLICANT: Schoenmakers, Ronald
/ TITLE OF INVENTION: CONTINGENT ADDITION REACTIONS FOR THE
/ FILE REFERENCE: 50154/003001
/ CURRENT APPLICATION NUMBER: US/09/586,937
/ CURRENT FILING DATE: 2000-06-02
/ PRIOR APPLICATION NUMBER: US 09/496,231
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```
/ PRIOR FILING DATE: 2000-02-01
/ PRIOR APPLICATION NUMBER: US 60/118,093
/ PRIOR FILING DATE: 1999-02-01
/ NUMBER OF SEQ ID NOS: 75
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO: 52
/ LENGTH: 19
/ TYPE: prt
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Based on Homo sapiens
US-09-586-937-52

Query Match          26.3%; Score 30; DB 2; Length 19;
Best Local Similarity 42.1%; Pred. No. 5.6e+02;
Matches 8; Conservative 1; Mismatches 6; Indels 4; Gaps 1;

QY 2 YEYPSRLGNPKAPLYKRP 20
   ||||| | : |||
Db 1 YEKPGS-----PPREVVRP 15

RESULT 68
US-09-798-338B-4
/ Sequence 4, Application US/09798338B
/ Patent No. 6960452
/ GENERAL INFORMATION:
/ APPLICANT: Hubbell, Jeffrey A.
/ APPLICANT: Schense, Jason C.
/ APPLICANT: Sakiyama, Shelly B.
/ TITLE OF INVENTION: Enzyme-mediated modifications of fibrin for tissue engineering:
/ FILE REFERENCE: ETH 107 CON
/ CURRENT APPLICATION NUMBER: US/09/798,338B
/ CURRENT FILING DATE: 2001-03-02
/ PRIOR APPLICATION NUMBER: 09/141,153
/ PRIOR FILING DATE: 1998-08-27
/ NUMBER OF SEQ ID NOS: 21
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO: 4
/ LENGTH: 19
/ TYPE: prt
/ ORGANISM: Homo sapiens
US-09-798-338B-4

Query Match          26.3%; Score 30; DB 2; Length 19;
Best Local Similarity 42.1%; Pred. No. 5.6e+02;
Matches 8; Conservative 1; Mismatches 6; Indels 4; Gaps 1;

QY 2 YEYPSRLGNPKAPLYKRP 20
   ||||| | : |||
Db 1 YEKPGS-----PPREVVRP 15

RESULT 69
PCT-US93-11781-1
/ Sequence 1, Application PC/TUS9311781
/ GENERAL INFORMATION:
/ APPLICANT: Regents of the University of Minnesota
/ APPLICANT: Morrill Hall
/ APPLICANT: 100 Church Street, S.E.
/ APPLICANT: Minneapolis, Minnesota 55455
/ APPLICANT: U.S.A.
/ APPLICANT: Represented By The Secretary of Health
/ APPLICANT: and Human Services
/ APPLICANT: 200 Independence Avenue S.W.
/ APPLICANT: Washington, D.C. 20201
/ APPLICANT: United States of America
/ TITLE OF INVENTION: Polypeptides useful for Treating
/ NUMBER OF SEQUENCES: 6
/ CORRESPONDENCE ADDRESSES:
/ ADDRESSEE: Merchant & Gould
```

STREET: 3100 Norwest Center  
CITY: Minneapolis  
STATE: MN  
COUNTRY: USA  
ZIP: 55402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/11781  
FILING DATE:  
CLASSIFICATION:  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 08/139,903  
FILING DATE: 21-OCT-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/990,296  
FILING DATE: 10-DEC-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Kowalchuk, Alan W.  
REGISTRATION NUMBER: 31,535  
REFERENCE/DOCKET NUMBER: 600.283-US-01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 612-332-5300  
TELEFAX: 612-332-9081  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
PCT-US93-11781-1

Query Match 26.3%; Score 30; DB 4; Length 19;  
Best Local Similarity 42.1%; Pred. No. 5.6e+02;  
Matches 8; Conservative 1; Mismatches 6; Indels 4; Gaps 1;

QY 2 YEYGSRLGNPKAPLYKRP 20  
DB 1 YEKFGS----PPREVVRP 15

RESULT 70  
PCT-US94-02051-2  
Sequence 2, Application PC/TUS9402051  
GENERAL INFORMATION:  
APPLICANT:  
TITLE OF INVENTION: ANALOGS FOR SPECIFIC OLIGOSACCHARIDE-  
NUMBER OF SEQUENCES: 4  
PROTEIN INTERACTIONS AND USES THEREFOR  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ &  
ADDRESS: THIBEAULT  
STREET: 53 STATE STREET  
CITY: BOSTON  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/02051  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/024,558  
FILING DATE: 01-MAR-1993  
ATTORNEY/AGENT INFORMATION:

NAME: KELLEY, ROBIN D.  
REGISTRATION NUMBER: 34,637  
REFERENCE/DOCKET NUMBER: GLY-003PC  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-248-7000  
TELEFAX: 617-248-7100  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FEATURE:  
NAME/KEY: Protein  
LOCATION: 1..19  
OTHER INFORMATION: /label= PP4  
OTHER INFORMATION: /note="OPPENHEIM ET AL. (1991) ANN. REV. IMMUNOL.  
OTHER INFORMATION: 9:617-648"  
PCT-US94-02051-2

Query Match 26.3%; Score 30; DB 4; Length 19;  
Best Local Similarity 71.4%; Pred. No. 5.6e+02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 13 KAPLYKR 19  
DB 5 QAPLYKK 11

RESULT 71  
PCT-US95-02478-9  
Sequence 9, Application PC/TUS9502478  
GENERAL INFORMATION:  
APPLICANT:  
TITLE OF INVENTION: Method for Treating Conditions  
OF THE EYE USING POLYPEPTIDES  
NUMBER OF SEQUENCES: 16  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/02478  
FILING DATE:  
CLASSIFICATION:  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 08/203,458  
FILING DATE: 28-FEB-1994  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
ORIGINAL SOURCE:  
STRAIN: FN-C/H-1  
PCT-US95-02478-9

Query Match 26.3%; Score 30; DB 4; Length 19;  
Best Local Similarity 42.1%; Pred. No. 5.6e+02;  
Matches 8; Conservative 1; Mismatches 6; Indels 4; Gaps 1;

QY 2 YEYGSRLGNPKAPLYKRP 20  
DB 1 YEKFGS----PPREVVRP 15

RESULT 72  
US-08-462-784-2  
Sequence 2, Application US/08462784  
Patent No. 5714313

GENERAL INFORMATION:  
APPLICANT: Dean, Richard T.  
CITY: Mober, Brian  
TITLE OF INVENTION: Technetium-99m Labeled Peptides for  
IMAGING INFLAMMATION  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff  
STREET: 300 South Wacker Drive Seventh Floor  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/462,784  
FILING DATE: 05-JUN-1995  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 571431nan, Kevin E  
REGISTRATION NUMBER: 35,303  
REFERENCE/DOCKET NUMBER: 90,1104-X  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312 913 0001  
TELEFAX: 312 913 0002  
TELEX:  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 1..5  
OTHER INFORMATION: /label= MODIFIED-CYS  
OTHER INFORMATION: /note= "The thiol group of each cysteine is  
protected by an acetamidomethyl group; the amino  
OTHER INFORMATION: terminal amine is acetylated."  
US-08-462-784-2  
Query Match 26.3%; Score 30; DB 1; Length 20;  
Best Local Similarity 71.4%; Pred. No. 66+02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 13 KAPLYR 19  
DB 6 QAPLYK 12  
RESULT 73  
US-07-923-724-43  
Sequence 43, Application US/07923724  
Patent No. 5780292  
GENERAL INFORMATION:  
APPLICANT: Nevalainen, Helena K.M.  
APPLICANT: Palohelmo, Marja T.  
APPLICANT: Miettinen-Oinonen, Arja S.K.  
APPLICANT: Torkkeli, Tuula K.  
APPLICANT: Cantrell, Michael  
APPLICANT: Piddington, Christopher S.  
APPLICANT: Rambosek, John A.  
APPLICANT: Turunen, Marja K.  
APPLICANT: Fagerstr m, Richard B.  
TITLE OF INVENTION: Production of Phytase Degrading Enzymes  
TITLE OF INVENTION: in Trichoderma  
NUMBER OF SEQUENCES: 66  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sterne, Kessler, Goldstein & Fox

STREET: 1100 New York Avenue, Suite 600  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/923,724  
FILING DATE: 31-JUL-1992  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/496,155  
FILING DATE: 19-MAR-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/044,077  
FILING DATE: 29-APR-1987  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: UK 8610600  
FILING DATE: 30-APR-1986  
ATTORNEY/AGENT INFORMATION:  
NAME: Cimbala, Michele A.  
REGISTRATION NUMBER: 33,851  
REFERENCE/DOCKET NUMBER: 1050.0240004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 371-2600  
TELEFAX: (202) 371-2540  
INFORMATION FOR SEQ ID NO: 43:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
TOPOLOGY: both  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 17  
OTHER INFORMATION: /label= Peptide  
OTHER INFORMATION: /note= "The amino acid at position 17 may also be  
OTHER INFORMATION: tyrosine."  
US-07-923-724-43  
Query Match 26.3%; Score 30; DB 1; Length 20;  
Best Local Similarity 50.0%; Pred. No. 66+02;  
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
QY 4 YPGSRIGNPKAP 15  
DB 1 YYGHGANGNPLGP 12  
RESULT 74  
US-08-609-426A-43  
Sequence 43, Application US/08609426A  
Patent No. 5830733  
GENERAL INFORMATION:  
APPLICANT: Nevalainen, Helena K.M.  
APPLICANT: Palohelmo, Marja T.  
APPLICANT: Miettinen-Oinonen, Arja S.K.  
APPLICANT: Torkkeli, Tuula K.  
APPLICANT: Cantrell, Michael  
APPLICANT: Piddington, Christopher S.  
APPLICANT: Rambosek, John A.  
APPLICANT: Turunen, Marja K.  
APPLICANT: Fagerstr m, Richard B.  
TITLE OF INVENTION: Production of Phytase Degrading Enzymes  
TITLE OF INVENTION: in Trichoderma  
NUMBER OF SEQUENCES: 69  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sterne, Kessler, Goldstein & Fox  
STREET: 1100 New York Avenue, Suite 600

CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/609,426A  
FILING DATE: 01-MAR-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/923,724  
FILING DATE: 31-JUL-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/496,155  
FILING DATE: 19-MAR-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/044,077  
FILING DATE: 29-APR-1987  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: UK 8610600  
FILING DATE: 30-APR-1986  
ATTORNEY/AGENT INFORMATION:  
NAME: Reed, Grant E.  
REGISTRATION NUMBER: P-41,264  
REFERENCE/DOCKET NUMBER: 1050,0080001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 371-2600  
TELEFAX: (202) 371-2540  
INFORMATION FOR SEQ ID NO: 43:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
TOPOLOGY: both  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 17  
OTHER INFORMATION: /label= Peptide  
OTHER INFORMATION: /note= "The amino acid at position 17 may also be  
OTHER INFORMATION: Tyrosine."  
US-08-609-426A-43  
Query Match 26.3%; Score 30; DB 1; Length 20;  
Best Local Similarity 50.0%; Pred. No. 6e+02;  
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
QY 4 YPSRLGNPKAP 15  
DB 1 YYGHGAGNPLGP 12  
RESULT 75  
US-08-564-315-2  
Sequence 2, Application US/08564315  
Patent No. 6019958  
GENERAL INFORMATION:  
APPLICANT: Dean, Richard T.  
APPLICANT: Moyer, Brian  
TITLE OF INVENTION: Technetium-99m Labeled Peptides for  
TITLE OF INVENTION: Imaging Inflammation  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESSES:  
ADDRESSER: McDonnell Boehnen Hulbert & Berghoff  
STREET: 300 South Wacker Drive Seventh Floor  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/564,315  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/462,784  
FILING DATE: 05-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 6019958nan, Kevin B  
REGISTRATION NUMBER: 35,303  
REFERENCE/DOCKET NUMBER: 90,1104-X  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312 913 0001  
TELEFAX: 312 913 0002  
TELEX:  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 1..5  
OTHER INFORMATION: /label= MODIFIED-CYS  
OTHER INFORMATION: /note= "The thiol group of each cysteine is  
OTHER INFORMATION: protected by an acetamidomethyl group; the amino  
OTHER INFORMATION: terminal amine is acetylated."  
US-08-564-315-2  
Query Match 26.3%; Score 30; DB 2; Length 20;  
Best Local Similarity 71.4%; Pred. No. 6e+02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 13 KAPLYR 19  
DB 6 QAPLYRK 12  
RESULT 76  
US-08-505-318-14  
Sequence 14, Application US/08505318  
Patent No. 6107459  
GENERAL INFORMATION:  
APPLICANT: Dean, Richard T.  
TITLE OF INVENTION: Technetium-99m Labeled Peptides for  
TITLE OF INVENTION: Diagnostic Imaging  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESSES:  
ADDRESSER: McDonnell Boehnen Hulbert & Berghoff  
STREET: 300 South Wacker Drive, Seventh Floor  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/505,318  
FILING DATE: 07-DEC-1995  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 6107459nan, Kevin B  
REGISTRATION NUMBER: 35,303  
REFERENCE/DOCKET NUMBER: 90,1104-FF  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-913-0001

TELEFAX: 312-913-0002  
 TELEX:  
 INFORMATION FOR SEQ ID NO: 14:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 20 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 FEATURE:  
 NAME/KEY: Modified-site  
 LOCATION: 1..5  
 OTHER INFORMATION: /label= Tc-99m-chelator  
 OTHER INFORMATION: /note= "The N-terminal amino group is acetylated,  
 OTHER INFORMATION: and the sidechain sulfur atoms of both Cys  
 OTHER INFORMATION: residues are each protected by an acetamidomethyl  
 OTHER INFORMATION: group"  
 US-08-505-318-14

Query Match 26.3%; Score 30; DB 2; Length 20;  
 Best Local Similarity 71.4%; Pred. No. 6e+02;  
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 13 KAPLYKR 19  
 :|||||:  
 DB 6 QAPLYKK 12

RESULT 77  
 US-09-600-432-42  
 Sequence 42, Application US/09600432  
 Patent No. 6849712  
 GENERAL INFORMATION:  
 APPLICANT: Regents of the University of Minnesota  
 TITLE OF INVENTION: PEPTIDES WITH R1 INTEGRIN SUBUNIT DEPENDENT CELL  
 FILE REFERENCE: 110.01130101  
 CURRENT APPLICATION NUMBER: US/09/600,432  
 PRIOR FILING DATE: 2000-10-02  
 PRIOR APPLICATION NUMBER: PCT/US99/01236  
 PRIOR FILING DATE: 1999-01-21  
 PRIOR APPLICATION NUMBER: 60/072,119  
 PRIOR FILING DATE: 1998-01-22  
 PRIOR APPLICATION NUMBER: 60/096,211  
 PRIOR FILING DATE: 1998-08-12  
 PRIOR APPLICATION NUMBER: 60/096,212  
 PRIOR FILING DATE: 1998-08-12  
 NUMBER OF SEQ ID NOS: 46  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO 42  
 LENGTH: 20  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-09-600-432-42

Query Match 26.3%; Score 30; DB 2; Length 20;  
 Best Local Similarity 42.1%; Pred. No. 6e+02;  
 Matches 8; Conservative 1; Mismatches 6; Indels 4; Gaps 1;

QY 2 YEYPSRLGNPKAPLYKRP 20  
 :|||||:  
 DB 1 YEKPSG----PPREVVPRP 15

RESULT 78  
 US-07-972-032-17  
 Sequence 17, Application US/07972032  
 Patent No. 5496712  
 GENERAL INFORMATION:  
 APPLICANT: Cappello, Joseph  
 APPLICANT: Ferrari, Franco A.  
 TITLE OF INVENTION: HIGH MOLECULAR WEIGHT COLLAGEN-LIKE  
 TITLE OF INVENTION: PROTEIN POLYMERS  
 NUMBER OF SEQUENCES: 85

CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Bertam I. Rowland  
 STREET: 4 Embarcadero Center, Suite 3400  
 CITY: San Francisco  
 STATE: California  
 COUNTRY: USA  
 ZIP: CA 94111  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/07/972,032  
 FILING DATE: 19921105  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/07/791,960  
 FILING DATE: 12-NOV-1991  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Rowland, Bertam I.  
 REGISTRATION NUMBER: 20,015  
 REFERENCE/DOCKET NUMBER: A-55556-1/BIR;PROP-08-1  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 781-1989  
 TELEFAX: (415) 398-3249  
 INFORMATION FOR SEQ ID NO: 17:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 18 amino acids  
 TYPE: AMINO ACID  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 US-07-972-032-17

Query Match 25.9%; Score 29.5; DB 1; Length 18;  
 Best Local Similarity 63.6%; Pred. No. 6.3e+02;  
 Matches 7; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

QY 5 PGRSLGNPKAP 15  
 :|||||:  
 DB 9 PGRS-GDPEPP 18

RESULT 79  
 US-07-972-032-83  
 Sequence 83, Application US/07972032  
 Patent No. 5496712  
 GENERAL INFORMATION:  
 APPLICANT: Cappello, Joseph  
 APPLICANT: Ferrari, Franco A.  
 TITLE OF INVENTION: HIGH MOLECULAR WEIGHT COLLAGEN-LIKE  
 TITLE OF INVENTION: PROTEIN POLYMERS  
 NUMBER OF SEQUENCES: 85  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Bertam I. Rowland  
 STREET: 4 Embarcadero Center, Suite 3400  
 CITY: San Francisco  
 STATE: California  
 COUNTRY: USA  
 ZIP: CA 94111  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/07/972,032  
 FILING DATE: 19921105  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/07/791,960  
 FILING DATE: 12-NOV-1991  
 ATTORNEY/AGENT INFORMATION:



NAME: Rowland, Bertram I.  
REGISTRATION NUMBER: 20,015  
REFERENCE/DOCKET NUMBER: A-55556-1/BIR;PROP-08-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 781-1989  
TELEFAX: (415) 398-3249  
INFORMATION FOR SEQ ID NO: 83:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: AMINO ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-07-972-032-83

Query Match 25.9%; Score 29.5; DB 1; Length 18;  
Best Local Similarity 63.6%; Pred. No. 6.3e+02;  
Matches 7; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

QY 5 PGSRLGNPKAP 15  
DB 9 PGSR-GDPGP 18

RESULT 80  
US-08-642-255-134  
Sequence 134, Application US/08642255  
Patent No. 5773249  
GENERAL INFORMATION:  
APPLICANT: CAPPELO, Joseph  
APPLICANT: FERRARI, Franco A.  
TITLE OF INVENTION: High Molecular Weight Collagen-Like  
NUMBER OF SEQUENCES: 135  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT  
STREET: 4 Embarcadero Center, Suite 3400  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-4187  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/642,255  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: ROWLAND, Bertram I.  
REGISTRATION NUMBER: 20,015  
REFERENCE/DOCKET NUMBER: A55556-3/BIR  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 494-8700  
TELEFAX: (415) 494-8771  
TELEX: 910 277299 FHT UR  
INFORMATION FOR SEQ ID NO: 134:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-642-255-134

Query Match 25.9%; Score 29.5; DB 1; Length 18;  
Best Local Similarity 63.6%; Pred. No. 6.3e+02;  
Matches 7; Conservative 1; Mismatches 2; Indels 1; Gaps 1;  
QY 5 PGSRLGNPKAP 15  
DB 9 PGSR-GDPGP 18

DB 9 PGSR-GDPGP 18

RESULT 81  
US-08-147-592A-36  
Sequence 36, Application US/08147592A  
Patent No. 6096513  
GENERAL INFORMATION:  
APPLICANT: Bell, Graeme I  
APPLICANT: Reisine, Terry  
APPLICANT: Yasuda, Kazuki  
TITLE OF INVENTION: Opioid Receptor Genes,  
TITLE OF INVENTION: Compositions and Methods  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold, White & Durkee  
STREET: P.O. Box 4433  
CITY: Houston  
STATE: Texas  
COUNTRY: United States of America  
ZIP: 77210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/147,592A  
FILING DATE: 05-NOV-1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/100,694  
FILING DATE: 30-JUL-1993  
CLASSIFICATION: 435  
APPLICATION NUMBER: 08/066,296  
FILING DATE: 20-MAY-1993  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Wilson, Mark B.  
REGISTRATION NUMBER: 37,259  
REFERENCE/DOCKET NUMBER: ARCD:105  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (512) 418-3000  
TELEFAX: (512) 474-7577  
TELEX: N/A  
INFORMATION FOR SEQ ID NO: 36:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-147-592A-36

Query Match 25.4%; Score 29; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 4e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 EYPGS 7  
DB 1 EYPGS 5

RESULT 82  
US-08-292-694A-36  
Sequence 36, Application US/08292694A  
Patent No. 6319686  
GENERAL INFORMATION:  
APPLICANT: BELL, GRAEME  
APPLICANT: REISINE, TERRY  
APPLICANT: YASUDA, KAZUKI  
TITLE OF INVENTION: OPIOID RECEPTORS: COMPOSITIONS AND METHODS  
NUMBER OF SEQUENCES: 46  
CORRESPONDENCE ADDRESS:

```
/ ADDRESS: Arnold, White & Durkee
/ STREET: P. O. Box 4433
/ CITY: Houston
/ STATE: Texas
/ COUNTRY: USA
/ ZIP: 77210
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
/ SOFTWARE: Patentin Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/292,694A
/ FILING DATE: August 19, 1994
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/066,296
/ FILING DATE: 20 May 1993
/ CLASSIFICATION: 435
/ APPLICATION NUMBER: 08/100,694
/ FILING DATE: 30 July, 1993
/ CLASSIFICATION: 435
/ APPLICATION NUMBER: 08/147,592
/ FILING DATE: 5 No. 631968ember 1993
/ CLASSIFICATION: 435
/ APPLICATION NUMBER: PCT/US94/05747
/ FILING DATE: 20 May 1994
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: MARK B. WILSON
/ REGISTRATION NUMBER: 37,259
/ REFERENCE/DOCKET NUMBER: ARCD:140/WIM
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (512) 418-3000
/ TELEFAX: (713) 789-2679
/ TELEX: 79-0924
/ INFORMATION FOR SEQ ID NO: 36:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 10 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-292-694A-36

Query Match          25.4%; Score 29; DB 2; Length 10;
Best Local Similarity 100.0%; Pred.No. 4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      3 EYPGS 7
      |||||
Db      1 EYPGS 5

RESULT 83
US-09-177-249-108
/ Sequence 108, Application US/09177249
/ Patent No. 6229064
/ GENERAL INFORMATION:
/ APPLICANT: Fischer, Robert L.
/ APPLICANT: Ohad, Nir
/ APPLICANT: Kiyosue, Tomohiro
/ APPLICANT: Yadegari, Ramlin
/ APPLICANT: Margossian, Linda
/ APPLICANT: Harada, John
/ APPLICANT: Goldberg, Robert B.
/ TITLE OF INVENTION: The Regents of the University of California
/ TITLE OF INVENTION: Nucleic Acids That Control Seed and Fruit
/ FILE REFERENCE: 023070-086120US
/ CURRENT APPLICATION NUMBER: US/09/177,249
/ FILING DATE: 1998-10-22
/ EARLIER APPLICATION NUMBER: US 09/071,838
/ EARLIER FILING DATE: 1998-05-01
```

```
/ NUMBER OF SEQ ID NOS: 324
/ SOFTWARE: Patentin Ver. 2.0
/ SEQ ID NO: 108
/ LENGTH: 12
/ TYPE: PRT
/ ORGANISM: Arabidopsis sp.
/ US-09-177-249-108

Query Match          25.4%; Score 29; DB 2; Length 12;
Best Local Similarity 44.4%; Pred.No. 4.9e+02;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      11 NPKAPLYR 19
      ||| :||:
Db      1 NPKVTIFPK 9

RESULT 84
US-09-812-283-108
/ Sequence 108, Application US/09812283
/ Patent No. 6828477
/ GENERAL INFORMATION:
/ APPLICANT: Fischer, Robert L.
/ APPLICANT: Ohad, Nir
/ APPLICANT: Kiyosue, Tomohiro
/ APPLICANT: Yadegari, Ramlin
/ APPLICANT: Margossian, Linda
/ APPLICANT: Harada, John
/ APPLICANT: Goldberg, Robert B.
/ TITLE OF INVENTION: The Regents of the University of California
/ TITLE OF INVENTION: Nucleic Acids That Control Seed and Fruit
/ FILE REFERENCE: 023070-086120US
/ CURRENT APPLICATION NUMBER: US/09/812,283
/ FILING DATE: 2001-03-19
/ PRIOR APPLICATION NUMBER: 09/177,249
/ PRIOR FILING DATE: 1998-10-22
/ PRIOR APPLICATION NUMBER: US 09/071,838
/ PRIOR FILING DATE: 1998-05-01
/ NUMBER OF SEQ ID NOS: 324
/ SOFTWARE: Patentin Ver. 2.0
/ SEQ ID NO: 108
/ LENGTH: 12
/ TYPE: PRT
/ ORGANISM: Arabidopsis sp.
/ US-09-812-283-108

Query Match          25.4%; Score 29; DB 2; Length 12;
Best Local Similarity 44.4%; Pred.No. 4.9e+02;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      11 NPKAPLYR 19
      ||| :||:
Db      1 NPKVTIFPK 9

RESULT 85
US-08-519-196-4
/ Sequence 4, Application US/08519196
/ Patent No. 5854206
/ GENERAL INFORMATION:
/ APPLICANT: Twardzik, Daniel R.
/ APPLICANT: Reed, Steven G.
/ APPLICANT: Vedvick, Thomas S.
/ TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT AND
/ TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
/ NUMBER OF SEQUENCES: 6
/ CORRESPONDENCE ADDRESS:
/ ADDRESS: SEED and BERRY
/ STREET: 6300 Columbia Center, 701 Fifth Avenue
/ CITY: Seattle
/ STATE: Washington
/ COUNTRY: USA
```

```

; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/519,196
; FILING DATE: 25-AUG-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Makl, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.412
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-08-519-196-4

Query Match      25.4%; Score 29; DB 1; Length 13;
Best Local Similarity 71.4%; Pred. No. 5.3e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      10 GNPAPL 16
Db      4 GEPKGPL 10

RESULT 86
; US-10-210-428-21
; Sequence 21, Application US/10210428
; Patent No. 6814969
; GENERAL INFORMATION:
; APPLICANT: David M. Koelle
; APPLICANT: Nancy A. Hoeken
; TITLE OF INVENTION: IMMUNOLOGICALLY SIGNIFICANT HERPES
; TITLE OF INVENTION: SIMPLEX VIRUS ANTIGENS AND METHODS FOR USING SAME
; FILE REFERENCE: 39967.8-US-01
; CURRENT APPLICATION NUMBER: US/10/210,428
; PRIOR FILING DATE: 2002-07-31
; PRIOR APPLICATION NUMBER: 60/308,923
; PRIOR FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: 60/309,428
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 16
; TYPE: PRP
; ORGANISM: Herpes simplex virus-1 (HSV-1)
; US-10-210-428-21

Query Match      25.4%; Score 29; DB 2; Length 16;
Best Local Similarity 35.7%; Pred. No. 6.6e+02;
Matches 5; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY      2 YEPGRLGNPKAP 15
Db      3 YTFSSGMASPDSP 16

RESULT 87
; US-08-436-420-24
; Sequence 24, Application US/08436420
; Patent No. 5840524
; GENERAL INFORMATION:
; APPLICANT: VAN DAMME, Jo; and
```

```

; APPLICANT: PROOST, Paul
; TITLE OF INVENTION: GRANULOCYTE CHEMOTACTIC PROTEIN
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HALB and DORR LLP
; STREET: 1455 PENNSYLVANIA AVENUE, N.W.
; CITY: WASHINGTON
; STATE: DISTRICT OF COLUMBIA
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/436,420
; FILING DATE: 24-MAY-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP93/03330
; FILING DATE: 26-NOV-1993
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/982,539
; FILING DATE: 27-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: BAKER, Hollie L.
; REGISTRATION NUMBER: 31,321
; REFERENCE/DOCKET NUMBER: 102378.215
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 942-8400
; TELEFAX: (202) 942-8484
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: C-terminal
; US-08-436-420-24

Query Match      25.4%; Score 29; DB 1; Length 19;
Best Local Similarity 62.5%; Pred. No. 8e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      12 PKAPLYR 19
Db      1 PEAPLTK 8

RESULT 88
; US-08-129-722A-8
; Sequence 8, Application US/08129722A
; Patent No. 6303369
; GENERAL INFORMATION:
; APPLICANT: Spana, Carl
; APPLICANT: Fargnoli, Joseph
; APPLICANT: Bolen, Joseph B.
; TITLE OF INVENTION: PROTEIN EXPRESSION SYSTEM
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burton Rodney
; STREET: P.O. Box 4000
; CITY: Princeton
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 08543-4000
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.25
```

```
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/129,722A
/ FILING DATE:
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Gaul, Timothy J.
/ REGISTRATION NUMBER: 33,111
/ REFERENCE/DOCKET NUMBER: DC25
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (609) 252-5901
/ TELEFAX: 609) 252-4526
/ INFORMATION FOR SEQ ID NO: 8:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 19 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
US-08-129-722A-8
```

```
Query Match 25.4%; Score 29; DB 2; Length 19;
Best Local Similarity 62.5%; Pred. No. 8e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 10 GNPXAPLYR 17
DB 5 GSPGIRPLY 12
```

```
RESULT 89
US-09-674-674D-42
/ Sequence 42, Application US/09674674D
/ Patent No. 6706859
/ GENERAL INFORMATION:
/ APPLICANT: Bitzer Sorensen
/ TITLE OF INVENTION: HIV Peptides, antigens, vaccine compositions, immunoassay kit and
/ FILE REFERENCE: 2833.400100
/ CURRENT APPLICATION NUMBER: US/09/674,674D
/ PRIOR FILING DATE: 2000-11-03
/ PRIOR APPLICATION NUMBER: PCT/NO00/00075
/ NUMBER OF SEQ ID NOS: 49
/ SOFTWARE: PatentIn Ver. 3.1
/ SEQ ID NO 42
/ LENGTH: 19
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-674-674D-42
```

```
Query Match 25.4%; Score 29; DB 2; Length 19;
Best Local Similarity 50.0%; Pred. No. 8e+02;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
```

```
QY 10 GNPXAPLYR 19
DB 4 GTPVGRIYR 13
```

```
RESULT 90
US-08-505-250-21
/ Sequence 21, Application US/08505250
/ Patent No. 6183983
/ GENERAL INFORMATION:
/ APPLICANT: Sato, Haruya
/ APPLICANT: Yamamoto, Keiji
/ APPLICANT: Suzuki, Kokiichi
/ APPLICANT: Ikeda, Masahiro
/ APPLICANT: Sakagami, Masahiro
/ APPLICANT: Taniguchi, Makoto
/ TITLE OF INVENTION: PROTEIN MODIFICATION METHOD
/ FILE REFERENCE: 110-511
/ CURRENT APPLICATION NUMBER: US/08/505,250
/ CURRENT FILING DATE: 1995-11-29
```

```
/ EARLIER APPLICATION NUMBER: PCT/JP95/00298
/ EARLIER FILING DATE: 1995-02-27
/ EARLIER APPLICATION NUMBER: JP 198187/94
/ EARLIER FILING DATE: 1994-08-23
/ NUMBER OF SEQ ID NOS: 53
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 21
/ LENGTH: 20
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-08-505-250-21
```

```
Query Match 25.4%; Score 29; DB 2; Length 20;
Best Local Similarity 45.5%; Pred. No. 8.4e+02;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
```

```
QY 3 EYPSRLGNPK 13
DB 5 ELPEQOVGP 15
```

```
RESULT 91
US-08-505-250-21
/ Sequence 21, Application US/08505250
/ Patent No. 6322996
/ GENERAL INFORMATION:
/ APPLICANT: Sato, Haruya
/ APPLICANT: Yamamoto, Keiji
/ APPLICANT: Suzuki, Kokiichi
/ APPLICANT: Ikeda, Masahiro
/ APPLICANT: Sakagami, Masahiro
/ APPLICANT: Taniguchi, Makoto
/ TITLE OF INVENTION: PROTEIN MODIFICATION METHOD
/ FILE REFERENCE: 110-511
/ CURRENT APPLICATION NUMBER: US/08/505,250
/ PRIOR FILING DATE: 1995-11-29
/ PRIOR APPLICATION NUMBER: PCT/JP95/00298
/ PRIOR FILING DATE: 1995-02-27
/ PRIOR APPLICATION NUMBER: JP 198187/94
/ PRIOR FILING DATE: 1994-08-23
/ NUMBER OF SEQ ID NOS: 53
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 21
/ LENGTH: 20
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-08-505-250-21
```

```
Query Match 25.4%; Score 29; DB 2; Length 20;
Best Local Similarity 45.5%; Pred. No. 8.4e+02;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
```

```
QY 3 EYPSRLGNPK 13
DB 5 ELPEQOVGP 15
```

```
RESULT 92
US-09-736-457-1844
/ Sequence 1844, Application US/09736457
/ Patent No. 6509448
/ GENERAL INFORMATION:
/ APPLICANT: Wang, Tongfong
/ APPLICANT: Bangur, Chaitanya S.
/ APPLICANT: Lodes, Michael A.
/ APPLICANT: Fanger, Gary
/ APPLICANT: Vedvick, Tom
```

```

/ APPLICANT: Carter, Darlick
/ APPLICANT: Recter, Marc
/ APPLICANT: Mannion, Jane
/ APPLICANT: Fan, Liqun
/ APPLICANT: Wang, Aijun
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
/ FILE OF INVENTION: DIAGNOSIS OF LUNG CANCER
/ FILE REFERENCE: 210121.478C15
/ CURRENT APPLICATION NUMBER: US/09/736,457
/ CURRENT FILING DATE: 2000-12-13
/ NUMBER OF SEQ ID NOS: 1864
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 1844
/ LENGTH: 20
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-736-457-1844

```

```

Query Match      25.4%; Score 29; DB 2; Length 20;
Best Local Similarity 46.7%; Pred. No. 8.4e+02;
Matches 7; Conservative 2; Mismatches 4; Indels 2; Gaps 1;

```

```

QY      6 GSRIGNPKAPLYKRP 20
DB      4 GKKKKDPNAP--KRP 16

```

```

RESULT 93
US-09-991-433-34
/ Sequence 34, Application US/09991433
/ Patent No. 6818612
/ GENERAL INFORMATION:
/ APPLICANT: Broiden, Kristina
/ TITLE OF INVENTION: USE OF PARVOVIRUS CAPSID PARTICLES IN
/ FILE OF INVENTION: THE INHIBITION OF CELL PROLIFERATION AND MIGRATION
/ FILE REFERENCE: TRIPR-019CP1
/ CURRENT APPLICATION NUMBER: US/09/991,433
/ CURRENT FILING DATE: 2001-11-16
/ PRIOR APPLICATION NUMBER: US 09/447,693
/ PRIOR FILING DATE: 1999-11-23
/ PRIOR APPLICATION NUMBER: SE 9804022-3
/ PRIOR FILING DATE: 1998-11-24
/ NUMBER OF SEQ ID NOS: 63
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 34
/ LENGTH: 20
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Peptide fragments derived from parvovirus capsid
US-09-991-433-34

```

```

Query Match      25.4%; Score 29; DB 2; Length 20;
Best Local Similarity 85.7%; Pred. No. 8.4e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY      6 GSRIGNPK 12
DB      8 GSRIGNPK 14

```

```

RESULT 94
US-10-017-754-1844
/ Sequence 1844, Application US/10017754
/ Patent No. 6858204
/ GENERAL INFORMATION:
/ APPLICANT: Henderson, Robert A.
/ APPLICANT: Wang, Tonglong
/ APPLICANT: Watanabe, Yoshihiro
/ APPLICANT: Johnson, Jeffrey C.
/ APPLICANT: Recter, Marc W.
/ APPLICANT: Marnerakis, Margarita

```

```

/ APPLICANT: Carter, Darlick
/ APPLICANT: Fanger, Gary R.
/ APPLICANT: Vedrick, Thomas S.
/ APPLICANT: Bangur, Chaitanya S.
/ APPLICANT: McNabb, Andria
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
/ FILE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
/ FILE REFERENCE: 210121.478C18
/ CURRENT APPLICATION NUMBER: US/10/017,754
/ CURRENT FILING DATE: 2001-10-29
/ NUMBER OF SEQ ID NOS: 2004
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 1844
/ LENGTH: 20
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-017-754-1844

```

```

Query Match      25.4%; Score 29; DB 2; Length 20;
Best Local Similarity 46.7%; Pred. No. 8.4e+02;
Matches 7; Conservative 2; Mismatches 4; Indels 2; Gaps 1;

```

```

QY      6 GSRIGNPKAPLYKRP 20
DB      4 GKKKKDPNAP--KRP 16

```

```

RESULT 95
PCT-US92-08094-68
/ Sequence 68, Application PC/TUS9208094
/ GENERAL INFORMATION:
/ APPLICANT: GENENTECH, INC.
/ APPLICANT: Amanto, Edward P.
/ TITLE OF INVENTION: DIAGNOSING AND TREATING AUTOIMMUNE
/ FILE OF INVENTION: DISORDERS
/ NUMBER OF SEQUENCES: 80
/ CORRESPONDENCE ADDRESS:
/ ADDRESSER: Genentech, Inc.
/ STREET: 460 Point San Bruno Blvd
/ CITY: South San Francisco
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94080-4990
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: patin (Genentech)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: PCT/US92/08094
/ FILING DATE: 19920923
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 07/765222
/ FILING DATE: 23-SEP-1991
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 07/779445
/ FILING DATE: 18-OCT-1991
/ APPLICATION NUMBER: 07/853362
/ FILING DATE: 18-MAR-1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Hensley, Max D.
/ REGISTRATION NUMBER: 27,043
/ REFERENCE/DOCKET NUMBER: 734P3
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 415/225-1994
/ TELEFAX: 415/952-9881
/ TELETYPE: 910/371-7168
/ INFORMATION FOR SEQ ID NO: 68:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 18 amino acids
/ TYPE: AMINO ACID

```

```

; TOPOLOGY: linear
PCT-US92-08094-68

Query Match          25.0%; Score 28.5; DB 4; Length 18;
Best Local Similarity 58.3%; Pred. No. 8.9e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 3; Gaps 1;

QY      1 DYEX---PGSRL 9
      ||| |||
      4 DYEXYRGPGTRL 15

Db

RESULT 96
US-08-331-394-43
; Sequence 43, Application US/08331394
; Patent No. 5670319
; GENERAL INFORMATION:
; APPLICANT: Goeddel, David V.
; APPLICANT: Roche, Mike
; TITLE OF INVENTION: Tumor Necrosis Factor
; TITLE OF INVENTION: Receptor-Associated Factors
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/331,394
; FILING DATE:
; CLASSIFICATION: 436
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/250858
; FILING DATE: 27-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Ginger R.
; REGISTRATION NUMBER: 33,055
; REFERENCE/DOCKET NUMBER: 897P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-3216
; TELEX: 910/371-7168
; TELEFAX: 415/952-9881
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-331-394-43

Query Match          24.6%; Score 28; DB 1; Length 7;
Best Local Similarity 71.4%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      5 PGSRLGN 11
      ||| |||
      1 PGSRLGS 7

Db

RESULT 97
US-08-250-858-43
; Sequence 43, Application US/08250858
; Patent No. 5708142
; GENERAL INFORMATION:
; APPLICANT: Goeddel, David V.
; APPLICANT: Roche, Mike
; TITLE OF INVENTION: Tumor Necrosis Factor Receptor-Associated Factors
```

```

; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/250,858
; FILING DATE: 27-May-1994
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Ginger R.
; REGISTRATION NUMBER: 33,055
; REFERENCE/DOCKET NUMBER: 897.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-3216
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-250-858-43

Query Match          24.6%; Score 28; DB 1; Length 7;
Best Local Similarity 71.4%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      5 PGSRLGN 11
      ||| |||
      1 PGSRLGS 7

Db

RESULT 98
US-08-446-915-43
; Sequence 43, Application US/08446915
; Patent No. 5741667
; GENERAL INFORMATION:
; APPLICANT: Goeddel, David V.
; APPLICANT: Roche, Mike
; TITLE OF INVENTION: Tumor Necrosis Factor Receptor-Associated Factors
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,915
; FILING DATE:
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/250858
; FILING DATE: 27-MAY-1994
; PRIORITY APPLICATION DATA:
```

APPLICATION NUMBER: 08/31394  
FILING DATE: 28-OCT-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Dreger, Ginger R.  
REGISTRATION NUMBER: 33,055  
REFERENCE/DOCKET NUMBER: 897P2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/225-3216  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 43:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-446-915-43

Query Match 24.6%; Score 28; DB 1; Length 7;  
Best Local Similarity 71.4%; Pred. No. 4.6e+05;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 PGSRLGN 11  
DB 1 PGSNLS 7

RESULT 99  
US-08-744-139-43  
Sequence 43, Application US/08744139  
Patent No. 5869612  
GENERAL INFORMATION:  
APPLICANT: Goeddel, David V  
ATTORNEY/AGENT INFORMATION:  
NAME: Dreger, Ginger R.  
REGISTRATION NUMBER: 33,055  
REFERENCE/DOCKET NUMBER: P0897C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/225-3216  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 43:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7 amino acids  
TYPE: Amino Acid  
TOPOLOGY: linear  
US-08-744-139-43

Query Match 24.6%; Score 28; DB 1; Length 7;  
Best Local Similarity 71.4%; Pred. No. 4.6e+05;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 PGSRLGN 11  
DB 1 PGSNLS 7

RESULT 100  
US-08-779-599-43  
Sequence 43, Application US/08779599  
Patent No. 6500922  
GENERAL INFORMATION:  
APPLICANT: Goeddel, David V.  
ATTORNEY/AGENT INFORMATION:  
NAME: Dreger, Ginger R.  
REGISTRATION NUMBER: 33,055  
REFERENCE/DOCKET NUMBER: P0897C2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/225-3216  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 43:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7 amino acids  
TYPE: Amino Acid  
TOPOLOGY: linear  
US-08-779-599-43

Query Match 24.6%; Score 28; DB 2; Length 7;  
Best Local Similarity 71.4%; Pred. No. 4.6e+05;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 PGSRLGN 11  
DB 1 PGSNLS 7

Search completed: January 20, 2006, 19:14:11  
Job time : 21.9615 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 20, 2006, 19:11:21 ! Search time 72.1154 Seconds  
(without alignments)  
115.878 Million cell updates/sec

Title: US-09-662-293-2

Perfect score: 114  
Sequence: 1 DYEPGSRRLGNPKAPLYKRP 20

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 380452

Minimum DB seq length: 0  
Maximum DB seq length: 20

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Littering filter 100 summaries

Database :

Published Applications AA Main: \*  
1: /cgn2\_6/ptodaca/1/pubppaa/US07\_PUBCOMB.pep: \*  
2: /cgn2\_6/ptodaca/1/pubppaa/US08\_PUBCOMB.pep: \*  
3: /cgn2\_6/ptodaca/1/pubppaa/US09\_PUBCOMB.pep: \*  
4: /cgn2\_6/ptodaca/1/pubppaa/US10A\_PUBCOMB.pep: \*  
5: /cgn2\_6/ptodaca/1/pubppaa/US10B\_PUBCOMB.pep: \*  
6: /cgn2\_6/ptodaca/1/pubppaa/US11\_PUBCOMB.pep: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	114	100.0	20	4 US-10-218-743-2	Sequence 2, Appl1
2	33	28.9	16	5 US-10-476-264-135	Sequence 135, App
3	33	28.9	19	4 US-10-394-980-17	Sequence 17, Appl
4	33	28.9	19	5 US-10-801-990-103	Sequence 103, App
5	33	28.9	19	5 US-10-952-557-17	Sequence 17, Appl
6	33	28.1	14	4 US-10-362-527-93	Sequence 93, Appl
7	32	28.1	16	4 US-10-224-999A-1541	Sequence 1541, App
8	32	28.1	17	2 US-08-424-550B-251	Sequence 251, App
9	32	28.1	17	3 US-09-879-857-226	Sequence 226, App
10	32	28.1	17	4 US-10-224-999A-1554	Sequence 1554, App
11	32	28.1	17	4 US-10-224-999A-1555	Sequence 1555, App
12	32	28.1	17	4 US-10-807-856-226	Sequence 226, Appl
13	32	28.1	17	4 US-10-723-606-19	Sequence 19, Appl
14	32	28.1	18	4 US-10-224-999A-1568	Sequence 1568, App
15	32	28.1	18	4 US-10-224-999A-1569	Sequence 1569, App
16	32	28.1	18	4 US-10-224-999A-1570	Sequence 1570, App
17	32	28.1	19	4 US-10-224-999A-1583	Sequence 1583, App
18	32	28.1	19	4 US-10-224-999A-1584	Sequence 1584, App
19	32	28.1	19	4 US-10-224-999A-1585	Sequence 1585, App
20	32	28.1	19	4 US-10-224-999A-1586	Sequence 1586, App
21	32	28.1	20	4 US-10-224-999A-1589	Sequence 1589, App
22	32	28.1	20	4 US-10-224-999A-1600	Sequence 1600, App
23	32	28.1	20	4 US-10-224-999A-1601	Sequence 1601, App
24	32	28.1	20	4 US-10-224-999A-1602	Sequence 1602, App
25	32	28.1	20	4 US-10-224-999A-1603	Sequence 1603, App
26	31	27.2	9	3 US-09-876-904A-119	Sequence 119, App
27	31	27.2	9	3 US-09-876-904A-125	Sequence 125, App

28	31	27.2	9	3 US-09-876-904A-128	Sequence 128, App
29	31	27.2	12	5 US-10-926-542-122	Sequence 122, App
30	31	27.2	13	5 US-10-948-707-803	Sequence 803, App
31	31	27.2	14	3 US-09-880-748-2501	Sequence 2501, App
32	31	27.2	14	4 US-10-293-418-2501	Sequence 2501, App
33	31	27.2	15	4 US-10-224-999A-1528	Sequence 1528, App
34	31	27.2	15	4 US-10-203-815A-58	Sequence 58, Appl
35	31	27.2	15	5 US-10-866-773-147	Sequence 147, App
36	31	27.2	15	5 US-10-862-195-182	Sequence 182, App
37	31	27.2	16	4 US-10-224-999A-1540	Sequence 1540, App
38	31	27.2	17	4 US-10-161-791-189	Sequence 244, App
39	31	27.2	17	4 US-10-211-088-254	Sequence 1553, App
40	31	27.2	17	4 US-10-224-999A-1553	Sequence 1553, App
41	31	27.2	17	4 US-10-350-405-155	Sequence 155, App
42	31	27.2	17	4 US-10-350-405-158	Sequence 158, App
43	31	27.2	17	5 US-10-482-029-373	Sequence 373, App
44	31	27.2	18	4 US-10-225-567A-2233	Sequence 2233, App
45	31	27.2	18	4 US-10-224-999A-1567	Sequence 1567, App
46	31	27.2	18	4 US-10-350-405-200	Sequence 200, App
47	31	27.2	19	4 US-10-224-999A-1582	Sequence 1582, App
48	31	27.2	19	5 US-10-862-195-1528	Sequence 1598, App
49	31	27.2	20	4 US-10-224-999A-1598	Sequence 459, App
50	30.5	26.8	13	5 US-10-481-261-459	Sequence 3190, App
51	30	26.3	10	3 US-09-572-404B-3190	Sequence 315, App
52	30	26.3	12	3 US-09-954-285-315	Sequence 315, App
53	30	26.3	12	5 US-10-912-512-315	Sequence 315, App
54	30	26.3	12	5 US-10-235-043-315	Sequence 2378, App
55	30	26.3	14	3 US-09-880-748-2378	Sequence 2378, App
56	30	26.3	15	4 US-10-293-418-2378	Sequence 44, Appl
57	30	26.3	15	4 US-09-829-549A-44	Sequence 45, Appl
58	30	26.3	15	3 US-09-992-665-45	Sequence 1857, App
59	30	26.3	15	5 US-10-862-195-1827	Sequence 522, App
60	30	26.3	16	3 US-09-974-879-522	Sequence 524, App
61	30	26.3	16	3 US-09-305-736-524	Sequence 524, App
62	30	26.3	16	3 US-09-818-683-524	Sequence 524, App
63	30	26.3	16	3 US-09-818-683-524	Sequence 524, App
64	30	26.3	16	4 US-10-621-401-522	Sequence 524, App
65	30	26.3	18	4 US-10-131-543-8	Sequence 522, App
66	30	26.3	18	4 US-10-131-546-8	Sequence 8, Appl1
67	30	26.3	18	4 US-10-131-346-8	Sequence 8, Appl1
68	30	26.3	18	4 US-10-405-339-6	Sequence 6, Appl1
69	30	26.3	18	4 US-10-325-810-163	Sequence 163, App
70	30	26.3	18	4 US-10-350-405-181	Sequence 181, App
71	30	26.3	18	4 US-10-415-024-8	Sequence 8, Appl1
72	30	26.3	18	5 US-10-877-124-163	Sequence 163, App
73	30	26.3	18	5 US-10-877-022-163	Sequence 163, App
74	30	26.3	18	5 US-10-877-146-163	Sequence 163, App
75	30	26.3	18	6 US-11-088-596-8	Sequence 8, Appl1
76	30	26.3	18	6 US-11-086-697A-1140	Sequence 1140, App
77	30	26.3	18	6 US-11-086-966-8	Sequence 8, Appl1
78	30	26.3	19	4 US-10-106-804B-11	Sequence 11, Appl1
79	30	26.3	19	4 US-10-323-046-13	Sequence 13, Appl1
80	30	26.3	19	4 US-10-297-229-52	Sequence 52, Appl1
81	30	26.3	19	4 US-10-225-567A-1514	Sequence 1514, App
82	29.5	25.9	15	4 US-10-327-598-150	Sequence 150, App
83	29.5	25.9	15	4 US-10-327-598-232	Sequence 232, App
84	29	25.4	10	4 US-10-304-443-99	Sequence 99, Appl1
85	29	25.4	10	4 US-10-415-389-12	Sequence 12, Appl1
86	29	25.4	11	4 US-10-322-210-4	Sequence 4, Appl1
87	29	25.4	11	4 US-10-304-443-4	Sequence 4, Appl1
88	29	25.4	11	4 US-10-362-527-63	Sequence 63, Appl1
89	29	25.4	11	6 US-11-004-771-4	Sequence 4, Appl1
90	29	25.4	12	3 US-09-071-838-108	Sequence 108, App
91	29	25.4	12	4 US-10-213-512-108	Sequence 108, App
92	29	25.4	12	4 US-10-304-443-111	Sequence 111, App
93	29	25.4	12	4 US-10-362-527-317	Sequence 317, App
94	29	25.4	12	4 US-10-815-389-24	Sequence 24, Appl1
95	29	25.4	13	4 US-10-322-210-20	Sequence 20, Appl1
96	29	25.4	13	4 US-10-304-443-20	Sequence 20, Appl1
97	29	25.4	13	4 US-10-082-014-272	Sequence 272, App
98	29	25.4	13	4 US-10-372-076-126	Sequence 126, App
99	29	25.4	13	4 US-10-362-527-79	Sequence 79, Appl1
100	29	25.4	13	4 US-10-732-862A-140	Sequence 140, App



Query Match 28.9%; Score 33; DB 5; Length 19;  
Best Local Similarity 46.2%; Pred. No. 9.7e+02;  
Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 DVEYPSRLGNPK 13  
| : ||||  
Db 7 DLSTPDVAVMGNPX 19

## RESULT 5

US-10-952-557-17  
Sequence 17, Application US/10952557  
Publication No. US20050196823A1  
GENERAL INFORMATION:  
APPLICANT: Vandekerckhove, Joel  
APPLICANT: Gevaert, Kt18  
TITLE OF INVENTION: METHODS AND APPARATUS FOR GEL-FREE QUALITATIVE AND  
FILE REFERENCE: VAV-001  
CURRENT APPLICATION NUMBER: US/10/952,557  
CURRENT FILING DATE: 2004-09-28  
PRIOR APPLICATION NUMBER: US/10/394,980  
PRIOR FILING DATE: 2003-03-21  
PRIOR APPLICATION NUMBER: PCT/EP02/03368  
PRIOR FILING DATE: 2002-03-22  
PRIOR APPLICATION NUMBER: US60/278,171  
PRIOR FILING DATE: 2001-03-22  
PRIOR APPLICATION NUMBER: US60/318,749  
PRIOR FILING DATE: 2001-09-12  
PRIOR APPLICATION NUMBER: US60/323,999  
PRIOR FILING DATE: 2001-09-20  
NUMBER OF SEQ ID NOS: 473  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 17  
LENGTH: 19  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: MISC\_FEATURE  
OTHER INFORMATION: part of HBB\_HUMAN ((P02023) hemoglobin beta chain)  
US-10-952-557-17

Query Match 28.9%; Score 33; DB 5; Length 19;  
Best Local Similarity 46.2%; Pred. No. 9.7e+02;  
Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 DVEYPSRLGNPK 13  
| : ||||  
Db 7 DLSTPDVAVMGNPX 19

## RESULT 6

US-10-362-527-93  
Sequence 93, Application US/10362527  
Publication No. US20040030106A1  
GENERAL INFORMATION:  
APPLICANT: Friede, Martin  
APPLICANT: Mason, Sean  
APPLICANT: Turnell, William Gordon  
APPLICANT: Vinals y De Baesols, Carlotia  
TITLE OF INVENTION: Vaccine Immunogens Comprising Disulphide Bridged Cyclised Peptide  
TITLE OF INVENTION: and Use thereof in the Treatment of Allergies  
FILE REFERENCE: B45236  
CURRENT APPLICATION NUMBER: US/10/362,527  
CURRENT FILING DATE: 2003-02-21  
PRIOR APPLICATION NUMBER: PCT/EP01/09576  
PRIOR FILING DATE: 2001-08-17  
PRIOR APPLICATION NUMBER: GB 0020717.5  
PRIOR FILING DATE: 2000-08-22  
NUMBER OF SEQ ID NOS: 328  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 93

LENGTH: 14  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-362-527-93

Query Match 28.1%; Score 32; DB 4; Length 14;  
Best Local Similarity 75.0%; Pred. No. 1.1e+03;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DVEYPSGR 8  
| : ||||  
Db 1 DPEWPGSR 8

## RESULT 7

US-10-224-999A-1541  
Sequence 1541, Application US/10224999A  
Publication No. US20030171318A1  
GENERAL INFORMATION:  
APPLICANT: Myriad Genetics, Inc.  
APPLICANT: Morham, Scott  
APPLICANT: Zavitz, Kenton  
APPLICANT: Hobden, Adrian  
TITLE OF INVENTION: Composition and Method for Treating Viral Infection  
FILE REFERENCE: 5004.01  
CURRENT APPLICATION NUMBER: US/10/224,999A  
CURRENT FILING DATE: 2003-03-03  
PRIOR APPLICATION NUMBER: US 60/313,695  
PRIOR FILING DATE: 2001-08-20  
NUMBER OF SEQ ID NOS: 3484  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 1541  
LENGTH: 16  
TYPE: PRT  
ORGANISM: Human papillomavirus  
US-10-224-999A-1541

Query Match 28.1%; Score 32; DB 4; Length 16;  
Best Local Similarity 31.2%; Pred. No. 1.1e+03;  
Matches 5; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 DVEYPSRLGNPKAPL 16  
| : ||||  
Db 1 DITPTAPWGTSPSPV 16

## RESULT 8

US-08-424-550B-251  
Sequence 251, Application US/08424550B  
Publication No. US20020119447A1  
GENERAL INFORMATION:  
APPLICANT: JOHN N. SIMONS  
APPLICANT: TAMI J. PILOT-MATIAS  
APPLICANT: GEORGE J. DAWSON  
APPLICANT: GEORGE G. SCHLAUDER  
APPLICANT: THOMAS P. DESAI  
APPLICANT: SURESH M. LIBAY  
APPLICANT: ANTHONY SCOTT MIERHOFF  
APPLICANT: JAMES C. ERKER  
APPLICANT: SHERI L. BUTIK  
APPLICANT: ISA K. MUSHAMMAR  
TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS  
TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE  
NUMBER OF SEQUENCES: 716  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: ABBOTT LABORATORIES D377/AP6D  
STREET: 100 ABBOTT PARK ROAD  
CITY: ABBOTT PARK  
STATE: IL  
COUNTRY: USA  
ZIP: 60064-3500  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/424,550B  
FILING DATE:  
CLASSIFICATION: 435435  
ATTORNEY/AGENT INFORMATION:  
NAME: FOREMSKI, PRISCILLA E.  
REGISTRATION NUMBER: 33,207  
REFERENCE/DOCKET NUMBER: 5527.PC.01  
TELEPHONE: 708-937-6365  
TELEFAX: 708-938-2623  
INFORMATION FOR SEQ ID NO: 251:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-424-550B-251

Query Match 28.1%; Score 32; DB 2; Length 17;  
Best Local Similarity 41.7%; Pred. No. 1.2e+03;  
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 5 GSRGNGPKAPL 16  
DB 1 PSRRSPKLPV 12

## RESULT 9

US-09-879-957-226  
Sequence 226, Application US/09879957  
Patent No. US20020034755A1

## GENERAL INFORMATION:

APPLICANT: SPARKS, Andrew B.  
HOFFMAN, No. US20020034755A1h  
KAY, Brian K.  
FOWLES, Dana M.

TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL

DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND  
USING SAME

NUMBER OF SEQUENCES: 227

CORRESPONDENCE ADDRESS:

ADDRESSER: Pennie & Edmonds LLP

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10036-2711

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/879,957

FILING DATE: 13-Jun-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/630,915

FILING DATE: 03-Apr-1996

ATTORNEY/AGENT INFORMATION:

NAME: Mistrock, S. Leslie

REGISTRATION NUMBER: 18,872

REFERENCE/DOCKET NUMBER: 1101-174

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-8864/9741

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 226:

SEQUENCE CHARACTERISTICS:  
LENGTH: 17 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
SEQUENCE DESCRIPTION: SEQ ID NO: 226:  
US-09-879-957-226

Query Match 28.1%; Score 32; DB 3; Length 17;  
Best Local Similarity 63.6%; Pred. No. 1.2e+03;  
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 6 GSRGNGPKAPL 16  
DB 2 GSGIAPPKPL 12

## RESULT 10

US-10-224-999A-1554  
Sequence 1554, Application US/10224999A  
Publication No. US20030171318A1

## GENERAL INFORMATION:

APPLICANT: Myriad Genetics, Inc.

APPLICANT: Morham, Scott

APPLICANT: Zavit, Kenton

APPLICANT: Hobden, Adrian

FILE REFERENCE: 5004.01

CURRENT APPLICATION NUMBER: US/10/224,999A

CURRENT FILING DATE: 2003-03-03

PRIOR APPLICATION NUMBER: US 60/313,695

PRIOR FILING DATE: 2001-08-20

NUMBER OF SEQ ID NOS: 3484

SOFTWARE: Patentin version 3.1

SEQ ID NO 1554

LENGTH: 17

TYPE: PRT

ORGANISM: Human papillomavirus

US-10-224-999A-1554

Query Match 28.1%; Score 32; DB 4; Length 17;  
Best Local Similarity 31.2%; Pred. No. 1.2e+03;  
Matches 5; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 DYEYPSRLGNPKAPL 16  
DB 2 DTFPTAPMGTFPSPV 17

## RESULT 11

US-10-224-999A-1555  
Sequence 1555, Application US/10224999A  
Publication No. US20030171318A1

## GENERAL INFORMATION:

APPLICANT: Myriad Genetics, Inc.

APPLICANT: Morham, Scott

APPLICANT: Zavit, Kenton

APPLICANT: Hobden, Adrian

TITLE OF INVENTION: Composition and Method for Treating Viral Infection

FILE REFERENCE: 5004.01

CURRENT APPLICATION NUMBER: US/10/224,999A

CURRENT FILING DATE: 2003-03-03

PRIOR APPLICATION NUMBER: US 60/313,695

PRIOR FILING DATE: 2001-08-20

NUMBER OF SEQ ID NOS: 3484

SOFTWARE: Patentin version 3.1

SEQ ID NO 1555

LENGTH: 17

TYPE: PRT

ORGANISM: Human papillomavirus



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; TITLE OF INVENTION: Composition and Method for Treating Viral Infection
; FILE REFERENCE: 5004.01
; CURRENT APPLICATION NUMBER: US/10/224,999A
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/313,695
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 3484
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1569
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Human papillomavirus
US-10-224-999A-1569

Query Match      28.1%; Score 32; DB 4; Length 18;
Best Local Similarity 31.2%; Pred. No. 1.3e+03;
Matches 5; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY      1 DYEYPSRLGNPKAPL 16
DB      2 DITFPTAPMGTPSPV 17

RESULT 16
US-10-224-999A-1570
; Sequence 1570, Application US/10224999A
; Publication No. US20030171318A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Composition and Method for Treating Viral Infection
; FILE REFERENCE: 5004.01
; CURRENT APPLICATION NUMBER: US/10/224,999A
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/313,695
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 3484
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1570
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Human papillomavirus
US-10-224-999A-1570

Query Match      28.1%; Score 32; DB 4; Length 18;
Best Local Similarity 31.2%; Pred. No. 1.3e+03;
Matches 5; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY      1 DYEYPSRLGNPKAPL 16
DB      1 DITFPTAPMGTPSPV 16

RESULT 17
US-10-224-999A-1583
; Sequence 1583, Application US/10224999A
; Publication No. US20030171318A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Composition and Method for Treating Viral Infection
; FILE REFERENCE: 5004.01
; CURRENT APPLICATION NUMBER: US/10/224,999A
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/313,695
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 3484
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1583

```

```

; LENGTH: 19
; TYPE: PRT
; ORGANISM: Human papillomavirus
US-10-224-999A-1583

Query Match      28.1%; Score 32; DB 4; Length 19;
Best Local Similarity 31.2%; Pred. No. 1.4e+03;
Matches 5; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY      1 DYEYPSRLGNPKAPL 16
DB      4 DITFPTAPMGTPSPV 19

RESULT 18
US-10-224-999A-1584
; Sequence 1584, Application US/10224999A
; Publication No. US20030171318A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Composition and Method for Treating Viral Infection
; FILE REFERENCE: 5004.01
; CURRENT APPLICATION NUMBER: US/10/224,999A
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/313,695
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 3484
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1584
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Human papillomavirus
US-10-224-999A-1584

Query Match      28.1%; Score 32; DB 4; Length 19;
Best Local Similarity 31.2%; Pred. No. 1.4e+03;
Matches 5; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY      1 DYEYPSRLGNPKAPL 16
DB      3 DITFPTAPMGTPSPV 18

RESULT 19
US-10-224-999A-1585
; Sequence 1585, Application US/10224999A
; Publication No. US20030171318A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Composition and Method for Treating Viral Infection
; FILE REFERENCE: 5004.01
; CURRENT APPLICATION NUMBER: US/10/224,999A
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/313,695
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 3484
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1585
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Human papillomavirus
US-10-224-999A-1585

Query Match      28.1%; Score 32; DB 4; Length 19;
Best Local Similarity 31.2%; Pred. No. 1.4e+03;
Matches 5; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

```

QY	1	DYEYPSRLGNPKAPL	16
		:  :  :  :	
Db	2	DITFPTAPMGTPFSPV	17

```

RESULT 20
US-10-224-999A-1586
/ Sequence 1586, Application US/1022499A
/ Publication No. US2003017318A1
/ GENERAL INFORMATION:
/ APPLICANT: Myriad Genetics, Inc.
/ APPLICANT: Morham, Scott
/ APPLICANT: Zavit, Kenton
/ APPLICANT: Hobden, Adrien
/ TITLE OF INVENTION: Composition and Method for Treating Viral Infection
/ FILE REFERENCE: 5004.01
/ CURRENT APPLICATION NUMBER: US/10/224,999A
/ CURRENT FILING DATE: 2003-03-03
/ PRIOR APPLICATION NUMBER: US 60/313,655
/ PRIOR FILING DATE: 2001-08-20
/ NUMBER OF SEQ ID NOS: 3484
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 1586
/ LENGTH: 19
/ TYPE: PR1
/ ORGANISM: Human papillomavirus
US-10-224-999A-1586

```

Query Match	28.1%	Score 32	DB 4	Length 19
Best Local Similarity	31.2%	Pred. No. 1.4e+03		
Matches	5	Conservative	5	Mismatches 6
			Indels	0
			Gaps	0

```
QY      1 DYEYPSRLGNPKAPL 16
          |  ::  ::  |  ::  |
Db      1 DTFPTAPMGTPSPV 16
```

```

RESULT 21
US-10-224-999A-1599
Sequence 1599, Application US/10224999A
Publication No. US2003017318A1
GENERAL INFORMATION:
APPLICANT: Myriad Genetics, Inc.
APPLICANT: Morham, Scott
APPLICANT: Zavit, Kenon
APPLICANT: Hobden, Adrien
TITLE OF INVENTION: Composition and Method for Treating Viral Infection
FILE REFERENCE: 5004.01
CURRENT APPLICATION NUMBER: US/10/224,999A
CURRENT FILING DATE: 2003-03-03
PRIOR APPLICATION NUMBER: US 60/313,655
PRIOR FILING DATE: 2001-08-20
NUMBER OF SEQ ID NOS: 3484
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1599
LENGTH: 20
TYPE: PRF
ORGANISM: Human papillomavirus
US-10-224-999A-1599

```

Query Match	28.1%	Score 32	DB 4	Length 20
Best Local Similarity	31.2%	Pred. No. 1.4e+03		
Matches	5	Conservative	6	Indels 0
				Gaps 0

```
QY      1 DYEPGSR LGNPKAPL 16
          | : | : | | : | :
Db      5 DITPTAPMGTPESPV 20
```

RESULT 22  
US-10-224-999A-1600  
; Sequence 1600, Application US/10224999A  
; Publication No. US20030171318A1

```

? GENERAL INFORMATION:
? APPLICANT: Myriad Genetics, Inc.
? APPLICANT: Morham, Scott
? APPLICANT: Zavitz, Kenton
? APPLICANT: Hobden, Adrian
? TITLE OF INVENTION: Composition and Method for Treating Viral Infection
? FILE REFERENCE: 5004.01
? CURRENT APPLICATION NUMBER: US/10/224,999A
? CURRENT FILING DATE: 2003-03-03
? PRIOR APPLICATION NUMBER: US 60/313,695
? PRIOR FILING DATE: 2001-08-20
? NUMBER OF SEQ ID NOS: 3484
? SOFTWARE: PatentIn version 3.1
? SEQ ID NO 1600
? LENGTH: 20
? TYPE: PR1
? ORGANISM: Human papillomavirus
US-10-224-999A-1600

```

Query Match	28.1%	Score 32;	DB 4;	Length 20;
Best Local Similarity	31.2%	Pred. No. 1.4e+03;		
Matches	5;	Conservative	5;	Mismatches 6;
			Indels	0;
			Gaps	0;

QY	1	DYEYPGSRLGNPKAPL	16
		:   :   :   :	
Db	4	DITFPTAPMGTPPSPV	19

```

RESULT 23
US-10-224-999A-1601
; Sequence 1601, Application US/10224999A
; Publication No. US2003017138A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Composition and Method for Treating Viral Infection
; FILE REFERENCE: 5004.01
; CURRENT APPLICATION NUMBER: US/10/224,999A
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/313,695
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 3484
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1601
; LENGTH: 20
; TYPE: PRN
; ORGANISM: Human papillomavirus
US-10-224-999A-1601

```

Query Match	28.1%	Score 32;	DB 4;	Length 20;
Best Local Similarity	31.2%	Pred. No. 1.4e+03;		
Matches	5;	Conservative	5;	Mismatches 6;
			Indels 0;	Gaps 0;

```
QY      1 DYBYPGSRLGNPKAPL 16
          |  ::::|::|
Db      3 DITFPTAPMGTFPSV 18
```

```

RESULT 24
US-10-224-999A-1602
/ Sequence 1602, Application US/10224999A
/ Publication No. US2003017138A1
/ GENERAL INFORMATION:
/ APPLICANT: Myriad Genetics, Inc.
/ APPLICANT: Morham, Scott
/ APPLICANT: Zavitz, Kenton
/ APPLICANT: Hobden, Adrian
/ TITLE OF INVENTION: Composition and Method for Treating Viral Infection
/ FILE REFERENCE: 5004.01
/ CURRENT APPLICATION NUMBER: US/10/224,999A
/ CURRENT FILING DATE: 2003-03-03

```

;; PRIOR APPLICATION NUMBER: US 60/313,695  
;; PRIOR FILING DATE: 2001-08-20  
;; NUMBER OF SEQ ID NOS: 3484  
;; SOFTWARE: PatentIn version 3.1  
;; SEQ ID NO 1602  
;; LENGTH: 20  
;; TYPE: PRT  
;; ORGANISM: Human papillomavirus  
US-10-224-999A-1602

Query Match 28.1%; Score 32; DB 4; Length 20;  
Best Local Similarity 31.2%; Pred. No. 1.4e+03;  
Matches 5; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

Qy 1 DYEYPSRLGNPKAPL 16  
Db 2 DTFPTAPMGTPSPV 17

RESULT 25  
US-10-224-999A-1603

;; Sequence 1603, Application US/10224999A  
;; Publication No. US20030171318A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Myriad Genetics, Inc.  
;; APPLICANT: Morham, Scott  
;; APPLICANT: Zavitz, Kenton  
;; APPLICANT: Hobden, Adrian  
;; TITLE OF INVENTION: Composition and Method for Treating Viral Infection  
;; FILE REFERENCE: 5004.01  
;; CURRENT APPLICATION NUMBER: US/10/224,999A  
;; PRIOR FILING DATE: 2003-03-03  
;; PRIOR APPLICATION NUMBER: US 60/313,695  
;; PRIOR FILING DATE: 2001-08-20  
;; NUMBER OF SEQ ID NOS: 3484  
;; SOFTWARE: PatentIn version 3.1  
;; SEQ ID NO 1603  
;; LENGTH: 20  
;; TYPE: PRT  
;; ORGANISM: Human papillomavirus  
US-10-224-999A-1603

Query Match 28.1%; Score 32; DB 4; Length 20;  
Best Local Similarity 31.2%; Pred. No. 1.4e+03;  
Matches 5; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

Qy 1 DYEYPSRLGNPKAPL 16  
Db 1 DTFPTAPMGTPSPV 16

RESULT 26  
US-09-876-904A-119

;; Sequence 119, Application US/09876904A  
;; Publication No. US20030072794A1  
;; GENERAL INFORMATION:  
;; APPLICANT: BOULIKAS, TENI  
;; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC  
;; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE  
;; FILE REFERENCE: TB-2002.00  
;; CURRENT APPLICATION NUMBER: US/09/876,904A  
;; PRIOR FILING DATE: 2001-06-08  
;; PRIOR APPLICATION NUMBER: US 60/210,925  
;; PRIOR FILING DATE: 2000-06-09  
;; NUMBER OF SEQ ID NOS: 629  
;; SOFTWARE: PatentIn Ver. 2.1  
;; SEQ ID NO 119  
;; LENGTH: 9  
;; TYPE: PRT  
;; ORGANISM: Bos sp.  
;; FEATURE:  
;; OTHER INFORMATION: Karyophilic peptide

US-09-876-904A-119

Query Match 27.2%; Score 31; DB 3; Length 9;  
Best Local Similarity 62.5%; Pred. No. 1.7e+06;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 EYPSRLG 10  
Db 2 KHPGRRLG 9

RESULT 27  
US-09-876-904A-125

;; Sequence 125, Application US/09876904A  
;; Publication No. US20030072794A1  
;; GENERAL INFORMATION:  
;; APPLICANT: BOULIKAS, TENI  
;; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC  
;; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE  
;; FILE REFERENCE: TB-2002.00  
;; CURRENT APPLICATION NUMBER: US/09/876,904A  
;; PRIOR FILING DATE: 2001-06-08  
;; PRIOR APPLICATION NUMBER: US 60/210,925  
;; PRIOR FILING DATE: 2000-06-09  
;; NUMBER OF SEQ ID NOS: 629  
;; SOFTWARE: PatentIn Ver. 2.1  
;; SEQ ID NO 125  
;; LENGTH: 9  
;; TYPE: PRT  
;; ORGANISM: Oryctolagus cuniculus  
;; FEATURE:  
;; OTHER INFORMATION: Karyophilic peptide  
US-09-876-904A-125

Query Match 27.2%; Score 31; DB 3; Length 9;  
Best Local Similarity 62.5%; Pred. No. 1.7e+06;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 EYPSRLG 10  
Db 2 KHPGRRLG 9

RESULT 28  
US-09-876-904A-128

;; Sequence 128, Application US/09876904A  
;; Publication No. US20030072794A1  
;; GENERAL INFORMATION:  
;; APPLICANT: BOULIKAS, TENI  
;; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC  
;; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE  
;; FILE REFERENCE: TB-2002.00  
;; CURRENT APPLICATION NUMBER: US/09/876,904A  
;; PRIOR FILING DATE: 2001-06-08  
;; PRIOR APPLICATION NUMBER: US 60/210,925  
;; PRIOR FILING DATE: 2000-06-09  
;; NUMBER OF SEQ ID NOS: 629  
;; SOFTWARE: PatentIn Ver. 2.1  
;; SEQ ID NO 128  
;; LENGTH: 9  
;; TYPE: PRT  
;; ORGANISM: Rattus sp.  
;; FEATURE:  
;; OTHER INFORMATION: Karyophilic peptide  
US-09-876-904A-128

Query Match 27.2%; Score 31; DB 3; Length 9;  
Best Local Similarity 62.5%; Pred. No. 1.7e+06;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 EYPSRLG 10



Db 2 KHFGKRLG 9

RESULT 29  
US-10-926-542-122  
Sequence 122, Application US/10926542  
Publication No. US20050053989A1  
GENERAL INFORMATION:  
APPLICANT: LABAN, ABRAHAM  
APPLICANT: SHARON, GIL  
TITLE OF INVENTION: LIBRARIES OF RECOMBINANT PROTEINS  
FILE REFERENCE: 178.002  
CURRENT APPLICATION NUMBER: US/10/926,542  
CURRENT FILING DATE: 2004-08-26  
PRIOR APPLICATION NUMBER: US 60/497,924  
PRIOR FILING DATE: 2003-08-27  
NUMBER OF SEQ ID NOS: 127  
SOFTWARE: PatentIn Ver. 3.2  
SEQ ID NO 122  
LENGTH: 12  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Consensus  
US-10-926-542-122

Query Match 27.2%; Score 31; DB 5; Length 12;  
Best Local Similarity 50.0%; Pred. No. 1.2e+03;  
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 DVEYPSGR 8  
Db 5 DWEPSGSK 12

RESULT 30  
US-10-948-707-803  
Sequence 803, Application US/10948707  
Publication No. US20050187147A1  
GENERAL INFORMATION:  
APPLICANT: Ballatore, Carlo  
APPLICANT: Castellino, Angelo  
APPLICANT: Desharnais, Joel  
APPLICANT: Guo, Zijian  
APPLICANT: Li, Qing  
APPLICANT: Newman, Michael James  
APPLICANT: Sun, Chengzao  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INCREASING  
TITLE OF INVENTION: DRUG EFFICIENCY  
FILE REFERENCE: 17967-003001  
CURRENT APPLICATION NUMBER: US/10/948,707  
CURRENT FILING DATE: 2004-09-22  
PRIOR APPLICATION NUMBER: 60/505,325  
PRIOR FILING DATE: 2003-09-22  
PRIOR APPLICATION NUMBER: 60/568,340  
PRIOR FILING DATE: 2004-05-04  
PRIOR APPLICATION NUMBER: 60/581,835  
PRIOR FILING DATE: 2004-06-22  
NUMBER OF SEQ ID NOS: 1422  
SOFTWARE: PasteSeq for Windows Version 4.0  
SEQ ID NO 803  
LENGTH: 13  
TYPE: PRT  
ORGANISM: Homo Sapiens  
US-10-948-707-803

Query Match 27.2%; Score 31; DB 5; Length 13;  
Best Local Similarity 54.5%; Pred. No. 1.3e+03;  
Matches 6; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
QY 5 PGSRLGNPKAP 15

Db 2 PGSRSRTPSLP 12

RESULT 31  
US-09-880-748-2501  
Sequence 2501, Application US/09880748  
Publication No. US2003005937A1  
GENERAL INFORMATION:  
APPLICANT: Ruben et al.  
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys  
FILE REFERENCE: PF523  
CURRENT APPLICATION NUMBER: US/09/880,748  
CURRENT FILING DATE: 2001-06-15  
PRIOR APPLICATION NUMBER: 60/212,210  
PRIOR FILING DATE: 2000-06-15  
PRIOR APPLICATION NUMBER: 60/240,816  
PRIOR FILING DATE: 2000-10-17  
PRIOR APPLICATION NUMBER: 60/276,248  
PRIOR FILING DATE: 2001-03-16  
PRIOR APPLICATION NUMBER: 60/277,379  
PRIOR FILING DATE: 2001-03-21  
PRIOR APPLICATION NUMBER: 60/293,499  
PRIOR FILING DATE: 2001-05-25  
NUMBER OF SEQ ID NOS: 3239  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 2501  
LENGTH: 14  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-880-748-2501

Query Match 27.2%; Score 31; DB 3; Length 14;  
Best Local Similarity 83.3%; Pred. No. 1.4e+03;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 12 PKAELY 17  
Db 8 PKAPLY 13

RESULT 32  
US-10-293-418-2501  
Sequence 2501, Application US/10293418  
Publication No. US20030223996A1  
GENERAL INFORMATION:  
APPLICANT: Ruben et al.  
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys  
FILE REFERENCE: PF523P2  
CURRENT APPLICATION NUMBER: US/10/293,418  
CURRENT FILING DATE: 2002-11-27  
PRIOR APPLICATION NUMBER: 60/331,469  
PRIOR FILING DATE: 2001-11-16  
PRIOR APPLICATION NUMBER: 60/340,817  
PRIOR FILING DATE: 2001-12-19  
PRIOR APPLICATION NUMBER: 09/880,748  
PRIOR FILING DATE: 2001-06-15  
PRIOR APPLICATION NUMBER: 60/293,499  
PRIOR FILING DATE: 2001-05-25  
PRIOR APPLICATION NUMBER: 60/277,379  
PRIOR FILING DATE: 2001-03-21  
PRIOR APPLICATION NUMBER: 60/276,248  
PRIOR FILING DATE: 2001-03-16  
PRIOR APPLICATION NUMBER: 60/240,816  
PRIOR FILING DATE: 2000-10-17  
PRIOR APPLICATION NUMBER: 60/212,210  
PRIOR FILING DATE: 2000-06-16  
NUMBER OF SEQ ID NOS: 3247  
SEQ ID NO 2501  
LENGTH: 14  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-293-418-2501

Query Match 27.2%; Score 31; DB 4; Length 14;  
 Best Local Similarity 83.3%; Pred. No. 1.4e+03;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 12 PRAPLY 17  
 |::|::|  
 Db 8 PRAPLY 13

RESULT 33

US-10-224-999A-1528  
 ; Sequence 1528, Application US/10224999A  
 ; Publication No. US20030171318A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Myriad Genetics, Inc.  
 ; APPLICANT: Morham, Scott  
 ; APPLICANT: Zavitz, Kenton  
 ; APPLICANT: Hobden, Adrian  
 ; TITLE OF INVENTION: Composition and Method for Treating Viral Infection  
 ; FILE REFERENCE: 5004.01  
 ; CURRENT APPLICATION NUMBER: US/10/224,999A  
 ; PRIOR FILING DATE: 2003-03-03  
 ; PRIOR APPLICATION NUMBER: US 60/313,695  
 ; NUMBER OF SEQ ID NOS: 3484  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 1528  
 ; LENGTH: 15  
 ; TYPE: PRT  
 ; ORGANISM: Human papillomavirus  
 US-10-224-999A-1528

Query Match 27.2%; Score 31; DB 4; Length 15;  
 Best Local Similarity 33.3%; Pred. No. 1.5e+03;  
 Matches 5; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 1 DYEYPSRLGNPKAP 15  
 |::|::|  
 Db 1 DITPPRAHPMGTPSP 15

RESULT 34

US-10-203-915A-58  
 ; Sequence 58, Application US/10203915A  
 ; Publication No. US20040106159A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Kern, Florian  
 ; TITLE OF INVENTION: Method for Antigen-Specific Stimulation of T  
 ; TITLE OF INVENTION: Lymphocytes with synthetic Peptide Libraries  
 ; FILE REFERENCE: 010266wo/JH/ml  
 ; CURRENT APPLICATION NUMBER: US/10/203,915A  
 ; PRIOR FILING DATE: 2002-08-15  
 ; NUMBER OF SEQ ID NOS: 260  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 58  
 ; LENGTH: 15  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: HCV IB-1  
 US-10-203-915A-58

Query Match 27.2%; Score 31; DB 4; Length 15;  
 Best Local Similarity 35.7%; Pred. No. 1.5e+03;  
 Matches 5; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 5 PPSRLGNPKAPLYK 18  
 |::|::|  
 Db 2 PSSKVPNPETPVTK 15

RESULT 35

US-10-886-773-147  
 ; Sequence 147, Application US/10886773  
 ; Publication No. US20050054107A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Chulay, Jeffrey D.  
 ; APPLICANT: Dryga, Sergey A.  
 ; APPLICANT: Read, Elizabeth A.  
 ; APPLICANT: Morris, John S.  
 ; APPLICANT: Olmsted, Robert A.  
 ; TITLE OF INVENTION: ALPHAVIRUS-BASED CYTOMEGALOVIRUS VACCINES  
 ; FILE REFERENCE: 9368-7  
 ; CURRENT APPLICATION NUMBER: US/10/886,773  
 ; PRIOR FILING DATE: 2004-07-08  
 ; PRIOR APPLICATION NUMBER: US 60/486,501  
 ; PRIOR FILING DATE: 2003-07-11  
 ; NUMBER OF SEQ ID NOS: 262  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 147  
 ; LENGTH: 15  
 ; TYPE: PRT  
 ; ORGANISM: Human cytomegalovirus  
 US-10-886-773-147

Query Match 27.2%; Score 31; DB 5; Length 15;  
 Best Local Similarity 35.7%; Pred. No. 1.5e+03;  
 Matches 5; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 5 PPSRLGNPKAPLYK 18  
 |::|::|  
 Db 2 PSSKVPNPETPVTK 15

RESULT 36

US-10-862-195-182  
 ; Sequence 182, Application US/10862195  
 ; Publication No. US20050164324A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: GYGI, STEVEN P.  
 ; TITLE OF INVENTION: SYSTEMS, METHODS AND KITS FOR CHARACTERIZING PHOSPHOPROTEOMES  
 ; FILE REFERENCE: 58890(70207)  
 ; CURRENT APPLICATION NUMBER: US/10/862,195  
 ; PRIOR FILING DATE: 2004-06-04  
 ; PRIOR APPLICATION NUMBER: 60/476,010  
 ; PRIOR FILING DATE: 2003-06-04  
 ; NUMBER OF SEQ ID NOS: 2245  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 182  
 ; LENGTH: 15  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; OTHER INFORMATION: See specification as filed for preferred embodiments  
 ; OTHER INFORMATION: and description of phosphorylation sites  
 US-10-862-195-182

Query Match 27.2%; Score 31; DB 5; Length 15;  
 Best Local Similarity 45.5%; Pred. No. 1.5e+03;  
 Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 5 PPSRLGNPKAP 15  
 |::|::|  
 Db 3 PPSQVPNPBSP 13

RESULT 37

US-10-224-999A-1540  
 ; Sequence 1540, Application US/10224999A  
 ; Publication No. US20030171318A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Myriad Genetics, Inc.  
 ; APPLICANT: Morham, Scott  
 ; APPLICANT: Zavitz, Kenton

APPLICANT: Hobden, Adrian  
TITLE OF INVENTION: Composition and Method for Treating Viral Infection  
FILE REFERENCE: 5004.01  
CURRENT APPLICATION NUMBER: US/10/224,999A  
CURRENT FILING DATE: 2003-03-03  
PRIOR APPLICATION NUMBER: US 60/313,695  
PRIOR FILING DATE: 2001-08-20  
NUMBER OF SEQ ID NOS: 3484  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 1540  
LENGTH: 16  
TYPE: PRT  
ORGANISM: Human papillomavirus  
US-10-224-999A-1540

Query Match 27.2%; Score 31; DB 4; Length 16;  
Best Local Similarity 33.3%; Pred. No. 1.6e+03;  
Matches 5; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 1 DYBYPGSRIGNPKAP 15  
Db 2 DTFPTAPWGTFFSP 16

RESULT 38  
US-10-161-791-189  
Sequence 189, Application US/10161791  
Publication No. US2003018685A1  
GENERAL INFORMATION:  
APPLICANT: SPARKS, Andrew B.  
APPLICANT: KAY, Brian K.  
APPLICANT: THORN, Judith M.  
APPLICANT: QUILIAM, Lawrence A.  
APPLICANT: DER, Channing J.  
APPLICANT: FOWLKES, Dana M.  
APPLICANT: RIDER, James E.  
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
TITLE OF INVENTION: ISOLATING AND USING SAME  
NUMBER OF SEQUENCES: 467  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/161,791  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/602,999  
FILING DATE: 16-FEB-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Mierock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 1101-202  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIR  
INFORMATION FOR SEQ ID NO: 189:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-10-161-791-189

Query Match 27.2%; Score 31; DB 4; Length 16;  
Best Local Similarity 60.0%; Pred. No. 1.6e+03;  
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 9 LGNPKAPLYK 18  
Db 4 LGRPEIFLKR 13

RESULT 39  
US-10-211-088-244  
Sequence 244, Application US/10211088  
Publication No. US20030104479A1  
GENERAL INFORMATION:  
APPLICANT: Bright, Gary R.  
APPLICANT: Premkumar, D. David  
APPLICANT: Chen, Yih-Tai  
TITLE OF INVENTION: No. US20030104479A1 Fusion Proteins And Assays For Molecular B  
FILE REFERENCE: 01-1022-US  
CURRENT APPLICATION NUMBER: US/10/211,088  
CURRENT FILING DATE: 2002-10-15  
PRIOR APPLICATION NUMBER: 60/309,395  
PRIOR FILING DATE: 2001-08-01  
PRIOR APPLICATION NUMBER: 60/341,589  
PRIOR FILING DATE: 2001-12-13  
NUMBER OF SEQ ID NOS: 366  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 244  
LENGTH: 17  
TYPE: PRT  
ORGANISM: Artificial sequence  
FEATURE:  
OTHER INFORMATION: Nuclear localization signal  
US-10-211-088-244

Query Match 27.2%; Score 31; DB 4; Length 17;  
Best Local Similarity 66.7%; Pred. No. 1.7e+03;  
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 10 GNPKAPLYK 18  
Db 7 GNPKPLK 15

RESULT 40  
US-10-224-999A-1553  
Sequence 1553, Application US/10224999A  
Publication No. US20030171318A1  
GENERAL INFORMATION:  
APPLICANT: Myriad Genetics, Inc.  
APPLICANT: Morham, Scott  
APPLICANT: Zavitz, Kenton  
APPLICANT: Hobden, Adrian  
TITLE OF INVENTION: Composition and Method for Treating Viral Infection  
FILE REFERENCE: 5004.01  
CURRENT APPLICATION NUMBER: US/10/224,999A  
CURRENT FILING DATE: 2003-03-03  
PRIOR APPLICATION NUMBER: US 60/313,695  
PRIOR FILING DATE: 2001-08-20  
NUMBER OF SEQ ID NOS: 3484  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 1553  
LENGTH: 17  
TYPE: PRT  
ORGANISM: Human papillomavirus  
US-10-224-999A-1553

Query Match 27.2%; Score 31; DB 4; Length 17;  
Best Local Similarity 33.3%; Pred. No. 1.7e+03;  
Matches 5; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 1 DYBYPGSRIGNPKAP 15

Db 3 DIFPPTAPWGTPEFSP 17

## RESULT 41

US-10-350-405-155  
; Sequence 155, Application US/10350405  
; Publication No. US20030215894A1  
; GENERAL INFORMATION:  
; APPLICANT: Niman, Henry L.  
; TITLE OF INVENTION: Polypeptide-Induced Monoclonal Receptors  
; FILE REFERENCE: TSRI 35.5 CON 7/LIG  
; CURRENT APPLICATION NUMBER: US/10/350,405  
; PRIOR FILING DATE: 2003-01-24  
; PRIOR APPLICATION NUMBER: 09/427,576  
; PRIOR FILING DATE: 1999-10-26  
; PRIOR APPLICATION NUMBER: 08/461,583  
; PRIOR FILING DATE: 1995-06-02  
; PRIOR APPLICATION NUMBER: 08/294,879  
; PRIOR FILING DATE: 1994-08-23  
; PRIOR APPLICATION NUMBER: 08/054,864  
; PRIOR FILING DATE: 1993-04-28  
; PRIOR APPLICATION NUMBER: 07/900,502  
; PRIOR FILING DATE: 1992-06-16  
; PRIOR APPLICATION NUMBER: 07/780,415  
; PRIOR FILING DATE: 1991-10-22  
; NUMBER OF SEQ ID NOS: 227  
; SOFTWARE: FaastSeq for Windows Version 4.0  
; SEQ ID NO 155  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: retrovirus  
US-10-350-405-155

Query Match 27.2%; Score 31; DB 4; Length 17;  
Best Local Similarity 62.5%; Pred. No. 1.7e+03;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 EYPSRLG 10  
Db 4 KHPGRRLG 11

## RESULT 42

US-10-350-405-158  
; Sequence 158, Application US/10350405  
; Publication No. US20030215894A1  
; GENERAL INFORMATION:  
; APPLICANT: Niman, Henry L.  
; TITLE OF INVENTION: Polypeptide-Induced Monoclonal Receptors  
; FILE REFERENCE: TSRI 35.5 CON 7/LIG  
; CURRENT APPLICATION NUMBER: US/10/350,405  
; PRIOR FILING DATE: 2003-01-24  
; PRIOR APPLICATION NUMBER: 09/427,576  
; PRIOR FILING DATE: 1999-10-26  
; PRIOR APPLICATION NUMBER: 08/461,583  
; PRIOR FILING DATE: 1995-06-02  
; PRIOR APPLICATION NUMBER: 08/294,879  
; PRIOR FILING DATE: 1994-08-23  
; PRIOR APPLICATION NUMBER: 08/054,864  
; PRIOR FILING DATE: 1993-04-28  
; PRIOR APPLICATION NUMBER: 07/900,502  
; PRIOR FILING DATE: 1992-06-16  
; PRIOR APPLICATION NUMBER: 07/780,415  
; PRIOR FILING DATE: 1991-10-22  
; NUMBER OF SEQ ID NOS: 227  
; SOFTWARE: FaastSeq for Windows Version 4.0  
; SEQ ID NO 158  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: retrovirus

US-10-350-405-158

Query Match 27.2%; Score 31; DB 4; Length 17;  
Best Local Similarity 62.5%; Pred. No. 1.7e+03;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 EYPSRLG 10  
Db 4 KHPGRRLG 11

## RESULT 43

US-10-482-029-373  
; Sequence 373, Application US/10482029  
; Publication No. US20050037445A1  
; GENERAL INFORMATION:  
; APPLICANT: ODIN medical A/S  
; TITLE OF INVENTION: Oncology drug innovation  
; FILE REFERENCE: P 573 PC00  
; CURRENT APPLICATION NUMBER: US/10/482,029  
; CURRENT FILING DATE: 2003-12-29  
; NUMBER OF SEQ ID NOS: 437  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 373  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-482-029-373

Query Match 27.2%; Score 31; DB 5; Length 17;  
Best Local Similarity 66.7%; Pred. No. 1.7e+03;  
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 10 GNPXPPLK 18  
Db 7 GNPXPPLK 15

## RESULT 44

US-10-225-567A-2233  
; Sequence 2233, Application US/10225567A  
; Publication No. US20030113798A1  
; GENERAL INFORMATION:  
; APPLICANT: Lifespan Biosciences  
; APPLICANT: Brown, Joseph P.  
; APPLICANT: Burner, Glenna C.  
; APPLICANT: Roush, Christine L.  
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS  
; FILE REFERENCE: 1920-4-4  
; CURRENT APPLICATION NUMBER: US/10/225,567A  
; CURRENT FILING DATE: 2001-12-19  
; PRIOR APPLICATION NUMBER: 60/257,144  
; PRIOR FILING DATE: 2000-12-19  
; NUMBER OF SEQ ID NOS: 2292  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2233  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-225-567A-2233

Query Match 27.2%; Score 31; DB 4; Length 18;  
Best Local Similarity 71.4%; Pred. No. 1.8e+03;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYQYPS 7  
Db 3 DYQYPS 9

## RESULT 45

US-10-224-999A-1567  
; Sequence 1567, Application US/10224999A

```
/ Publication No. US20030171318A1
/ GENERAL INFORMATION:
/ APPLICANT: Myriad Genetics, Inc.
/ APPLICANT: Morham, Scott
/ APPLICANT: Zavitz, Kenton
/ APPLICANT: Hobden, Adrian
/ TITLE OF INVENTION: Composition and Method for Treating Viral Infection
/ FILE REFERENCE: 5004.01
/ CURRENT APPLICATION NUMBER: US/10/224,999A
/ CURRENT FILING DATE: 2003-03-03
/ PRIOR APPLICATION NUMBER: US 60/313,695
/ PRIOR FILING DATE: 2001-08-20
/ NUMBER OF SEQ ID NOS: 3484
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 1567
/ LENGTH: 18
/ TYPE: PRT
/ ORGANISM: Human papillomavirus
US-10-224-999A-1567
```

```
Query Match          27.2% Score 31; DB 4; Length 18;
Best Local Similarity 33.3%; Pred. No. 1.8e+03;
Matches 5; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
```

```
Qy 1 DYEYPSRLGNPKAP 15
| : : : : : : : :
Db 4 DITFPTAPWGTTPSP 18
```

```
RESULT 46
US-10-350-405-200
/ Sequence 200, Application US/10350405
/ Publication No. US20030215894A1
/ GENERAL INFORMATION:
/ APPLICANT: Niman, Henry L.
/ TITLE OF INVENTION: Polypeptide-Induced Monoclonal Receptors
/ FILE REFERENCE: TSRI 35.5 CON 7/LIG
/ CURRENT APPLICATION NUMBER: US/10/350,405
/ CURRENT FILING DATE: 2003-01-24
/ PRIOR APPLICATION NUMBER: 09/427,576
/ PRIOR FILING DATE: 1999-10-26
/ PRIOR APPLICATION NUMBER: 08/461,583
/ PRIOR FILING DATE: 1995-06-02
/ PRIOR APPLICATION NUMBER: 08/294,879
/ PRIOR FILING DATE: 1994-08-23
/ PRIOR APPLICATION NUMBER: 08/054,864
/ PRIOR FILING DATE: 1993-04-28
/ PRIOR APPLICATION NUMBER: 07/900,502
/ PRIOR FILING DATE: 1992-06-16
/ PRIOR APPLICATION NUMBER: 07/780,415
/ NUMBER OF SEQ ID NOS: 227
/ SOFTWARE: FaastSeq for Windows Version 4.0
/ SEQ ID NO 200
/ LENGTH: 18
/ TYPE: PRT
/ ORGANISM: retrovirus
US-10-350-405-200
```

```
Query Match          27.2% Score 31; DB 4; Length 18;
Best Local Similarity 44.4%; Pred. No. 1.8e+03;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy 12 PKAPLYKRP 20
| : : : : : : : :
Db 3 PQVPAFRRP 11
```

```
RESULT 47
US-10-224-999A-1582
/ Sequence 1582, Application US/10224999A
/ Publication No. US20030171318A1
```

```
/ GENERAL INFORMATION:
/ APPLICANT: Myriad Genetics, Inc.
/ APPLICANT: Morham, Scott
/ APPLICANT: Zavitz, Kenton
/ APPLICANT: Hobden, Adrian
/ TITLE OF INVENTION: Composition and Method for Treating Viral Infection
/ FILE REFERENCE: 5004.01
/ CURRENT APPLICATION NUMBER: US/10/224,999A
/ CURRENT FILING DATE: 2003-03-03
/ PRIOR APPLICATION NUMBER: US 60/313,695
/ PRIOR FILING DATE: 2001-08-20
/ NUMBER OF SEQ ID NOS: 3484
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 1582
/ LENGTH: 19
/ TYPE: PRT
/ ORGANISM: Human papillomavirus
US-10-224-999A-1582
```

```
Query Match          27.2% Score 31; DB 4; Length 19;
Best Local Similarity 33.3%; Pred. No. 1.9e+03;
Matches 5; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
```

```
Qy 1 DYEYPSRLGNPKAP 15
| : : : : : : : :
Db 5 DITFPTAPWGTTPSP 19
```

```
RESULT 48
US-10-862-195-1528
/ Sequence 1528, Application US/10862195
/ Publication No. US20050164324A1
/ GENERAL INFORMATION:
/ APPLICANT: GYGI, STEVEN P.
/ TITLE OF INVENTION: SYSTEMS, METHODS AND KITS FOR CHARACTERIZING PHOSPHOPROTEOMES
/ FILE REFERENCE: 58890(70207)
/ CURRENT APPLICATION NUMBER: US/10/862,195
/ CURRENT FILING DATE: 2004-06-04
/ PRIOR APPLICATION NUMBER: 60/476,010
/ PRIOR FILING DATE: 2003-06-04
/ NUMBER OF SEQ ID NOS: 2245
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 1528
/ LENGTH: 19
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ OTHER INFORMATION: See specification as filed for preferred embodiments
/ OTHER INFORMATION: and description of phosphorylation sites
US-10-862-195-1528
```

```
Query Match          27.2% Score 31; DB 5; Length 19;
Best Local Similarity 50.0%; Pred. No. 1.9e+03;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
```

```
Qy 11 NPKAPLYKRP 20
| : : : : : : : :
Db 1 NPQMPQYSSP 10
```

```
RESULT 49
US-10-224-999A-1598
/ Sequence 1598, Application US/10224999A
/ Publication No. US20030171318A1
/ GENERAL INFORMATION:
/ APPLICANT: Myriad Genetics, Inc.
/ APPLICANT: Morham, Scott
/ APPLICANT: Zavitz, Kenton
/ APPLICANT: Hobden, Adrian
/ TITLE OF INVENTION: Composition and Method for Treating Viral Infection
/ FILE REFERENCE: 5004.01
/ CURRENT APPLICATION NUMBER: US/10/224,999A
/ CURRENT FILING DATE: 2003-03-03
```

;; PRIOR APPLICATION NUMBER: US 60/313,695  
;; PRIOR FILING DATE: 2001-08-20  
;; NUMBER OF SEQ ID NOS: 3484  
;; SOFTWARE: PatentIn version 3.1  
;; SEQ ID NO 1598  
;; LENGTH: 20  
;; TYPE: PRT  
;; ORGANISM: Human papillomavirus  
US-10-224-999A-1598

Query Match 27.2%; Score 31; DB 4; Length 20;  
Best Local Similarity 33.3%; Pred. No. 2e+03;  
Matches 5; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 1 DYEPGSRGNPKAP 15  
| : : : : :  
Db 6 DTFPPAPWGPSP 20

RESULT 50  
US-10-481-261-459  
;; Sequence 459, Application US/10481261  
;; Publication No. US20040265792A1  
;; GENERAL INFORMATION:  
;; APPLICANT: GLENN, Jeffrey S.  
;; APPLICANT: GLASS, John I.  
;; APPLICANT: MYERS, Tina M.  
;; TITLE OF INVENTION: AGENTS FOR TREATMENT OF HCV AND METHODS OF USE  
;; FILE REFERENCE: STAN-344  
;; CURRENT APPLICATION NUMBER: US/10/481,261  
;; CURRENT FILING DATE: 2003-12-17  
;; PRIOR APPLICATION NUMBER: PCT/US 02/13951  
;; PRIOR FILING DATE: 2002-05-03  
;; PRIOR APPLICATION NUMBER: US 60/288,687  
;; PRIOR FILING DATE: 2001-05-03  
;; PRIOR APPLICATION NUMBER: US 60/316,805  
;; PRIOR FILING DATE: 2001-08-31  
;; NUMBER OF SEQ ID NOS: 470  
;; SOFTWARE: PatentIn version 3.1  
;; SEQ ID NO 459  
;; LENGTH: 13  
;; TYPE: PRT  
;; ORGANISM: Hepatitis C virus  
US-10-481-261-459

Query Match 26.8%; Score 30.5; DB 5; Length 13;  
Best Local Similarity 64.3%; Pred. No. 1.5e+03;  
Matches 9; Conservative 1; Mismatches 1; Indels 3; Gaps 2;

Qy 4 YPGSRGN--PKAP 15  
| : : : : :  
Db 1 YP-SKPGNTPKAP 13

RESULT 51  
US-09-572-404B-3190  
;; Sequence 3190, Application US/09572404B  
;; Publication No. US20030078374A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Proteom Ltd  
;; TITLE OF INVENTION: Complementary peptide ligands from the human genome  
;; FILE REFERENCE: Human Patent  
;; CURRENT APPLICATION NUMBER: US/09/572,404B  
;; CURRENT FILING DATE: 2000-05-17  
;; NUMBER OF SEQ ID NOS: 4203  
;; SOFTWARE: Protolent version 1.0  
;; SEQ ID NO 3190  
;; LENGTH: 10  
;; TYPE: PRT  
;; ORGANISM: Homo Sapiens  
;; FEATURE:  
;; OTHER INFORMATION: Sequence located in K1AA0411 at 417-426 and may interact with Seq  
;; OTHER INFORMATION: 3189 in this patent.

US-09-572-404B-3190

Query Match 26.3%; Score 30; DB 3; Length 10;  
Best Local Similarity 62.5%; Pred. No. 1.4e+03;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 5 PGSRGNP 12  
| : : : : :  
Db 3 PGALGSP 10

RESULT 52  
US-09-954-385-315  
;; Sequence 315, Application US/09954385  
;; Publication No. US20030100467A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Aehle, Wolfgang  
;; APPLICANT: Baldwin, Toby L.  
;; APPLICANT: Van Gastel, Franciscus J.C.  
;; APPLICANT: Janssen, Giselle G.  
;; APPLICANT: Murray, Christopher J.  
;; APPLICANT: Wang, Huaming  
;; APPLICANT: Winetzkry, Deborah S.  
;; TITLE OF INVENTION: Binding Phenol Oxidizing Enzyme-peptide  
;; FILE REFERENCE: GC690  
;; CURRENT APPLICATION NUMBER: US/09/954,385  
;; CURRENT FILING DATE: 2001-09-12  
;; NUMBER OF SEQ ID NOS: 433  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 315  
;; LENGTH: 12  
;; TYPE: PRT  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: binding peptide  
US-09-954-385-315

Query Match 26.3%; Score 30; DB 3; Length 12;  
Best Local Similarity 54.5%; Pred. No. 1.6e+03;  
Matches 6; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 5 PGSRGNPKAP 15  
| : : : : :  
Db 2 PHSMLQNPSP 12

RESULT 53  
US-10-912-512-315  
;; Sequence 315, Application US/10912512  
;; Publication No. US20050042684A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Aehle, Wolfgang  
;; APPLICANT: Baldwin, Toby L.  
;; APPLICANT: Van Gastel, Franciscus J.C.  
;; APPLICANT: Janssen, Giselle G.  
;; APPLICANT: Murray, Christopher J.  
;; APPLICANT: Wang, Huaming  
;; APPLICANT: Winetzkry, Deborah S.  
;; TITLE OF INVENTION: Binding Phenol Oxidizing Enzyme-peptide  
;; FILE REFERENCE: GC690  
;; CURRENT APPLICATION NUMBER: US/10/912,512  
;; CURRENT FILING DATE: 2004-08-05  
;; PRIOR APPLICATION NUMBER: US/09/954,385  
;; PRIOR FILING DATE: 2001-09-12  
;; NUMBER OF SEQ ID NOS: 433  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 315  
;; LENGTH: 12  
;; TYPE: PRT  
;; ORGANISM: Artificial Sequence  
;; FEATURE:

OTHER INFORMATION: binding peptide  
US-10-912-512-315

Query Match 26.3%; Score 30; DB 5; Length 12;  
Best Local Similarity 54.5%; Pred. No. 1.6e+03;  
Matches 6; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5 PGSRLGNPKAP 15  
DB 2 PHSMLQNPSCP 12

RESULT 54  
US-10-235-043-315  
Sequence 315, Application US/10235043  
Publication No. US20050058996A1  
GENERAL INFORMATION:  
APPLICANT: Aehle, Wolfgang  
APPLICANT: Baldwin, Toby M.  
APPLICANT: Van Gastel, Franciscus J.C.  
APPLICANT: Janssen, Christoffer J.  
APPLICANT: Murray, Christopher J.  
APPLICANT: Wang, Huaming  
APPLICANT: Wietzky, Deborah S.  
TITLE OF INVENTION: Binding Phenol Oxidizing Enzyme-Peptide  
FILE REFERENCE: GC690-2  
CURRENT APPLICATION NUMBER: US/10/235,043  
CURRENT FILING DATE: 2002-09-03  
NUMBER OF SEQ ID NOS: 446  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 315  
LENGTH: 12  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: binding peptide  
US-10-235-043-315

Query Match 26.3%; Score 30; DB 5; Length 12;  
Best Local Similarity 54.5%; Pred. No. 1.6e+03;  
Matches 6; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5 PGSRLGNPKAP 15  
DB 2 PHSMLQNPSCP 12

RESULT 55  
US-09-880-748-2378  
Sequence 2378, Application US/09880748  
Publication No. US2003005937A1  
GENERAL INFORMATION:  
APPLICANT: Ruben et al.  
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys  
FILE REFERENCE: P5523  
CURRENT APPLICATION NUMBER: US/09/880,748  
CURRENT FILING DATE: 2001-06-15  
PRIOR APPLICATION NUMBER: 60/212,210  
PRIOR FILING DATE: 2000-06-15  
PRIOR APPLICATION NUMBER: 60/240,816  
PRIOR FILING DATE: 2000-10-17  
PRIOR APPLICATION NUMBER: 60/276,248  
PRIOR FILING DATE: 2001-03-16  
PRIOR APPLICATION NUMBER: 60/277,379  
PRIOR FILING DATE: 2001-03-21  
PRIOR APPLICATION NUMBER: 60/293,499  
PRIOR FILING DATE: 2001-05-25  
NUMBER OF SEQ ID NOS: 3239  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 2378  
LENGTH: 14  
TYPE: PRT

ORGANISM: Homo sapiens  
US-09-880-748-2378

Query Match 26.3%; Score 30; DB 3; Length 14;  
Best Local Similarity 83.3%; Pred. No. 1.9e+03;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 12 PKAPLY 17  
DB 8 PQAPLY 13

RESULT 56  
US-10-293-418-2378  
Sequence 2378, Application US/10293418  
Publication No. US20030223996A1  
GENERAL INFORMATION:  
APPLICANT: Ruben et al.  
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys  
FILE REFERENCE: P5523P2  
CURRENT APPLICATION NUMBER: US/10/293,418  
CURRENT FILING DATE: 2002-11-27  
PRIOR APPLICATION NUMBER: 60/331,469  
PRIOR FILING DATE: 2001-11-16  
PRIOR APPLICATION NUMBER: 60/340,817  
PRIOR FILING DATE: 2001-12-19  
PRIOR APPLICATION NUMBER: 09/880,748  
PRIOR FILING DATE: 2001-06-15  
PRIOR APPLICATION NUMBER: 60/293,499  
PRIOR FILING DATE: 2001-05-25  
PRIOR APPLICATION NUMBER: 60/277,379  
PRIOR FILING DATE: 2001-03-21  
PRIOR APPLICATION NUMBER: 60/276,248  
PRIOR FILING DATE: 2001-03-16  
PRIOR APPLICATION NUMBER: 60/240,816  
PRIOR FILING DATE: 2000-10-17  
PRIOR APPLICATION NUMBER: 60/212,210  
PRIOR FILING DATE: 2000-06-16  
NUMBER OF SEQ ID NOS: 3247  
SEQ ID NO 2378  
LENGTH: 14  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-293-418-2378

Query Match 26.3%; Score 30; DB 4; Length 14;  
Best Local Similarity 83.3%; Pred. No. 1.9e+03;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 12 PKAPLY 17  
DB 8 PQAPLY 13

RESULT 57  
US-09-829-549A-44  
Sequence 44, Application US/09829549A  
Patent No. US20020052484A1  
GENERAL INFORMATION:  
APPLICANT: The Curators of the University of Missouri  
TITLE OF INVENTION: PHAGE DISPLAY SELECTION OF ANTI FUNGAL PEPTIDES  
FILE REFERENCE: UMO 1521.1  
CURRENT APPLICATION NUMBER: US/09/829,549A  
CURRENT FILING DATE: 2001-04-10  
PRIOR APPLICATION NUMBER: US 60/195,785  
PRIOR FILING DATE: 2000-04-10  
NUMBER OF SEQ ID NOS: 48  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 44  
LENGTH: 15  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:

```
/ NAME/KEY: DOMAIN
/ LOCATION: (1)...(15)
/ OTHER INFORMATION: Random peptide insert
US-09-829-549A-44
```

```
Query Match          26.3%; Score 30; DB 3; Length 15;
Best Local Similarity 83.3%; Pred. No. 2.1e+03;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      15 PLYKRP 20
      |||||
Db       2 PLYKRP 7
```

```
RESULT 58
US-09-992-665-45
/ Sequence 45, Application US/09992665
/ Publication No. US20030092009A1
/ GENERAL INFORMATION:
/ APPLICANT: Kala Palm
/ TITLE OF INVENTION: PROFILING TUMOR SPECIFIC MARKERS FOR THE
/ FILE REFERENCE: CEMINES.002A
/ CURRENT FILING DATE: 2001-11-13
/ PRIOR APPLICATION NUMBER: 60/249,508
/ PRIOR FILING DATE: 2000-11-16
/ NUMBER OF SEQ ID NOS: 380
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 45
/ LENGTH: 15
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Probe
US-09-992-665-45
```

```
Query Match          26.3%; Score 30; DB 3; Length 15;
Best Local Similarity 50.0%; Pred. No. 2.1e+03;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      10 GNPAPLYKR 19
      |||||
Db       5 GSPAPAHSR 14
```

```
RESULT 59
US-10-862-195-1857
/ Sequence 1857, Application US/10862195
/ Publication No. US20050164324A1
/ GENERAL INFORMATION:
/ APPLICANT: GYGI, STEVEN P.
/ TITLE OF INVENTION: SYSTEMS, METHODS AND KITS FOR CHARACTERIZING PHOSPHOPROTEOMES
/ FILE REFERENCE: 58890(70207)
/ CURRENT APPLICATION NUMBER: US/10/862,195
/ CURRENT FILING DATE: 2004-06-04
/ PRIOR APPLICATION NUMBER: 60/476,010
/ PRIOR FILING DATE: 2003-06-04
/ NUMBER OF SEQ ID NOS: 2245
/ SOFTWARE: Patentin version 3.2
/ SEQ ID NO 1857
/ LENGTH: 15
/ TYPE: PRT
/ ORGANISM: Saccharomyces cerevisiae
US-10-862-195-1857
```

```
Query Match          26.3%; Score 30; DB 5; Length 15;
Best Local Similarity 57.1%; Pred. No. 2.1e+03;
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
```

```
QY      6 GSRLLGNPKAPLYKR 19
      |||||
Db       2 GSOLKNLKAALYKR 15
```

```
RESULT 60
US-09-974-879-522
```

```
/ Sequence 522, Application US/09974879
/ Publication No. US20030028003A1
/ GENERAL INFORMATION:
/ APPLICANT: Rosen et al.
/ TITLE OF INVENTION: 125 Human Secreted Proteins
/ FILE REFERENCE: P2020P2
/ CURRENT APPLICATION NUMBER: US/09/974,879
/ CURRENT FILING DATE: 2001-10-12
/ PRIOR APPLICATION NUMBER: US 60/239,893
/ PRIOR FILING DATE: 2000-10-13
/ PRIOR APPLICATION NUMBER: US 09/818,683
/ PRIOR FILING DATE: 2001-03-28
/ PRIOR APPLICATION NUMBER: US 09/305,736
/ PRIOR FILING DATE: 1999-05-05
/ PRIOR APPLICATION NUMBER: PCT/US98/23435
/ PRIOR FILING DATE: 1998-11-04
/ PRIOR APPLICATION NUMBER: US 60/064,911
/ PRIOR FILING DATE: 1997-11-07
/ PRIOR APPLICATION NUMBER: US 60/064,912
/ PRIOR FILING DATE: 1997-11-07
/ PRIOR APPLICATION NUMBER: US 60/064,983
/ PRIOR FILING DATE: 1997-11-07
/ PRIOR APPLICATION NUMBER: US 60/064,900
/ PRIOR FILING DATE: 1997-11-07
/ PRIOR APPLICATION NUMBER: US 60/064,988
/ PRIOR FILING DATE: 1997-11-07
/ PRIOR APPLICATION NUMBER: US 60/064,987
/ PRIOR FILING DATE: 1997-11-07
/ PRIOR APPLICATION NUMBER: US 60/064,908
/ PRIOR FILING DATE: 1997-11-07
/ PRIOR APPLICATION NUMBER: US 60/064,984
/ PRIOR FILING DATE: 1997-11-07
/ PRIOR APPLICATION NUMBER: US 60/064,985
/ PRIOR FILING DATE: 1997-11-07
/ PRIOR APPLICATION NUMBER: US 60/066,094
/ PRIOR FILING DATE: 1997-11-17
/ PRIOR APPLICATION NUMBER: US 60/066,100
/ PRIOR FILING DATE: 1997-11-17
/ PRIOR APPLICATION NUMBER: US 60/066,089
/ PRIOR FILING DATE: 1997-11-17
/ PRIOR APPLICATION NUMBER: US 60/066,095
/ PRIOR FILING DATE: 1997-11-17
/ PRIOR APPLICATION NUMBER: US 60/066,090
/ PRIOR FILING DATE: 1997-11-17
/ NUMBER OF SEQ ID NOS: 611
/ SOFTWARE: Patentin Ver. 2.0
/ SEQ ID NO 522
/ LENGTH: 16
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-974-879-522
```

```
Query Match          26.3%; Score 30; DB 3; Length 16;
Best Local Similarity 46.2%; Pred. No. 2.2e+03;
Matches 6; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
```

```
QY      8 RLGNPKAPLYKRP 20
      |||||
Db       2 RFLNPKRLFSVP 14
```

```
RESULT 61
US-09-305-736-524
/ Sequence 524, Application US/09305736
/ Publication No. US20030088078A1
/ GENERAL INFORMATION:
/ APPLICANT: Feng et al.
/ TITLE OF INVENTION: 125 Human Secreted Proteins
/ FILE REFERENCE: P2020P1
```



CURRENT APPLICATION NUMBER: US/09/305,736  
CURRENT FILING DATE: 1999-05-05  
EARLIER APPLICATION NUMBER: PCT/US98/23435  
EARLIER FILING DATE: 1998-11-04  
EARLIER APPLICATION NUMBER: 60/064,911  
EARLIER FILING DATE: 1997-11-07  
EARLIER APPLICATION NUMBER: 60/064,912  
EARLIER FILING DATE: 1997-11-07  
EARLIER APPLICATION NUMBER: 60/064,983  
EARLIER FILING DATE: 1997-11-07  
EARLIER APPLICATION NUMBER: 60/064,900  
EARLIER FILING DATE: 1997-11-07  
EARLIER APPLICATION NUMBER: 60/064,988  
EARLIER FILING DATE: 1997-11-07  
EARLIER APPLICATION NUMBER: 60/064,987  
EARLIER FILING DATE: 1997-11-07  
EARLIER APPLICATION NUMBER: 60/064,908  
EARLIER FILING DATE: 1997-11-07  
EARLIER APPLICATION NUMBER: 60/064,984  
EARLIER FILING DATE: 1997-11-07  
EARLIER APPLICATION NUMBER: 60/064,985  
EARLIER FILING DATE: 1997-11-07  
EARLIER APPLICATION NUMBER: 60/066,094  
EARLIER FILING DATE: 1997-11-17  
EARLIER APPLICATION NUMBER: 60/066,100  
EARLIER FILING DATE: 1997-11-17  
EARLIER APPLICATION NUMBER: 60/066,089  
EARLIER FILING DATE: 1997-11-17  
EARLIER APPLICATION NUMBER: 60,066,095  
EARLIER FILING DATE: 1997-11-17  
EARLIER APPLICATION NUMBER: 60/066,090  
EARLIER FILING DATE: 1997-11-17  
NUMBER OF SEQ ID NOS: 612  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 524  
LENGTH: 16  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-305-736-524

Query Match 26.3%; Score 30; DB 3; Length 16;  
Best Local Similarity 46.2%; Pred. No. 2.2e+03;  
Matches 6; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 8 RLGNPKAPLYKRP 20  
DB 2 RFGNPKCRLFSVP 14

RESULT 62  
US-09-818-683-524  
Sequence 524, Application US/09818683  
Publication No. US20030211472A1  
GENERAL INFORMATION:  
APPLICANT: Peng et al.  
TITLE OF INVENTION: 125 Human Secreted Proteins  
FILE REFERENCE: P2020P1  
CURRENT APPLICATION NUMBER: US/09/818,683  
CURRENT FILING DATE: 2001-03-28  
Prior application data removed - consult PALM or file wrapper  
NUMBER OF SEQ ID NOS: 612  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 524  
LENGTH: 16  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-818-683-524

Query Match 26.3%; Score 30; DB 3; Length 16;  
Best Local Similarity 46.2%; Pred. No. 2.2e+03;  
Matches 6; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 8 RLGNPKAPLYKRP 20

DB 2 RFGNPKCRLFSVP 14

RESULT 63  
US-09-818-683-524  
Sequence 524, Application US/09818683  
Publication No. US20040185440A9  
GENERAL INFORMATION:  
APPLICANT: Peng et al.  
TITLE OF INVENTION: 125 Human Secreted Proteins  
FILE REFERENCE: P2020P1  
CURRENT APPLICATION NUMBER: US/09/818,683  
CURRENT FILING DATE: 2001-03-28  
Prior application data removed - consult PALM or file wrapper  
NUMBER OF SEQ ID NOS: 612  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 524  
LENGTH: 16  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-818-683-524

Query Match 26.3%; Score 30; DB 3; Length 16;  
Best Local Similarity 46.2%; Pred. No. 2.2e+03;  
Matches 6; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 8 RLGNPKAPLYKRP 20  
DB 2 RFGNPKCRLFSVP 14

RESULT 64  
US-10-621-401-522  
Sequence 522, Application US/10621401  
Publication No. US20040038277A1  
GENERAL INFORMATION:  
APPLICANT: Rosen et al.  
TITLE OF INVENTION: 125 Human Secreted Proteins  
FILE REFERENCE: P2020P2C1  
CURRENT APPLICATION NUMBER: US/10/621,401  
CURRENT FILING DATE: 2003-07-18  
PRIOR APPLICATION NUMBER: US 09/974,879  
PRIOR FILING DATE: 2001-10-12  
PRIOR APPLICATION NUMBER: US 60/239,893  
PRIOR FILING DATE: 2000-10-13  
PRIOR APPLICATION NUMBER: US 09/818,683  
PRIOR FILING DATE: 2001-03-28  
PRIOR APPLICATION NUMBER: US 09/305,736  
PRIOR FILING DATE: 1999-05-05  
PRIOR APPLICATION NUMBER: PCT/US98/23435  
PRIOR FILING DATE: 1998-11-04  
PRIOR APPLICATION NUMBER: US 60/064,911  
PRIOR FILING DATE: 1997-11-07  
PRIOR APPLICATION NUMBER: US 60/064,912  
PRIOR FILING DATE: 1997-11-07  
PRIOR APPLICATION NUMBER: US 60/064,983  
PRIOR FILING DATE: 1997-11-07  
PRIOR APPLICATION NUMBER: US 60/064,900  
PRIOR FILING DATE: 1997-11-07  
PRIOR APPLICATION NUMBER: US 60/064,988  
PRIOR FILING DATE: 1997-11-07  
Remaining Prior Application data removed - See file wrapper or PALM.  
NUMBER OF SEQ ID NOS: 611  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 522  
LENGTH: 16  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-621-401-522

Query Match 26.3%; Score 30; DB 4; Length 16;  
Best Local Similarity 46.2%; Pred. No. 2.2e+03;

Query Match	26.3%	Score 30	DB 4	Length 18
Similarity	71.4%	Pred. No.	2.5e+03	
Best Local	1.4%	Mismatches	0	Gaps 0
Matches	5	Conservative	0	Indels 0

RESULT 69  
US-10-325-810-163

```

/ Sequence 163, Application US/10325810
/ Publication No. US20030204069A1
/ GENERAL INFORMATION:
/ APPLICANT: Cech, Thomas R.
/           Ligner, Joachim
/           Nakamura, Toru
/           Chapman, Karen B.
/           Morin, Gregg B.
/           Harley, Calvin B.
/           Andrew, William H.
/ TITLE OF INVENTION: Human Telomerase Catalytic Subunit
/ NUMBER OF SEQUENCES: 633
/ CORRESPONDENCE ADDRESS:
/ ADDRESS: Townsend and Townsend and Crew LLP
/ STREET: Two Embarcadero Center, Eighth Floor
/ CITY: San Francisco
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94111-3834
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/325,810
/ FILING DATE: 20-Dec-2002
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/09/402,181
/ FILING DATE: 29-Sep-1997
/ APPLICATION NUMBER: US 08/724,643
/ FILING DATE: 01-Oct-1996
/ APPLICATION NUMBER: US 08/844,419
/ FILING DATE: 18-Apr-1997
/ APPLICATION NUMBER: US 08/846,017
/ FILING DATE: 25-Apr-1997
/ APPLICATION NUMBER: US 08/851,843
/ FILING DATE: 06-May-1997
/ APPLICATION NUMBER: US 08/854,050
/ FILING DATE: 09-May-1997
/ APPLICATION NUMBER: US 08/911,312
/ FILING DATE: 14-Aug-1997
/ APPLICATION NUMBER: US 08/912,951
/ FILING DATE: 14-Aug-1997
/ APPLICATION NUMBER: US 08/915,503
/ FILING DATE: 14-Aug-1997
/ APPLICATION NUMBER: WO PCT/US97/17865
/ FILING DATE: 01-Oct-1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Aueenhub, Scott L.
/ REGISTRATION NUMBER: 42,271
/ REFERENCE/DOCKET NUMBER: 015369-002620US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 576-0300
/ TELEFAX: (415) 576-0300
/ INFORMATION FOR SEQ ID NO: 163:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 18 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: <Unknown>
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ SEQUENCE DESCRIPTION: SEQ ID NO: 163:
US-10-325-810-163

```

```

Query Match      26.3%; Score 30; DB 4; Length 18;
Best Local Similarity 62.5%; Pred. No. 2.5e+03;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY      11 NPKAPLYK 18
      |||||
      5 NPKTPYK 12
DB

```

```

RESULT 70
US-10-350-405-181
/ Sequence 181, Application US/10350405
/ Publication No. US20030215894A1
/ GENERAL INFORMATION:
/ APPLICANT: Niman, Henry L.
/ TITLE OF INVENTION: Polypeptide-Induced Monoclonal Receptors
/ FILE REFERENCE: TSRI 35.5 CON 7/LIG
/ CURRENT APPLICATION NUMBER: US/10/350,405
/ CURRENT FILING DATE: 2003-01-24
/ PRIOR APPLICATION NUMBER: 09/427,576
/ PRIOR FILING DATE: 1999-10-26
/ PRIOR APPLICATION NUMBER: 08/461,583
/ PRIOR FILING DATE: 1995-06-02
/ PRIOR APPLICATION NUMBER: 08/294,879
/ PRIOR FILING DATE: 1994-08-23
/ PRIOR APPLICATION NUMBER: 08/054,864
/ PRIOR FILING DATE: 1993-04-28
/ PRIOR APPLICATION NUMBER: 07/900,502
/ PRIOR FILING DATE: 1992-06-16
/ PRIOR APPLICATION NUMBER: 07/780,415
/ PRIOR FILING DATE: 1991-10-22
/ NUMBER OF SEQ ID NOS: 227
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 181
/ LENGTH: 18
/ TYPE: PRT
/ ORGANISM: retrovirus
US-10-350-405-181

```

```

Query Match      26.3%; Score 30; DB 4; Length 18;
Best Local Similarity 66.7%; Pred. No. 2.5e+03;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY      5 PGRRLNPK 13
      |||||
      10 PSERLGNLK 18
DB

```

```

RESULT 71
US-10-415-024-8
/ Sequence 8, Application US/10415024
/ Publication No. US20040058984A1
/ GENERAL INFORMATION:
/ APPLICANT: Diatide, Inc.
/ TITLE OF INVENTION: STABILIZATION OF RADIOPHARMACEUTICAL COMPOSITIONS
/ FILE REFERENCE: CHROMANS
/ FILE REFERENCE: 09744-015W01
/ CURRENT APPLICATION NUMBER: US/10/415,024
/ CURRENT FILING DATE: 2003-04-24
/ PRIOR APPLICATION NUMBER: US 09/694,992
/ PRIOR FILING DATE: 2000-10-24
/ PRIOR APPLICATION NUMBER: US 09/695,360
/ PRIOR FILING DATE: 2000-10-24
/ PRIOR APPLICATION NUMBER: US 09/695,494
/ PRIOR FILING DATE: 2000-10-24
/ NUMBER OF SEQ ID NOS: 29
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 8
/ LENGTH: 18
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Synthetic construct
US-10-415-024-8

```

```

Query Match      26.3%; Score 30; DB 4; Length 18;
Best Local Similarity 71.4%; Pred. No. 2.5e+03;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY
DB

```

OY 13 KAPLYK 19  
:||||:  
Db 4 QAPLYK 10

## RESULT 72

US-10-877-124-163  
; Sequence 163, Application US/10877124  
; Publication No. US20040242529A1  
; GENERAL INFORMATION:  
; APPLICANT: Cech, Thomas R.  
; Lingner, Joachim  
; Nakamura, Toru  
; Chapman, Karen B.  
; Morin, Gregg B.  
; Hartley, Calvin B.  
; Andrews, William H.

TITLE OF INVENTION: Human Telomerase Catalytic Subunit  
NUMBER OF SEQUENCES: 727  
CORRESPONDENCE ADDRESS:  
ADDRESS: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/877,124  
FILING DATE: 24-Jun-2004  
CLASSIFICATION: <Unknown>

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/432,503  
FILING DATE: 02-Nov-1999  
APPLICATION NUMBER: 08/974,549  
FILING DATE: <Unknown>  
APPLICATION NUMBER: US 08/844,419  
FILING DATE: 18-Apr-1997  
APPLICATION NUMBER: US 08/846,017  
FILING DATE: 25-Apr-1997  
APPLICATION NUMBER: US 08/851,843  
FILING DATE: 06-May-1997  
APPLICATION NUMBER: US 08/854,050  
FILING DATE: 09-May-1997  
APPLICATION NUMBER: US 08/911,312  
FILING DATE: 14-Aug-1997  
APPLICATION NUMBER: US 08/912,951  
FILING DATE: 14-Aug-1997  
APPLICATION NUMBER: US 08/915,503  
FILING DATE: 14-Aug-1997  
APPLICATION NUMBER: WO PCT/US97/17618  
FILING DATE: 01-Oct-1997  
APPLICATION NUMBER: WO PCT/US97/17885  
FILING DATE: 01-Oct-1997

## ATTORNEY/AGENT INFORMATION:

NAME: Apple, Randolph Ted  
REGISTRATION NUMBER: 36,429  
REFERENCE/DOCKET NUMBER: 015389-002610US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300

## INFORMATION FOR SEQ ID NO: 163:

SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: peptide

; SEQUENCE DESCRIPTION: SEQ ID NO: 163:  
US-10-877-124-163

Query Match 26.3%; Score 30; DB 5; Length 18;  
Best Local Similarity 62.5%; Pred. No. 2.5e+03;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 11 NPKAPLYK 18  
|||||:  
Db 5 NPKAPIK 12

## RESULT 73

US-10-877-022-163  
; Sequence 163, Application US/10877022  
; Publication No. US20040247613A1  
; GENERAL INFORMATION:  
; APPLICANT: Cech, Thomas R.  
; Lingner, Joachim  
; Nakamura, Toru  
; Chapman, Karen B.  
; Morin, Gregg B.  
; Hartley, Calvin B.  
; Andrews, William H.

TITLE OF INVENTION: Human Telomerase Catalytic Subunit  
NUMBER OF SEQUENCES: 727  
CORRESPONDENCE ADDRESS:  
ADDRESS: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/877,022  
FILING DATE: 24-Jun-2004  
CLASSIFICATION: <Unknown>

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/432,503  
FILING DATE: 02-Nov-1999  
APPLICATION NUMBER: 08/974,549  
FILING DATE: <Unknown>  
APPLICATION NUMBER: US 08/844,419  
FILING DATE: 18-Apr-1997  
APPLICATION NUMBER: US 08/846,017  
FILING DATE: 25-Apr-1997  
APPLICATION NUMBER: US 08/851,843  
FILING DATE: 06-May-1997  
APPLICATION NUMBER: US 08/854,050  
FILING DATE: 09-May-1997  
APPLICATION NUMBER: US 08/911,312  
FILING DATE: 14-Aug-1997  
APPLICATION NUMBER: US 08/912,951  
FILING DATE: 14-Aug-1997  
APPLICATION NUMBER: US 08/915,503  
FILING DATE: 14-Aug-1997  
APPLICATION NUMBER: WO PCT/US97/17618  
FILING DATE: 01-Oct-1997  
APPLICATION NUMBER: WO PCT/US97/17885  
FILING DATE: 01-Oct-1997

## ATTORNEY/AGENT INFORMATION:

NAME: Apple, Randolph Ted  
REGISTRATION NUMBER: 36,429  
REFERENCE/DOCKET NUMBER: 015389-002610US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300

## INFORMATION FOR SEQ ID NO: 163:

SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 163:  
US-10-877-022-163

Query Match 26.3%; Score 30; DB 5; Length 18;  
Best Local Similarity 62.5%; Pred. No. 2.5e+03;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 11 NPKAPLYK 18  
DB 5 NPKTPYK 12

RESULT 74  
US-10-877-146-163  
Sequence 163, Application US/10877146  
Publication No. US20050013825A1  
GENERAL INFORMATION:  
APPLICANT: Cech, Thomas R.  
Lingner, Joachim  
Nakamura, Toru  
Chapman, Karen B.  
Morin, Gregg B.  
Harley, Calvin B.  
Andrews, William H.  
TITLE OF INVENTION: Human Telomerase Catalytic Subunit  
NUMBER OF SEQUENCES: 727  
CORRESPONDING ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/877,146  
FILING DATE: 24-Jun-2004  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/432,503  
FILING DATE: 02-Nov-1999  
APPLICATION NUMBER: 08/974,549  
FILING DATE: <Unknown>  
APPLICATION NUMBER: US 08/844,419  
FILING DATE: 18-Apr-1997  
APPLICATION NUMBER: US 08/846,017  
FILING DATE: 25-Apr-1997  
APPLICATION NUMBER: US 08/851,843  
FILING DATE: 06-May-1997  
APPLICATION NUMBER: US 08/854,050  
FILING DATE: 09-May-1997  
APPLICATION NUMBER: US 08/911,312  
FILING DATE: 14-Aug-1997  
APPLICATION NUMBER: US 08/912,951  
FILING DATE: 14-Aug-1997  
APPLICATION NUMBER: US 08/915,503  
FILING DATE: 14-Aug-1997  
APPLICATION NUMBER: WO PCT/US97/17618  
FILING DATE: 01-Oct-1997  
APPLICATION NUMBER: WO PCT/US97/17885  
FILING DATE: 01-Oct-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Apple, Randolph Ted

REGISTRATION NUMBER: 36,429  
REFERENCE/DOCKET NUMBER: 015389-002610US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 163:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 163:  
US-10-877-146-163

Query Match 26.3%; Score 30; DB 5; Length 18;  
Best Local Similarity 62.5%; Pred. No. 2.5e+03;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 11 NPKAPLYK 18  
DB 5 NPKTPYK 12

RESULT 75  
US-11-088-596-8  
Sequence 8, Application US/11088596  
Publication No. US20050180918A1  
GENERAL INFORMATION:  
APPLICANT: Cyr, John B.  
APPLICANT: Pearson, Daniel A.  
TITLE OF INVENTION: STABILIZATION OF RADIOPHARMACEUTICAL COMPOSITIONS  
TITLE OF INVENTION: USING HYDROPHILIC THIOETHERS  
FILE REFERENCE: 09744-016001  
CURRENT APPLICATION NUMBER: US/11/088,596  
FILING DATE: 2005-03-24  
PRIOR APPLICATION NUMBER: US/10/131,543  
PRIOR FILING DATE: 2002-04-24  
PRIOR APPLICATION NUMBER: US 09/694,992  
PRIOR FILING DATE: 2000-10-24  
PRIOR APPLICATION NUMBER: PCT/US01/50423  
PRIOR FILING DATE: 2001-10-24  
NUMBER OF SEQ ID NOS: 29  
SOFTWARE: PaetSeq for Windows Version 4.0  
SEQ ID NO 8  
LENGTH: 18  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURES:  
OTHER INFORMATION: Synthetic construct  
US-11-088-596-8

Query Match 26.3%; Score 30; DB 6; Length 18;  
Best Local Similarity 71.4%; Pred. No. 2.5e+03;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 13 KAPLYK 19  
DB 4 QAPLYK 10

RESULT 76  
US-11-066-697-1140  
Sequence 1140, Application US/11066697  
Publication No. US20050187159A1  
GENERAL INFORMATION:  
APPLICANT: Brlidon, Dominique P.  
APPLICANT: Ezrin, Alan M.  
APPLICANT: Milner, Peter G.  
APPLICANT: Holmes, Darren L.  
APPLICANT: Thibodeau, Karen  
TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM  
PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD

```

; TITLE OF INVENTION: COMPONENTS
; FILE REFERENCE: 500862002301
; CURRENT APPLICATION NUMBER: US/11/066,697
; CURRENT FILING DATE: 2005-02-25
; PRIOR APPLICATION NUMBER: 09/657,276
; PRIOR FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-15
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1140
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-11-066-697-1140
```

```
Query Match      26.3%; Score 30; DB 6; Length 18;
Best Local Similarity 42.1%; Pred. No. 2.5e+03;
Matches      8; Conservative 1; Mismatches 6; Indels 4; Gaps 1;
```

```
QY      2 YEYPSRLGNPKAPLYKRP 20
      ||||| : ||
Db      1 YEKPSG---PPREVPRP 15
```

```

RESULT 77
US-11-086-966-8
; Sequence 8, Application US/11086966
; Publication No. US20050207973A1
; GENERAL INFORMATION:
; APPLICANT: CYT, John E.
; TITLE OF INVENTION: STABILIZATION OF RADIOPHARMACEUTICAL COMPOSITIONS
; FILE REFERENCE: 09744-017001
; CURRENT APPLICATION NUMBER: US/11/086,966
; CURRENT FILING DATE: 2005-03-22
; PRIOR APPLICATION NUMBER: US/10/131,346
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 09/695,360
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: PCT/US01/50423
; PRIOR FILING DATE: 2001-10-24
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-11-086-966-8
```

```
Query Match      26.3%; Score 30; DB 6; Length 18;
Best Local Similarity 71.4%; Pred. No. 2.5e+03;
Matches      5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      13 KAPLYRK 19
      :|||:
Db      4 QAPLYRK 10
```

```

RESULT 78
US-10-106-804B-11
; Sequence 11, Application US/10106804B
; Publication No. US2003019186A1
; GENERAL INFORMATION:
; APPLICANT: Hubbell, Jeffrey A.
; APPLICANT: Schense, Jason C.
```

```

; APPLICANT: Sakiyama-Bibert, Shelly E.
; TITLE OF INVENTION: Enzyme-Mediated Modification of Fibrin For Tissue Engineering: F
; FILE REFERENCE: ETH 106 CON
; CURRENT APPLICATION NUMBER: US/10/106,804B
; CURRENT FILING DATE: 2003-03-04
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 19
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: heparin binding sequence
US-10-106-804B-11
```

```
Query Match      26.3%; Score 30; DB 4; Length 19;
Best Local Similarity 42.1%; Pred. No. 2.6e+03;
Matches      8; Conservative 1; Mismatches 6; Indels 4; Gaps 1;
```

```
QY      2 YEYPSRLGNPKAPLYKRP 20
      ||||| : ||
Db      1 YEKPSG---PPREVPRP 15
```

```

RESULT 79
US-10-323-046-13
; Sequence 13, Application US/10323046
; Publication No. US20030187232A1
; GENERAL INFORMATION:
; APPLICANT: Hubbell, Jeffrey A
; APPLICANT: Schense, Jason C
; APPLICANT: Sakiyama-Bibert, Shelly E
; TITLE OF INVENTION: Growth Factor Modified Protein Matrices for Tissue
; FILE REFERENCE: ETH 107 CIP (2)
; CURRENT APPLICATION NUMBER: US/10/323,046
; CURRENT FILING DATE: 2002-12-17
; PRIOR APPLICATION NUMBER: 09/141,153
; PRIOR FILING DATE: 1998-08-27
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 13
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Heparin-binding sequence
US-10-323-046-13
```

```
Query Match      26.3%; Score 30; DB 4; Length 19;
Best Local Similarity 42.1%; Pred. No. 2.6e+03;
Matches      8; Conservative 1; Mismatches 6; Indels 4; Gaps 1;
```

```
QY      2 YEYPSRLGNPKAPLYKRP 20
      ||||| : ||
Db      1 YEKPSG---PPREVPRP 15
```

```

RESULT 80
US-10-297-229-52
; Sequence 52, Application US/10297229
; Publication No. US20030220245A1
; GENERAL INFORMATION:
; APPLICANT: HUBBELL, Jeffrey A.
; APPLICANT: ELBERT, Donald
; APPLICANT: SCHOENMAKERS, Ronald
; TITLE OF INVENTION: CONJUGATE ADDITION REACTIONS FOR THE
; FILE REFERENCE: 50154/003002
; CURRENT APPLICATION NUMBER: US/10/297,229
; CURRENT FILING DATE: 2002-10-02
```

/ PRIOR APPLICATION NUMBER: PCT/US01/18101  
/ PRIOR FILING DATE: 2001-06-04  
/ PRIOR APPLICATION NUMBER: US 09/586,937  
/ PRIOR FILING DATE: 2000-06-02  
/ NUMBER OF SEQ ID NOS: 77  
/ SOFTWARE: FastSeq for Windows Version 4.0  
/ SEQ ID NO 52  
/ LENGTH: 19  
/ TYPE: PRT  
/ ORGANISM: Artificial Sequence  
/ FEATURES:  
/ OTHER INFORMATION: Based on Homo sapiens  
US-10-297-229-52

Query Match 26.3%; Score 30; DB 4; Length 19;  
Best Local Similarity 42.1%; Pred. No. 2.6e+03;  
Matches 8; Conservative 1; Mismatches 6; Indels 4; Gaps 1;

QY 2 YEYGSRLGNPKAPLYRKP 20  
|||:|:|:  
DB 1 YEKFGS---PPEVVRP 15

RESULT 81  
US-10-225-567A-1614  
/ Sequence 1614, Application US/10225567A  
/ Publication No. US20030113798A1  
/ GENERAL INFORMATION:  
/ APPLICANT: LifeSpan Biosciences  
/ APPLICANT: Brown, Joseph P.  
/ APPLICANT: Burmer, Glenna C.  
/ APPLICANT: Roush, Christine L.  
/ TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS  
/ FILE REFERENCE: 1920-4-4  
/ CURRENT APPLICATION NUMBER: US/10/225,567A  
/ CURRENT FILING DATE: 2001-12-19  
/ PRIOR APPLICATION NUMBER: 60/257,144  
/ PRIOR FILING DATE: 2000-12-19  
/ NUMBER OF SEQ ID NOS: 2292  
/ SOFTWARE: PatentIn version 3.1  
/ SEQ ID NO 1614  
/ LENGTH: 20  
/ TYPE: PRT  
/ ORGANISM: Homo sapiens  
US-10-225-567A-1614

Query Match 26.3%; Score 30; DB 4; Length 20;  
Best Local Similarity 62.5%; Pred. No. 2.8e+03;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 PGSRLGNP 12  
||:|:|:  
DB 12 PGTTPGSP 19

RESULT 82  
US-10-327-598-150  
/ Sequence 150, Application US/10327598  
/ Publication No. US20040181039A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Krah, Eugene  
/ APPLICANT: Guo, Hongliang  
/ APPLICANT: Aliyappa, Ashok  
/ APPLICANT: Lawton, Robert  
/ TITLE OF INVENTION: Canine Immunoglobulin Variable Domains, Caninized Antibodies, and  
/ FILE REFERENCE: 01-799-A  
/ CURRENT APPLICATION NUMBER: US/10/327,598  
/ CURRENT FILING DATE: 2002-12-20  
/ PRIOR APPLICATION NUMBER: US 60/344,874  
/ PRIOR FILING DATE: 2001-12-21  
/ NUMBER OF SEQ ID NOS: 1139  
/ SOFTWARE: PatentIn version 3.0

/ SEQ ID NO 150  
/ LENGTH: 15  
/ TYPE: PRT  
/ ORGANISM: canis familiaris;  
US-10-327-598-150

Query Match 25.9%; Score 29.5; DB 4; Length 15;  
Best Local Similarity 40.0%; Pred. No. 2.4e+03;  
Matches 6; Conservative 3; Mismatches 3; Indels 3; Gaps 1;

QY 3 EYPSRLGNPKAPLY 17  
:|:|:|:|:  
DB 4 QYPTG---GPKTLY 15

RESULT 83  
US-10-327-598-232  
/ Sequence 232, Application US/10327598  
/ Publication No. US20040181039A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Krah, Eugene  
/ APPLICANT: Guo, Hongliang  
/ APPLICANT: Aliyappa, Ashok  
/ APPLICANT: Lawton, Robert  
/ TITLE OF INVENTION: Canine Immunoglobulin Variable Domains, Caninized Antibodies, an  
/ FILE REFERENCE: 01-799-A  
/ CURRENT APPLICATION NUMBER: US/10/327,598  
/ CURRENT FILING DATE: 2002-12-20  
/ PRIOR APPLICATION NUMBER: US 60/344,874  
/ PRIOR FILING DATE: 2001-12-21  
/ NUMBER OF SEQ ID NOS: 1139  
/ SOFTWARE: PatentIn version 3.0  
/ SEQ ID NO 232  
/ LENGTH: 15  
/ TYPE: PRT  
/ ORGANISM: canis familiaris;  
US-10-327-598-232

Query Match 25.9%; Score 29.5; DB 4; Length 15;  
Best Local Similarity 53.8%; Pred. No. 2.4e+03;  
Matches 7; Conservative 2; Mismatches 1; Indels 3; Gaps 1;

QY 5 PGSR---LGNPKA 14  
||:|:|:|:  
DB 3 PGTQLTVLGQPKA 15

RESULT 84  
US-10-304-443-99  
/ Sequence 99, Application US/10304443  
/ Publication No. US20030170229A1  
/ GENERAL INFORMATION:  
/ APPLICANT: SmithKline Beecham Biologicals s.a.  
/ APPLICANT: Peptide Therapeutics Ltd.  
/ TITLE OF INVENTION: Vaccine  
/ FILE REFERENCE: B45173CIP  
/ CURRENT APPLICATION NUMBER: US/10/304,443  
/ CURRENT FILING DATE: 2002-11-26  
/ PRIOR APPLICATION NUMBER: US/09/698,906A  
/ PRIOR FILING DATE: 2001-02-20  
/ NUMBER OF SEQ ID NOS: 121  
/ SOFTWARE: FastSeq for Windows Version 3.0  
/ SEQ ID NO 99  
/ LENGTH: 10  
/ TYPE: PRT  
/ ORGANISM: Human peptide sequence  
US-10-304-443-99

Query Match 25.4%; Score 29; DB 4; Length 10;  
Best Local Similarity 83.3%; Pred. No. 1.9e+03;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
OY      3 EYPSR 8
        |||||
Db      2 EWPGR 7

RESULT 85
US-10-415-389-12
/ Sequence 12, Application US/10415389
/ Publication No. US20040115220A1
/ GENERAL INFORMATION:
/ APPLICANT: De Basois, Carlota Vinals Y
/ TITLE OF INVENTION: Vaccine
/ FILE REFERENCE: B45251
/ CURRENT APPLICATION NUMBER: US/10/415,389
/ PRIOR FILING DATE: 2003-04-25
/ PRIOR APPLICATION NUMBER: PCT/EP01/12932
/ PRIOR FILING DATE: 2001-10-24
/ PRIOR APPLICATION NUMBER: GB 0026334.3
/ NUMBER OF SEQ ID NOS: 34
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 12
/ LENGTH: 10
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Human IGE peptide mimotope
US-10-415-389-12

Query Match      25.4%; Score 29; DB 4; Length 10;
Best Local Similarity 83.3%; Pred. No. 1.9e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY      3 EYPSR 8
        |||||
Db      2 EWPGR 7

RESULT 86
US-10-322-210-4
/ Sequence 4, Application US/10322210
/ Publication No. US20030147906A1
/ GENERAL INFORMATION:
/ APPLICANT: Friede, Martin
/ APPLICANT: Mason, Sean
/ APPLICANT: Turnell, William Gordon
/ APPLICANT: Van Mechelen, Marcelle Paulette
/ APPLICANT: Vinals y de Basois, Carlota
/ TITLE OF INVENTION: Epitopes or Mimotopes Derived from the
/ TITLE OF INVENTION: C-Epsilon-3 or C-Epsilon-4 Domains of IGE, Antagonists
/ FILE REFERENCE: B45173
/ CURRENT APPLICATION NUMBER: US/10/322,210
/ CURRENT FILING DATE: 2002-12-18
/ PRIOR APPLICATION NUMBER: US/09/914,089
/ PRIOR FILING DATE: 2001-08-22
/ PRIOR APPLICATION NUMBER: GB 9904408.3
/ PRIOR FILING DATE: 1999-02-25
/ PRIOR APPLICATION NUMBER: GB 9917144.9
/ PRIOR FILING DATE: 1999-07-21
/ PRIOR APPLICATION NUMBER: GB 9918598.5
/ PRIOR FILING DATE: 1999-08-07
/ PRIOR APPLICATION NUMBER: GB 9918599.3
/ PRIOR FILING DATE: 1999-08-07
/ PRIOR APPLICATION NUMBER: GB 9918601.7
/ PRIOR FILING DATE: 1999-08-07
/ PRIOR APPLICATION NUMBER: GB 9918604.1
/ PRIOR FILING DATE: 1999-08-07
/ PRIOR APPLICATION NUMBER: GB 9918606.6
/ PRIOR FILING DATE: 1999-08-07
/ PRIOR APPLICATION NUMBER: GB 9925618.2
/ PRIOR FILING DATE: 1999-10-29
/ NUMBER OF SEQ ID NOS: 86
```

```
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 4
/ LENGTH: 11
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Chimeric
US-10-322-210-4

Query Match      25.4%; Score 29; DB 4; Length 11;
Best Local Similarity 83.3%; Pred. No. 2.1e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY      3 EYPSR 8
        |||||
Db      2 EWPGR 7

RESULT 87
US-10-304-443-4
/ Sequence 4, Application US/10304443
/ Publication No. US20030170229A1
/ GENERAL INFORMATION:
/ APPLICANT: SmithKline Beecham Biologicals s.a.
/ APPLICANT: Peptide Therapeutics Ltd.
/ TITLE OF INVENTION: Vaccine
/ FILE REFERENCE: B45173CIP
/ CURRENT APPLICATION NUMBER: US/10/304,443
/ CURRENT FILING DATE: 2002-11-26
/ PRIOR APPLICATION NUMBER: US/09/698,906A
/ PRIOR FILING DATE: 2001-02-20
/ NUMBER OF SEQ ID NOS: 121
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 4
/ LENGTH: 11
/ TYPE: PRT
/ ORGANISM: Human peptide sequence
US-10-304-443-4

Query Match      25.4%; Score 29; DB 4; Length 11;
Best Local Similarity 83.3%; Pred. No. 2.1e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY      3 EYPSR 8
        |||||
Db      2 EWPGR 7

RESULT 88
US-10-362-527-63
/ Sequence 63, Application US/10362527
/ Publication No. US20040030106A1
/ GENERAL INFORMATION:
/ APPLICANT: Friede, Martin
/ APPLICANT: Mason, Sean
/ APPLICANT: Turnell, William Gordon
/ APPLICANT: Vinals y de Basois, Carlota
/ TITLE OF INVENTION: Vaccine Immunogens Comprising Disulphide Bridged Cycled Peptide
/ TITLE OF INVENTION: and Use Thereof in the Treatment of Allergies
/ FILE REFERENCE: B45236
/ CURRENT APPLICATION NUMBER: US/10/362,527
/ CURRENT FILING DATE: 2003-02-21
/ PRIOR APPLICATION NUMBER: PCT/EP01/09576
/ PRIOR FILING DATE: 2001-08-17
/ PRIOR APPLICATION NUMBER: GB 0020717.5
/ PRIOR FILING DATE: 2000-08-22
/ NUMBER OF SEQ ID NOS: 328
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 63
/ LENGTH: 11
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-362-527-63
```



Query Match 25.4%; Score 29; DB 4; Length 11;  
 Best Local Similarity 83.3%; Pred. No. 2.1e+03;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 EYPSGR 8  
 | : |||||  
 Db 2 EWPGR 7

RESULT 89  
 US-11-004-771-4  
 / Sequence 4, Application US/11004771  
 / Publication No. US20050152892A1  
 / GENERAL INFORMATION:  
 / APPLICANT: Friede, Martin  
 / APPLICANT: Mason, Sean  
 / APPLICANT: Turnell, William Gordon  
 / APPLICANT: Van Mechelen, Marcelle Paulette  
 / APPLICANT: Vinals y de Bascoles, Carlota  
 / TITLE OF INVENTION: Epitopes or Mimotopes Derived from the  
 / TITLE OF INVENTION: C-Epsilon-3 or C-Epsilon-4 Domains of IGE, Antagonists  
 / TITLE OF INVENTION: thereof, and Their Therapeutic Uses  
 / FILE REFERENCE: B45173  
 / CURRENT APPLICATION NUMBER: US/11/004,771  
 / CURRENT FILING DATE: 2004-12-03  
 / PRIOR APPLICATION NUMBER: US/10/322,210  
 / PRIOR FILING DATE: 2002-12-18  
 / PRIOR APPLICATION NUMBER: US/09/914,089  
 / PRIOR FILING DATE: 2001-08-22  
 / PRIOR APPLICATION NUMBER: GB 9904408.3  
 / PRIOR FILING DATE: 1999-02-25  
 / PRIOR APPLICATION NUMBER: GB 9917144.9  
 / PRIOR FILING DATE: 1999-07-21  
 / PRIOR APPLICATION NUMBER: GB 9918598.5  
 / PRIOR FILING DATE: 1999-08-07  
 / PRIOR APPLICATION NUMBER: GB 9918599.3  
 / PRIOR FILING DATE: 1999-08-07  
 / PRIOR APPLICATION NUMBER: GB 9918601.7  
 / PRIOR FILING DATE: 1999-08-07  
 / PRIOR APPLICATION NUMBER: GB 9918604.1  
 / PRIOR FILING DATE: 1999-08-07  
 / PRIOR APPLICATION NUMBER: GB 9918606.6  
 / PRIOR FILING DATE: 1999-08-07  
 / PRIOR APPLICATION NUMBER: GB 9925618.2  
 / PRIOR FILING DATE: 1999-10-29  
 / NUMBER OF SEQ ID NOS: 86  
 / SOFTWARE: FastSeq for Windows Version 4.0  
 / SEQ ID NO 4  
 / LENGTH: 11  
 / TYPE: PRT  
 / ORGANISM: Artificial Sequence  
 / FEATURE:  
 / OTHER INFORMATION: Chimeric  
 US-11-004-771-4

Query Match 25.4%; Score 29; DB 6; Length 11;  
 Best Local Similarity 83.3%; Pred. No. 2.1e+03;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 EYPSGR 8  
 | : |||||  
 Db 2 EWPGR 7

RESULT 90  
 US-09-071-838-108  
 / Sequence 108, Application US/09071838  
 / Patent No. US20020152501A1  
 / GENERAL INFORMATION:  
 / APPLICANT: Fischer, Robert L.  
 / APPLICANT: Ohad, Nir  
 / APPLICANT: Klyosue, Tomohiro

APPLICANT: Yadegari, Ramin  
 APPLICANT: Margosian, Linda  
 APPLICANT: Harada, John  
 APPLICANT: Goldberg, Robert B.  
 TITLE OF INVENTION: Nucleic Acids That Control Seed and  
 TITLE OF INVENTION: Fruit Development in Plants  
 NUMBER OF SEQUENCES: 324  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Townsend and Townsend and Crew LLP  
 STREET: Two Embarcadero Center, Eighth Floor  
 CITY: San Francisco  
 STATE: California  
 COUNTRY: USA  
 ZIP: 94111-3834  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/071,838  
 FILING DATE: 01-MAY-1998  
 CLASSIFICATION: 800  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Bastian, Kevin L.  
 REGISTRATION NUMBER: 34,774  
 REFERENCE/DOCKET NUMBER: 023070-086100US  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 576-0200  
 TELEFAX: (415) 576-0300  
 INFORMATION FOR SEQ ID NO: 108:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 12 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 / MOLECULAR TYPE: peptide  
 US-09-071-838-108

Query Match 25.4%; Score 29; DB 3; Length 12;  
 Best Local Similarity 44.4%; Pred. No. 2.3e+03;  
 Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 11 NPKAPLYKR 19  
 | : |||||  
 Db 1 NPKVTIFPK 9

RESULT 91  
 US-10-213-512-108  
 / Sequence 108, Application US/10213512  
 / Publication No. US20030110536A1  
 / GENERAL INFORMATION:  
 / APPLICANT: Fischer, Robert L.  
 / APPLICANT: Ohad, Nir  
 / APPLICANT: Klyosue, Tomohiro  
 / APPLICANT: Yadegari, Ramin  
 / APPLICANT: Margosian, Linda  
 / APPLICANT: Harada, John  
 / APPLICANT: Goldberg, Robert B.  
 TITLE OF INVENTION: The Regents of the University of California  
 TITLE OF INVENTION: Fruit Development in Plants  
 TITLE OF INVENTION: Nucleic Acids That Control Seed and  
 FILE REFERENCE: 023070-086100US  
 CURRENT APPLICATION NUMBER: US/10/213,512  
 CURRENT FILING DATE: 2002-08-06  
 PRIOR APPLICATION NUMBER: US/09/177,206  
 PRIOR FILING DATE: 1998-10-22  
 PRIOR APPLICATION NUMBER: US 09/071,838  
 PRIOR FILING DATE: 1998-05-01  
 NUMBER OF SEQ ID NOS: 324  
 SOFTWARE: Patentin Ver. 2.0  
 / SEQ ID NO 108  
 / LENGTH: 12

TYPE: PRT  
ORGANISM: Arabidopsis sp.  
US-10-213-512-108

Query Match 25.4%; Score 29; DB 4; Length 12;  
Best Local Similarity 44.4%; Pred. No. 2.3e+03;  
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 11 NPKAPLYKR 19  
DB 1 NPKVTTFKK 9

RESULT 92  
US-10-304-443-111  
Sequence 111, Application US/10304443  
Publication No. US20030170229A1  
GENERAL INFORMATION:  
APPLICANT: SmithKline Beecham Biologicals s.a.  
APPLICANT: Peptide Therapeutics Ltd.  
TITLE OF INVENTION: Vaccine  
FILE REFERENCE: B45173C1P  
CURRENT APPLICATION NUMBER: US/10/304,443  
CURRENT FILING DATE: 2002-11-26  
PRIOR APPLICATION NUMBER: US/09/698,906A  
PRIOR FILING DATE: 2001-02-20  
NUMBER OF SEQ ID NOS: 121  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 111  
LENGTH: 12  
TYPE: PRT  
ORGANISM: Human peptide sequence  
US-10-304-443-111

Query Match 25.4%; Score 29; DB 4; Length 12;  
Best Local Similarity 83.3%; Pred. No. 2.3e+03;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 EYPSGR 8  
DB 3 EWPGR 8

RESULT 93  
US-10-362-527-317  
Sequence 317, Application US/10362527  
Publication No. US20040030106A1  
GENERAL INFORMATION:  
APPLICANT: Friede, Martin  
APPLICANT: Mason, Sean  
APPLICANT: Turnell, William Gordon  
APPLICANT: Vinals y De Basols, Carlota  
TITLE OF INVENTION: Vaccine Immunogens Comprising Disulphide Bridged Cyclised Peptide  
TITLE OF INVENTION: and Use Thereof in the Treatment of Allergies  
FILE REFERENCE: B45236  
CURRENT APPLICATION NUMBER: US/10/362,527  
CURRENT FILING DATE: 2003-02-21  
PRIOR APPLICATION NUMBER: PCT/EP01/09576  
PRIOR FILING DATE: 2001-08-17  
PRIOR APPLICATION NUMBER: GB 0020717.5  
PRIOR FILING DATE: 2000-08-22  
NUMBER OF SEQ ID NOS: 328  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 317  
LENGTH: 12  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Artificial variant of Homo sapiens IGE peptide  
US-10-362-527-317

Query Match 25.4%; Score 29; DB 4; Length 12;  
Best Local Similarity 83.3%; Pred. No. 2.3e+03;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 3 EYPSGR 8  
DB 3 EWPGR 8

RESULT 94  
US-10-415-389-24  
Sequence 24, Application US/10415389  
Publication No. US20040115220A1  
GENERAL INFORMATION:  
APPLICANT: De Basols, Carlota Vinals y  
APPLICANT: Vaccine  
FILE REFERENCE: B45251  
CURRENT APPLICATION NUMBER: US/10/415,389  
CURRENT FILING DATE: 2003-04-25  
PRIOR APPLICATION NUMBER: PCT/EP01/12932  
PRIOR FILING DATE: 2001-10-24  
PRIOR APPLICATION NUMBER: GB 0026334.3  
PRIOR FILING DATE: 2000-10-27  
NUMBER OF SEQ ID NOS: 34  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 24  
LENGTH: 12  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Human IGE peptide mimotope  
US-10-415-389-24

Query Match 25.4%; Score 29; DB 4; Length 12;  
Best Local Similarity 83.3%; Pred. No. 2.3e+03;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 EYPSGR 8  
DB 3 EWPGR 8

RESULT 95  
US-10-322-210-20  
Sequence 20, Application US/10322210  
Publication No. US20030147906A1  
GENERAL INFORMATION:  
APPLICANT: Friede, Martin  
APPLICANT: Mason, Sean  
APPLICANT: Turnell, William Gordon  
APPLICANT: Van Mechelen, Marcelle Paulette  
APPLICANT: Vinals y de Basols, Carlota  
TITLE OF INVENTION: Biotopes or Mimotopes Derived from the  
TITLE OF INVENTION: C-Epsilon-3 or C-Epsilon-4 Domains of IGE, Antagonists  
TITLE OF INVENTION: thereof, and their Therapeutic Uses  
FILE REFERENCE: B45173  
CURRENT APPLICATION NUMBER: US/10/322,210  
CURRENT FILING DATE: 2002-12-18  
PRIOR APPLICATION NUMBER: US/09/914,089  
PRIOR FILING DATE: 2001-08-22  
PRIOR APPLICATION NUMBER: GB 9904408.3  
PRIOR FILING DATE: 1999-02-25  
PRIOR APPLICATION NUMBER: GB 9917144.9  
PRIOR FILING DATE: 1999-07-21  
PRIOR APPLICATION NUMBER: GB 9918598.5  
PRIOR FILING DATE: 1999-08-07  
PRIOR APPLICATION NUMBER: GB 9918599.3  
PRIOR FILING DATE: 1999-08-07  
PRIOR APPLICATION NUMBER: GB 9918601.7  
PRIOR FILING DATE: 1999-08-07  
PRIOR APPLICATION NUMBER: GB 9918604.1  
PRIOR FILING DATE: 1999-08-07  
PRIOR APPLICATION NUMBER: GB 9918606.6  
PRIOR FILING DATE: 1999-08-07  
PRIOR APPLICATION NUMBER: GB 9925618.2

PRIOR FILING DATE: 1999-10-29  
NUMBER OF SEQ ID NOS: 86  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 20  
LENGTH: 13  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Chimeric  
US-10-322-210-20

Query Match 25.4%; Score 29; DB 4; Length 13;  
Best Local Similarity 83.3%; Pred. No. 2.5e+03;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 EYFGSR 8  
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DB 3 EWPGR 8

RESULT 96  
US-10-304-443-20  
Sequence 20, Application US/10304443  
Publication No. US20030170229A1  
GENERAL INFORMATION:  
APPLICANT: SmithKline Beecham Biologicals s.a.  
TITLE OF INVENTION: Vaccine  
FILE REFERENCE: B45173CIP  
CURRENT APPLICATION NUMBER: US/10/304,443  
CURRENT FILING DATE: 2002-11-26  
PRIOR APPLICATION NUMBER: US/09/698,906A  
PRIOR FILING DATE: 2001-02-20  
NUMBER OF SEQ ID NOS: 121  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 20  
LENGTH: 13  
TYPE: PRT  
ORGANISM: Human peptide sequence  
US-10-304-443-20

Query Match 25.4%; Score 29; DB 4; Length 13;  
Best Local Similarity 83.3%; Pred. No. 2.5e+03;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 EYFGSR 8  
|:||||  
DB 3 EWPGR 8

RESULT 97  
US-10-082-014-272  
Sequence 272, Application US/10082014  
Publication No. US2003018585A1  
GENERAL INFORMATION:  
APPLICANT: Birkett, Ashley J.  
TITLE OF INVENTION: IMMUNOGENIC HBC CHIMER PARTICLES STABILIZED WITH AN N-TERMINAL CY  
FILE REFERENCE: ICC-130.0 4564/85124  
CURRENT APPLICATION NUMBER: US/10/082,014  
CURRENT FILING DATE: 2002-02-22  
PRIOR APPLICATION NUMBER: 09/930,915  
PRIOR FILING DATE: 2001-08-15  
NUMBER OF SEQ ID NOS: 280  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 272  
LENGTH: 13  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-082-014-272

Query Match 25.4%; Score 29; DB 4; Length 13;  
Best Local Similarity 83.3%; Pred. No. 2.5e+03;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 EYFGSR 8  
|:||||  
DB 3 EWPGR 8

RESULT 98  
US-10-372-076-126  
Sequence 126, Application US/10372076  
Publication No. US20030198645A1  
GENERAL INFORMATION:  
APPLICANT: Page, Mark  
TITLE OF INVENTION: STABILIZED HBC CHIMER PARTICLES AS THERAPEUTIC VACCINE FOR  
FILE REFERENCE: 4564/87179  
CURRENT APPLICATION NUMBER: US/10/372,076  
CURRENT FILING DATE: 2003-02-21  
PRIOR APPLICATION NUMBER: 10/080,299  
PRIOR FILING DATE: 2002-02-21  
PRIOR APPLICATION NUMBER: 10/082,014  
PRIOR FILING DATE: 2002-02-22  
NUMBER OF SEQ ID NOS: 308  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 126  
LENGTH: 13  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-372-076-126

Query Match 25.4%; Score 29; DB 4; Length 13;  
Best Local Similarity 83.3%; Pred. No. 2.5e+03;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 EYFGSR 8  
|:||||  
DB 3 EWPGR 8

RESULT 99  
US-10-362-527-79  
Sequence 79, Application US/10362527  
Publication No. US20040030106A1  
GENERAL INFORMATION:  
APPLICANT: Friele, Martin  
APPLICANT: Mason, Sean  
APPLICANT: Turnell, William Gordon  
APPLICANT: Vinals y De Baesols, Carlota  
TITLE OF INVENTION: Vaccine Immunogens Comprising Disulphide Bridged Cyclised Peptid  
TITLE OF INVENTION: and Use Thereof in the Treatment of Allergies  
FILE REFERENCE: B45236  
CURRENT APPLICATION NUMBER: US/10/362,527  
CURRENT FILING DATE: 2003-02-21  
PRIOR APPLICATION NUMBER: PCT/EP01/09576  
PRIOR FILING DATE: 2001-08-17  
PRIOR APPLICATION NUMBER: GB 0020717.5  
PRIOR FILING DATE: 2000-08-22  
NUMBER OF SEQ ID NOS: 328  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 79  
LENGTH: 13  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-362-527-79

Query Match 25.4%; Score 29; DB 4; Length 13;  
Best Local Similarity 83.3%; Pred. No. 2.5e+03;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 EYFGSR 8  
|:||||  
DB 3 EWPGR 8

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RESULT 100
US-10-732-862A-140
; Sequence 140, Application US/10732862A
; Publication No. US20040146524A1
; GENERAL INFORMATION:
; APPLICANT: ASHLEY, BIRKETT J.
; APPLICANT: Lyons, Katelyne J.
; APPLICANT: Jay, Haron J.
; TITLE OF INVENTION: STABILIZED IMMUNOGENIC HBC CHIMER PARTICLES
; FILE REFERENCE: ICC-136.0 (4564-88881)
; CURRENT APPLICATION NUMBER: US/10/732,862A
; PRIOR FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: US 60/432,123
; PRIOR FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: US 10/274,616
; PRIOR FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US 10/080,299
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 10/082,014
; PRIOR FILING DATE: 2002-02-22
; NUMBER OF SEQ ID NOS: 455
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 140
; LENGTH: 13
; TYPE: PRF
; ORGANISM: Homo sapiens
US-10-732-862A-140

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Query Match      25.4%; Score 29; DB 4; Length 13;
Best Local Similarity 83.3%; Pred. No. 2.5e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY      3 EYPSGR 8
Db      3 EWPGRS 8

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Search completed: January 20, 2006, 19:45:36  
 Job time : 73.1154 secs

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OM protein - protein search, using bw model

Run on: January 20, 2006, 19:12:21 ; Search time 8.07692 Seconds  
(without alignments)  
25.093 Million cell updates/sec

Title: US-09-662-293-2

Perfect score: 114  
Sequence: 1 DYEPGSRILGNPKAPLYKRP 20

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 70606 seqs, 10133881 residues

Total number of hits satisfying chosen parameters: 34662

Minimum DB seq length: 0  
Maximum DB seq length: 20

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 100 summaries

Database :

Published Applications AA\_New:\*  
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2: /cgn2\_6/prodata/1/pubppaa/US06\_NEW\_PUB.pep:\*  
3: /cgn2\_6/prodata/1/pubppaa/US07\_NEW\_PUB.pep:\*  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	33	28.9	18	6	US-10-956-755A-6
2	31	27.2	14	7	US-11-054-515-2501
3	30	26.3	14	7	US-11-054-515-2378
4	30	26.3	20	6	US-10-889-197-30
5	29	25.4	11	7	US-11-033-365-51
6	29	25.4	11	7	US-11-033-365-52
7	29	25.4	11	7	US-11-033-365-54
8	29	25.4	14	7	US-11-054-515-2387
9	28	24.6	9	7	US-11-010-748A-408
10	28	24.6	9	7	US-11-010-748A-409
11	28	24.6	9	7	US-11-010-748A-410
12	28	24.6	9	7	US-11-010-748A-415
13	28	24.6	9	7	US-11-010-748A-416
14	28	24.6	9	7	US-11-010-748A-417
15	28	24.6	11	7	US-11-033-365-45
16	28	24.6	14	7	US-11-054-515-2535
17	28	24.6	14	7	US-11-054-515-2589
18	28	24.6	14	7	US-11-054-515-2592
19	28	24.6	17	7	US-11-010-748A-405
20	28	24.6	17	7	US-11-010-748A-412
21	27	23.7	9	7	US-11-010-748A-617
22	27	23.7	9	7	US-11-010-748A-621
23	27	23.7	9	7	US-11-010-748A-635
24	27	23.7	12	7	US-11-058-735-35
25	27	23.7	13	6	US-10-511-559-465

26	27	23.7	13	7	US-11-041-893-182	Sequence 182, App
27	27	23.7	14	7	US-11-054-515-2148	Sequence 2148, App
28	27	23.7	14	7	US-11-054-515-2382	Sequence 2382, App
29	27	23.7	14	7	US-11-054-515-2466	Sequence 2466, App
30	27	23.7	14	7	US-11-054-515-2486	Sequence 2486, App
31	27	23.7	14	7	US-11-054-515-2534	Sequence 2534, App
32	27	23.7	14	7	US-11-054-515-2544	Sequence 2544, App
33	27	23.7	14	7	US-11-054-515-2697	Sequence 2697, App
34	27	23.7	19	6	US-10-503-575-271	Sequence 271, App
35	26	22.8	9	7	US-11-105-668-20	Sequence 20, App1
36	26	22.8	9	7	US-11-110-374-331	Sequence 331, App
37	26	22.8	11	7	US-11-033-365-213	Sequence 48, App1
38	26	22.8	11	7	US-11-073-347-150	Sequence 150, App
39	26	22.8	11	7	US-11-073-347-151	Sequence 151, App
40	26	22.8	12	7	US-11-073-347-152	Sequence 152, App
41	26	22.8	13	7	US-11-073-347-153	Sequence 153, App
42	26	22.8	14	7	US-11-054-515-2683	Sequence 2683, App
43	26	22.8	14	7	US-11-054-515-2689	Sequence 2689, App
44	26	22.8	14	7	US-11-054-515-2720	Sequence 2720, App
45	26	22.8	14	7	US-11-073-347-153	Sequence 153, App
46	26	22.8	15	7	US-11-073-347-154	Sequence 154, App
47	26	22.8	16	7	US-11-073-347-156	Sequence 156, App
48	26	22.8	16	7	US-11-152-697-55	Sequence 55, App1
49	26	22.8	17	7	US-11-073-347-158	Sequence 158, App
50	26	22.8	18	7	US-11-220-439-4	Sequence 4, App1
51	26	22.8	18	7	US-11-220-439-22	Sequence 22, App1
52	26	22.8	18	7	US-11-220-439-24	Sequence 24, App1
53	26	22.8	19	7	US-11-220-439-10	Sequence 10, App1
54	26	22.8	19	7	US-11-220-439-25	Sequence 25, App1
55	26	22.8	20	7	US-11-133-665A-6	Sequence 6, App1
56	26	22.8	20	7	US-11-220-439-2	Sequence 2, App1
57	26	22.8	20	7	US-11-220-439-6	Sequence 6, App1
58	26	22.8	20	7	US-11-220-439-11	Sequence 11, App1
59	26	22.8	20	7	US-11-220-439-12	Sequence 12, App1
60	26	22.8	20	7	US-11-220-439-13	Sequence 13, App1
61	26	22.8	20	7	US-11-220-439-16	Sequence 16, App1
62	26	22.8	20	7	US-11-220-439-23	Sequence 23, App1
63	26	22.8	20	7	US-11-220-439-26	Sequence 26, App1
64	25.5	22.4	15	7	US-11-022-562-64	Sequence 64, App1
65	25.5	22.4	15	7	US-11-045-024-13027	Sequence 13027, App
66	25.5	22.4	17	7	US-11-045-024-13086	Sequence 13086, App
67	25.5	22.4	20	7	US-11-022-562-304	Sequence 304, App
68	25.5	22.4	20	7	US-11-022-562-305	Sequence 305, App
69	25	21.9	10	6	US-10-859-643-418	Sequence 418, App
70	25	21.9	10	6	US-10-859-643-429	Sequence 429, App
71	25	21.9	10	7	US-11-097-864-418	Sequence 418, App
72	25	21.9	10	7	US-11-097-864-429	Sequence 429, App
73	25	21.9	10	7	US-11-097-912-418	Sequence 418, App
74	25	21.9	10	7	US-11-097-912-429	Sequence 429, App
75	25	21.9	10	7	US-11-156-843-119	Sequence 119, App
76	25	21.9	10	7	US-11-045-024-2015	Sequence 2015, App
77	25	21.9	11	7	US-11-033-365-49	Sequence 49, App1
78	25	21.9	11	7	US-11-156-843-28	Sequence 28, App1
79	25	21.9	11	7	US-11-156-843-35	Sequence 35, App1
80	25	21.9	11	7	US-11-045-024-2247	Sequence 2247, App
81	25	21.9	11	7	US-11-045-024-5360	Sequence 5360, App
82	25	21.9	11	7	US-11-045-024-7847	Sequence 7847, App
83	25	21.9	13	6	US-10-511-559-464	Sequence 464, App
84	25	21.9	13	7	US-11-054-515-2470	Sequence 2470, App
85	25	21.9	13	7	US-11-006-119-35	Sequence 35, App1
86	25	21.9	14	6	US-10-983-174-6	Sequence 6, App1
87	25	21.9	14	6	US-10-719-150-1	Sequence 1, App1
88	25	21.9	14	7	US-11-054-515-2529	Sequence 2529, App
89	25	21.9	14	7	US-11-054-515-2691	Sequence 2691, App
90	25	21.9	15	6	US-10-719-150-4	Sequence 4, App1
91	25	21.9	15	7	US-11-045-024-13167	Sequence 13167, App
92	25	21.9	15	7	US-11-045-024-13259	Sequence 13259, App
93	25	21.9	15	7	US-11-045-024-13283	Sequence 13283, App
94	25	21.9	17	6	US-10-201-525-23	Sequence 23, App1
95	25	21.9	17	7	US-11-006-119-38	Sequence 38, App1
96	25	21.9	19	7	US-11-128-059-11	Sequence 11, App1
97	25	21.9	20	6	US-10-623-155-493	Sequence 493, App
98	24.5	21.5	15	7	US-11-045-024-13091	Sequence 13091, App

99 24 21.1 9 7 US-11-105-708-25 Sequence 25, Appl  
100 24 21.1 10 6 US-10-859-643-448 Sequence 448, App

## ALIGNMENTS

RESULT 1  
US-10-956-755A-6  
; Sequence 6, Application US/10956755A  
; Publication No. US20050282747A1  
; GENERAL INFORMATION:  
; APPLICANT: Clark, Richard A.  
; APPLICANT: Prestwich, Glenn  
; TITLE OF INVENTION: Methods and Compositions for Wound Healing  
; FILE REFERENCE: STONYB-09223  
; CURRENT APPLICATION NUMBER: US/10/956,755A  
; CURRENT FILING DATE: 2004-10-01  
; NUMBER OF SEQ ID NOS: 100  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 6  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
US-10-956-755A-6

Query Match 28.9%; Score 33; DB 6; Length 18;  
Best Local Similarity 42.1%; Pred. No. 20;  
Matches 8; Conservative 2; Mismatches 5; Indels 4; Gaps 1;

QY 2 YEYPSRLGNPKAPLYKRP 20  
DB 1 YEKPS---PREVVPRP 15

RESULT 2  
US-11-054-515-2501  
; Sequence 2501, Application US/11054515  
; Publication No. US2005023532A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys  
; FILE REFERENCE: PFS23P3  
; CURRENT APPLICATION NUMBER: US/11/054,515  
; CURRENT FILING DATE: 2005-02-10  
; PRIOR APPLICATION NUMBER: 60/543,296  
; PRIOR FILING DATE: 2004-02-11  
; PRIOR APPLICATION NUMBER: 60/580,347  
; PRIOR FILING DATE: 2004-06-18  
; PRIOR APPLICATION NUMBER: 10/293,418  
; PRIOR FILING DATE: 2002-11-14  
; PRIOR APPLICATION NUMBER: 60/331,469  
; PRIOR FILING DATE: 2001-11-16  
; PRIOR APPLICATION NUMBER: 60/340,817  
; PRIOR FILING DATE: 2001-12-19  
; PRIOR APPLICATION NUMBER: 09/880,748  
; PRIOR FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/293,499  
; PRIOR FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: 60/277,379  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/276,248  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/240,816  
; PRIOR FILING DATE: 2000-10-17  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 3247  
; SEQ ID NO 2501  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Homo sapiens

US-11-054-515-2501

Query Match 27.2%; Score 31; DB 7; Length 14;  
Best Local Similarity 83.3%; Pred. No. 32;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 12 PKAPLY 17  
DB 8 PKAPLY 13

RESULT 3  
US-11-054-515-2378  
; Sequence 2378, Application US/11054515  
; Publication No. US20050255532A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys  
; FILE REFERENCE: PFS23P3  
; CURRENT APPLICATION NUMBER: US/11/054,515  
; CURRENT FILING DATE: 2005-02-10  
; PRIOR APPLICATION NUMBER: 60/543,296  
; PRIOR FILING DATE: 2004-02-11  
; PRIOR APPLICATION NUMBER: 60/580,347  
; PRIOR FILING DATE: 2004-06-18  
; PRIOR APPLICATION NUMBER: 10/293,418  
; PRIOR FILING DATE: 2002-11-14  
; PRIOR APPLICATION NUMBER: 60/331,469  
; PRIOR FILING DATE: 2001-11-16  
; PRIOR APPLICATION NUMBER: 60/340,817  
; PRIOR FILING DATE: 2001-12-19  
; PRIOR APPLICATION NUMBER: 09/880,748  
; PRIOR FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/293,499  
; PRIOR FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: 60/277,379  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/276,248  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/240,816  
; PRIOR FILING DATE: 2000-10-17  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 3247  
; SEQ ID NO 2378  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-054-515-2378

Query Match 26.3%; Score 30; DB 7; Length 14;  
Best Local Similarity 83.3%; Pred. No. 45;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 12 PKAPLY 17  
DB 8 PKAPLY 13

RESULT 4  
US-10-889-197-30  
; Sequence 30, Application US/10889197  
; Publication No. US20050271689A1  
; GENERAL INFORMATION:  
; APPLICANT: HUANG, CHUN-MING  
; APPLICANT: ZHANG, JIANFENG  
; APPLICANT: TANG, DE-CHU  
; TITLE OF INVENTION: NOVEL TARGETS AND COMPOSITIONS FOR USE IN  
; TITLE OF INVENTION: DECONTAMINATION, IMMUNOPROPHYLAXIS, AND POST-EXPOSURE  
; TITLE OF INVENTION: THERAPY AGAINST ANTHRAX  
; FILE REFERENCE: 858610-2006.1  
; CURRENT APPLICATION NUMBER: US/10/889,197  
; CURRENT FILING DATE: 2004-07-12  
; PRIOR APPLICATION NUMBER: 60/486,369

/ PRIOR FILING DATE: 2003-07-11  
/ NUMBER OF SEQ ID NOS: 44  
/ SOFTWARE: PatentIn Ver. 3.2  
/ SEQ ID NO 30  
/ LENGTH: 20  
/ TYPE: PRT  
/ ORGANISM: Bacillus anthracis  
US-10-889-197-30

Query Match 26.3%; Score 30; DB 6; Length 20;  
Best Local Similarity 62.5%; Pred. No. 66;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 YPGSRLLG 11  
: ||| : ||  
Db 12 HPGSGVGN 19

RESULT 5  
US-11-033-365-51  
/ Sequence 51, Application US/11033365  
/ Publication No. US20050250678A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Neose Technologies Inc.  
/ APPLICANT: Defrees, Shawn  
/ APPLICANT: Zopf, David  
/ APPLICANT: Wang, ZhiGuang  
/ APPLICANT: Clausen, Henrik  
/ TITLE OF INVENTION: O-Linked Glycosylation of peptides  
/ FILE REFERENCE: 040853-01-5138  
/ CURRENT APPLICATION NUMBER: US/11/033,365  
/ PRIOR FILING DATE: 2005-01-10  
/ PRIOR APPLICATION NUMBER: 60/535,284  
/ PRIOR FILING DATE: 2004-01-08  
/ PRIOR APPLICATION NUMBER: 60/544,411  
/ PRIOR FILING DATE: 2004-02-12  
/ PRIOR APPLICATION NUMBER: 60/546,631  
/ PRIOR FILING DATE: 2004-02-20  
/ PRIOR APPLICATION NUMBER: 60/555,813  
/ PRIOR FILING DATE: 2004-03-23  
/ PRIOR APPLICATION NUMBER: 60/570,891  
/ PRIOR FILING DATE: 2004-05-12  
/ NUMBER OF SEQ ID NOS: 213  
/ SOFTWARE: PatentIn version 3.2  
/ SEQ ID NO 51  
/ LENGTH: 11  
/ TYPE: PRT  
/ ORGANISM: Homo sapiens  
US-11-033-365-51

Query Match 25.4%; Score 29; DB 7; Length 11;  
Best Local Similarity 75.0%; Pred. No. 50;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 9 LGNPKAPL 16  
: ||| : |||  
Db 1 LGTPWAPL 8

RESULT 6  
US-11-033-365-52  
/ Sequence 52, Application US/11033365  
/ Publication No. US20050250678A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Neose Technologies Inc.  
/ APPLICANT: Defrees, Shawn  
/ APPLICANT: Zopf, David  
/ APPLICANT: Wang, ZhiGuang  
/ APPLICANT: Clausen, Henrik  
/ TITLE OF INVENTION: O-Linked Glycosylation of peptides  
/ FILE REFERENCE: 040853-01-5138  
/ CURRENT APPLICATION NUMBER: US/11/033,365  
/ CURRENT FILING DATE: 2005-01-10

/ PRIOR APPLICATION NUMBER: 60/535,284  
/ PRIOR FILING DATE: 2004-01-08  
/ PRIOR APPLICATION NUMBER: 60/544,411  
/ PRIOR FILING DATE: 2004-02-12  
/ PRIOR APPLICATION NUMBER: 60/546,631  
/ PRIOR FILING DATE: 2004-02-20  
/ PRIOR APPLICATION NUMBER: 60/555,813  
/ PRIOR FILING DATE: 2004-03-23  
/ PRIOR APPLICATION NUMBER: 60/570,891  
/ PRIOR FILING DATE: 2004-05-12  
/ NUMBER OF SEQ ID NOS: 213  
/ SOFTWARE: PatentIn version 3.2  
/ SEQ ID NO 52  
/ LENGTH: 11  
/ TYPE: PRT  
/ ORGANISM: Homo sapiens  
US-11-033-365-52

Query Match 25.4%; Score 29; DB 7; Length 11;  
Best Local Similarity 75.0%; Pred. No. 50;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 9 LGNPKAPL 16  
: ||| : |||  
Db 1 LGTPWAPL 8

RESULT 7  
US-11-033-365-54  
/ Sequence 54, Application US/11033365  
/ Publication No. US20050250678A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Neose Technologies Inc.  
/ APPLICANT: Defrees, Shawn  
/ APPLICANT: Zopf, David  
/ APPLICANT: Wang, ZhiGuang  
/ APPLICANT: Clausen, Henrik  
/ TITLE OF INVENTION: O-Linked Glycosylation of peptides  
/ FILE REFERENCE: 040853-01-5138  
/ CURRENT APPLICATION NUMBER: US/11/033,365  
/ PRIOR FILING DATE: 2005-01-10  
/ PRIOR APPLICATION NUMBER: 60/535,284  
/ PRIOR FILING DATE: 2004-01-08  
/ PRIOR APPLICATION NUMBER: 60/544,411  
/ PRIOR FILING DATE: 2004-02-12  
/ PRIOR APPLICATION NUMBER: 60/546,631  
/ PRIOR FILING DATE: 2004-02-20  
/ PRIOR APPLICATION NUMBER: 60/555,813  
/ PRIOR FILING DATE: 2004-03-23  
/ PRIOR APPLICATION NUMBER: 60/570,891  
/ PRIOR FILING DATE: 2004-05-12  
/ NUMBER OF SEQ ID NOS: 213  
/ SOFTWARE: PatentIn version 3.2  
/ SEQ ID NO 54  
/ LENGTH: 11  
/ TYPE: PRT  
/ ORGANISM: Homo sapiens  
US-11-033-365-54

Query Match 25.4%; Score 29; DB 7; Length 11;  
Best Local Similarity 75.0%; Pred. No. 50;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 9 LGNPKAPL 16  
: ||| : |||  
Db 2 LGAPTAAPL 9

RESULT 8  
US-11-054-515-2387  
/ Sequence 2387, Application US/11054515  
/ Publication No. US20050255532A1  
/ GENERAL INFORMATION:

APPLICANT: Ruben et al.  
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys  
FILE REFERENCE: PR523P3  
CURRENT APPLICATION NUMBER: US/11/054,515  
CURRENT FILING DATE: 2005-02-10  
PRIOR APPLICATION NUMBER: 60/543,296  
PRIOR FILING DATE: 2004-02-11  
PRIOR APPLICATION NUMBER: 60/580,347  
PRIOR FILING DATE: 2004-06-18  
PRIOR APPLICATION NUMBER: 10/293,418  
PRIOR FILING DATE: 2002-11-14  
PRIOR APPLICATION NUMBER: 60/331,469  
PRIOR FILING DATE: 2001-11-16  
PRIOR APPLICATION NUMBER: 60/340,817  
PRIOR FILING DATE: 2001-12-19  
PRIOR APPLICATION NUMBER: 09/880,748  
PRIOR FILING DATE: 2001-06-15  
PRIOR APPLICATION NUMBER: 60/293,499  
PRIOR FILING DATE: 2001-05-25  
PRIOR APPLICATION NUMBER: 60/277,379  
PRIOR FILING DATE: 2001-03-21  
PRIOR APPLICATION NUMBER: 60/276,248  
PRIOR FILING DATE: 2001-03-16  
PRIOR APPLICATION NUMBER: 60/240,816  
PRIOR FILING DATE: 2000-10-17  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 3247  
SEQ ID NO 2387  
LENGTH: 14  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-11-054-515-2387

Query Match 25.4%; Score 29; DB 7; Length 14;  
Best Local Similarity 83.3%; Pred. No. 65;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 12 PRAPLY 17  
Db 8 PSHPLY 13

RESULT 9  
US-11-010-748A-408  
Sequence 408, Application US/11010748A  
Publication No. US2005024421A1  
GENERAL INFORMATION:  
APPLICANT: Merck Patent GmbH  
APPLICANT: STRITTMAYER, Wolfgang  
APPLICANT: MOLL, Heidrun  
APPLICANT: SCHARM, Burkhard  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING IMMUNE RESPONSE  
FILE REFERENCE: MER-136  
CURRENT APPLICATION NUMBER: US/11/010,748A  
CURRENT FILING DATE: 2004-12-13  
PRIOR APPLICATION NUMBER: PCT/EP03/06251  
PRIOR FILING DATE: 2003-06-13  
PRIOR APPLICATION NUMBER: EP02013423.5  
PRIOR FILING DATE: 2002-06-13  
NUMBER OF SEQ ID NOS: 926  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 408  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: HLA-binding peptide of Seq. No. 405  
US-11-010-748A-408

Query Match 24.6%; Score 28; DB 7; Length 9;  
Best Local Similarity 80.0%; Pred. No. 5.5e+04;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 YEYPG 6  
Db 1 YKYPG 5

RESULT 10  
US-11-010-748A-409  
Sequence 409, Application US/11010748A  
Publication No. US2005024421A1  
GENERAL INFORMATION:  
APPLICANT: Merck Patent GmbH  
APPLICANT: STRITTMAYER, Wolfgang  
APPLICANT: MOLL, Heidrun  
APPLICANT: SCHARM, Burkhard  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING IMMUNE RESPONSE  
FILE REFERENCE: MER-136  
CURRENT APPLICATION NUMBER: US/11/010,748A  
CURRENT FILING DATE: 2004-12-13  
PRIOR APPLICATION NUMBER: PCT/EP03/06251  
PRIOR FILING DATE: 2003-06-13  
PRIOR APPLICATION NUMBER: EP02013423.5  
PRIOR FILING DATE: 2002-06-13  
NUMBER OF SEQ ID NOS: 926  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 409  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: HLA-binding peptide of Seq. No. 405  
US-11-010-748A-409

Query Match 24.6%; Score 28; DB 7; Length 9;  
Best Local Similarity 80.0%; Pred. No. 5.5e+04;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Qy 2 YEYPG 6  
Db 3 YKYPG 7

RESULT 11  
US-11-010-748A-410  
Sequence 410, Application US/11010748A  
Publication No. US2005024421A1  
GENERAL INFORMATION:  
APPLICANT: Merck Patent GmbH  
APPLICANT: STRITTMAYER, Wolfgang  
APPLICANT: MOLL, Heidrun  
APPLICANT: SCHARM, Burkhard  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING IMMUNE RESPONSE  
FILE REFERENCE: MER-136  
CURRENT APPLICATION NUMBER: US/11/010,748A  
CURRENT FILING DATE: 2004-12-13  
PRIOR APPLICATION NUMBER: PCT/EP03/06251  
PRIOR FILING DATE: 2003-06-13  
PRIOR APPLICATION NUMBER: EP02013423.5  
PRIOR FILING DATE: 2002-06-13  
NUMBER OF SEQ ID NOS: 926  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 410  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: HLA-binding peptide of Seq. No. 405  
US-11-010-748A-410

Query Match 24.6%; Score 28; DB 7; Length 9;  
Best Local Similarity 80.0%; Pred. No. 5.5e+04;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Qy 2 YEYPG 6



Db 1 YKYPG 5

RESULT 12  
US-11-010-748A-415  
Sequence 415, Application US/11010748A  
Publication No. US20050244421A1  
GENERAL INFORMATION:  
APPLICANT: Merck Patent GmbH  
APPLICANT: STRITTMAYER, Wolfgang  
APPLICANT: MOLL, Heidrun  
APPLICANT: SCHARM, Burhard  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING IMMUNE RESPONSE  
FILE REFERENCE: MER-136  
CURRENT APPLICATION NUMBER: US/11/010,748A  
CURRENT FILING DATE: 2004-12-13  
PRIOR APPLICATION NUMBER: PCT/EP03/06251  
PRIOR FILING DATE: 2003-06-13  
PRIOR APPLICATION NUMBER: EP02013423.5  
PRIOR FILING DATE: 2002-06-13  
NUMBER OF SEQ ID NOS: 926  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 415  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: HLA-binding peptide of Seq. No. 412  
US-11-010-748A-415

Query Match 24.6%; Score 28; DB 7; Length 9;  
Best Local Similarity 80.0%; Pred. No. 5.5e+04;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 YKYPG 6  
|:|:|  
Db 1 YKYPG 5

RESULT 13  
US-11-010-748A-416  
Sequence 416, Application US/11010748A  
Publication No. US20050244421A1  
GENERAL INFORMATION:  
APPLICANT: Merck Patent GmbH  
APPLICANT: STRITTMAYER, Wolfgang  
APPLICANT: MOLL, Heidrun  
APPLICANT: SCHARM, Burhard  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING IMMUNE RESPONSE  
FILE REFERENCE: MER-136  
CURRENT APPLICATION NUMBER: US/11/010,748A  
CURRENT FILING DATE: 2004-12-13  
PRIOR APPLICATION NUMBER: PCT/EP03/06251  
PRIOR FILING DATE: 2003-06-13  
PRIOR APPLICATION NUMBER: EP02013423.5  
PRIOR FILING DATE: 2002-06-13  
NUMBER OF SEQ ID NOS: 926  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 416  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: HLA-binding peptide of Seq. No. 412  
US-11-010-748A-416

Query Match 24.6%; Score 28; DB 7; Length 9;  
Best Local Similarity 80.0%; Pred. No. 5.5e+04;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 YKYPG 6  
|:|:|

Db 3 YKYPG 7

RESULT 14  
US-11-010-748A-417  
Sequence 417, Application US/11010748A  
Publication No. US20050244421A1  
GENERAL INFORMATION:  
APPLICANT: Merck Patent GmbH  
APPLICANT: STRITTMAYER, Wolfgang  
APPLICANT: MOLL, Heidrun  
APPLICANT: SCHARM, Burhard  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING IMMUNE RESPONSE  
FILE REFERENCE: MER-136  
CURRENT APPLICATION NUMBER: US/11/010,748A  
CURRENT FILING DATE: 2004-12-13  
PRIOR APPLICATION NUMBER: PCT/EP03/06251  
PRIOR FILING DATE: 2003-06-13  
PRIOR APPLICATION NUMBER: EP02013423.5  
PRIOR FILING DATE: 2002-06-13  
NUMBER OF SEQ ID NOS: 926  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 417  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: HLA-binding peptide of Seq. No. 412  
US-11-010-748A-417

Query Match 24.6%; Score 28; DB 7; Length 9;  
Best Local Similarity 80.0%; Pred. No. 5.5e+04;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 YKYPG 6  
|:|:|  
Db 1 YKYPG 5

RESULT 15  
US-11-033-365-45  
Sequence 45, Application US/11033365  
Publication No. US20050250678A1  
GENERAL INFORMATION:  
APPLICANT: Neose Technologies Inc.  
APPLICANT: Defrees, Shawn  
APPLICANT: Zopf, David  
APPLICANT: Wang, ZhiGuang  
APPLICANT: Clausen, Henrik  
TITLE OF INVENTION: O-linked glycosylation of peptides  
FILE REFERENCE: 040853-01-5138  
CURRENT APPLICATION NUMBER: US/11/033,365  
CURRENT FILING DATE: 2005-01-10  
PRIOR APPLICATION NUMBER: 60/535,284  
PRIOR FILING DATE: 2004-01-08  
PRIOR APPLICATION NUMBER: 60/544,411  
PRIOR FILING DATE: 2004-02-12  
PRIOR APPLICATION NUMBER: 60/546,631  
PRIOR FILING DATE: 2004-02-20  
PRIOR APPLICATION NUMBER: 60/555,813  
PRIOR FILING DATE: 2004-03-23  
PRIOR APPLICATION NUMBER: 60/570,891  
PRIOR FILING DATE: 2004-05-12  
NUMBER OF SEQ ID NOS: 213  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 45  
LENGTH: 11  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-11-033-365-45

Query Match 24.6%; Score 28; DB 7; Length 11;  
Best Local Similarity 75.0%; Pred. No. 71;

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Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 9 LGNPKAPL 16
Db 1 LGIPTAPL 8

RESULT 16
US-11-054-515-2535
; Sequence 2535, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2535
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-2535

Query Match 24.6%; Score 28; DB 7; Length 14;
Best Local Similarity 83.3%; Pred. No. 92;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 12 PKAPLY 17
Db 8 PTPAPLY 13

RESULT 17
US-11-054-515-2589
; Sequence 2589, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2592
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-2592
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; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2589
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-2589

Query Match 24.6%; Score 28; DB 7; Length 14;
Best Local Similarity 83.3%; Pred. No. 92;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 12 PKAPLY 17
Db 8 PTPAPLY 13

RESULT 18
US-11-054-515-2592
; Sequence 2592, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2592
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-2592
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## RESULT 19

US-11-010-748A-405  
Sequence 405, Application US/11010748A  
Publication No. US20050244421A1  
GENERAL INFORMATION:  
APPLICANT: Merck Patent GmbH  
APPLICANT: STRITTMATTER, Wolfgang  
APPLICANT: MOLL, Heidrun  
APPLICANT: SCHARM, Burkhard  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING IMMUNE RESPONSE  
FILE REFERENCE: MER-136  
CURRENT APPLICATION NUMBER: US/11/010,748A  
CURRENT FILING DATE: 2004-12-13  
PRIOR APPLICATION NUMBER: PCT/EP03/06251  
PRIOR FILING DATE: 2003-06-13  
PRIOR APPLICATION NUMBER: EP02013423.5  
PRIOR FILING DATE: 2002-06-13  
NUMBER OF SEQ ID NOS: 926  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 405  
LENGTH: 17  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: CD42b peptide fragment  
US-11-010-748A-405

## Query Match

Best Local Similarity 24.6%; Score 28; DB 7; Length 17;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 YKYPG 6  
DB 3 YKYPG 7

## RESULT 20

US-11-010-748A-412  
Sequence 412, Application US/11010748A  
Publication No. US20050244421A1  
GENERAL INFORMATION:  
APPLICANT: Merck Patent GmbH  
APPLICANT: STRITTMATTER, Wolfgang  
APPLICANT: MOLL, Heidrun  
APPLICANT: SCHARM, Burkhard  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING IMMUNE RESPONSE  
FILE REFERENCE: MER-136  
CURRENT APPLICATION NUMBER: US/11/010,748A  
CURRENT FILING DATE: 2004-12-13  
PRIOR APPLICATION NUMBER: PCT/EP03/06251  
PRIOR FILING DATE: 2003-06-13  
PRIOR APPLICATION NUMBER: EP02013423.5  
PRIOR FILING DATE: 2002-06-13  
NUMBER OF SEQ ID NOS: 926  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 412  
LENGTH: 17  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: CD42b peptide fragment  
US-11-010-748A-412

## Query Match

Best Local Similarity 24.6%; Score 28; DB 7; Length 17;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 YKYPG 6  
DB 3 YKYPG 7

## RESULT 21

US-11-010-748A-617  
Sequence 617, Application US/11010748A  
Publication No. US20050244421A1  
GENERAL INFORMATION:  
APPLICANT: Merck Patent GmbH  
APPLICANT: STRITTMATTER, Wolfgang  
APPLICANT: MOLL, Heidrun  
APPLICANT: SCHARM, Burkhard  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING IMMUNE RESPONSE  
FILE REFERENCE: MER-136  
CURRENT APPLICATION NUMBER: US/11/010,748A  
CURRENT FILING DATE: 2004-12-13  
PRIOR APPLICATION NUMBER: PCT/EP03/06251  
PRIOR FILING DATE: 2003-06-13  
PRIOR APPLICATION NUMBER: EP02013423.5  
PRIOR FILING DATE: 2002-06-13  
NUMBER OF SEQ ID NOS: 926  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 617  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: HLA-binding peptide of Seq. No. 611  
US-11-010-748A-617

## Query Match

Best Local Similarity 23.7%; Score 27; DB 7; Length 9;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 PGSRLGNP 12  
DB 1 PGFPLGSP 8

## RESULT 22

US-11-010-748A-621  
Sequence 621, Application US/11010748A  
Publication No. US20050244421A1  
GENERAL INFORMATION:  
APPLICANT: Merck Patent GmbH  
APPLICANT: STRITTMATTER, Wolfgang  
APPLICANT: MOLL, Heidrun  
APPLICANT: SCHARM, Burkhard  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING IMMUNE RESPONSE  
FILE REFERENCE: MER-136  
CURRENT APPLICATION NUMBER: US/11/010,748A  
CURRENT FILING DATE: 2004-12-13  
PRIOR APPLICATION NUMBER: PCT/EP03/06251  
PRIOR FILING DATE: 2003-06-13  
PRIOR APPLICATION NUMBER: EP02013423.5  
PRIOR FILING DATE: 2002-06-13  
NUMBER OF SEQ ID NOS: 926  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 621  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: HLA-binding peptide of Seq. No. 611  
US-11-010-748A-621

## Query Match

Best Local Similarity 23.7%; Score 27; DB 7; Length 9;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 PGSRLGNP 12  
DB 2 PGFPLGSP 9

RESULT 23  
US-11-010-748A-635  
; Sequence 635, Application US/11010748A  
; Publication No. US2005024421A1  
; GENERAL INFORMATION:  
; APPLICANT: Merck Patent GmbH  
; APPLICANT: STRITTMAYER, Wolfgang  
; APPLICANT: MOLL, Heidrun  
; APPLICANT: SCHAM, Burkhard  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING IMMUNE RESPONSE  
; FILE REFERENCE: MER-136  
; CURRENT APPLICATION NUMBER: US/11/010,748A  
; CURRENT FILING DATE: 2004-12-13  
; PRIOR APPLICATION NUMBER: PCT/EP03/06251  
; PRIOR FILING DATE: 2003-06-13  
; PRIOR APPLICATION NUMBER: EP02013423.5  
; PRIOR FILING DATE: 2002-06-13  
; NUMBER OF SEQ ID NOS: 926  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO: 635  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: HLA-binding peptide of Seq. No. 611  
US-11-010-748A-635

Query Match 23.7%; Score 27; DB 7; Length 9;  
Best Local Similarity 62.5%; Pred. No. 5.5e+04;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 5 PGSRLGNP 12  
Db 1 PGEPPLGSP 8

RESULT 24  
US-11-058-735-35  
; Sequence 35, Application US/11058735  
; Publication No. US20050261475A1  
; GENERAL INFORMATION:  
; APPLICANT: TSENG, HUANG-CHUN  
; APPLICANT: TSAI, LI-HUEI  
; TITLE OF INVENTION: SOLID-PHASE CAPTURE-RELEASE-TAG METHODS FOR  
; TITLE OF INVENTION: PHOSPHOPROTEOMIC ANALYSES  
; FILE REFERENCE: HMV-094.01  
; CURRENT APPLICATION NUMBER: US/11/058,735  
; CURRENT FILING DATE: 2005-02-14  
; PRIOR APPLICATION NUMBER: 60/544,748  
; PRIOR FILING DATE: 2004-02-13  
; NUMBER OF SEQ ID NOS: 80  
; SOFTWARE: PatentIn Ver. 3.3  
; SEQ ID NO: 35  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-058-735-35

Query Match 23.7%; Score 27; DB 7; Length 12;  
Best Local Similarity 50.0%; Pred. No. 1.1e+02;  
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 10 GNPKAPLYKR 19  
Db 3 GTPTGTPSYR 12

RESULT 25  
US-10-511-559-465  
; Sequence 465, Application US/10511559  
; Publication No. US20050256304A1  
; GENERAL INFORMATION:  
; APPLICANT: JONES, Tlm

; APPLICANT: BAKER, Matthew  
; APPLICANT: CARR, Francis, J.  
; TITLE OF INVENTION: MODIFIED FACTOR VIII  
; FILE REFERENCE: MER-133  
; CURRENT APPLICATION NUMBER: US/10/511,559  
; CURRENT FILING DATE: 2004-10-15  
; PRIOR APPLICATION NUMBER: PCT/EP03/04063  
; PRIOR FILING DATE: 2003-04-17  
; PRIOR APPLICATION NUMBER: EP 02008712.8  
; PRIOR FILING DATE: 2002-04-18  
; PRIOR APPLICATION NUMBER: EP 03006554.4  
; PRIOR FILING DATE: 2003-03-24  
; NUMBER OF SEQ ID NOS: 1147  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO: 465  
; LENGTH: 13  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Potential Epitope of human Factor VIII  
US-10-511-559-465

Query Match 23.7%; Score 27; DB 6; Length 13;  
Best Local Similarity 45.5%; Pred. No. 1.2e+02;  
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 7 SRLGNPKAPLY 17  
Db 1 SSLGPPSMFVH 11

RESULT 26  
US-11-041-893-182  
; Sequence 182, Application US/11041893  
; Publication No. US20060002941A1  
; GENERAL INFORMATION:  
; APPLICANT: Mahalirae, Gregory G.  
; TITLE OF INVENTION: COMPOSITIONS COMPRISING IMMUNE RESPONSE  
; TITLE OF INVENTION: ALTERING AGENTS AND METHODS OF USE  
; FILE REFERENCE: 100123.401  
; CURRENT APPLICATION NUMBER: US/11/041,893  
; CURRENT FILING DATE: 2005-01-24  
; PRIOR APPLICATION NUMBER: US 60/616,855  
; PRIOR FILING DATE: 2004-10-06  
; PRIOR APPLICATION NUMBER: US 60/538,713  
; PRIOR FILING DATE: 2004-01-23  
; NUMBER OF SEQ ID NOS: 295  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO: 182  
; LENGTH: 13  
; TYPE: PRT  
; ORGANISM: Babesia bovis  
US-11-041-893-182

Query Match 23.7%; Score 27; DB 7; Length 13;  
Best Local Similarity 71.4%; Pred. No. 1.2e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 13 KAPLYKR 19  
Db 1 EAPWYKR 7

RESULT 27  
US-11-054-515-2148  
; Sequence 2148, Application US/11054515  
; Publication No. US20050255532A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Anticodules that Immunospecifically Bind Blys  
; FILE REFERENCE: PR523P3  
; CURRENT APPLICATION NUMBER: US/11/054,515  
; CURRENT FILING DATE: 2005-02-10

```
/ PRIOR APPLICATION NUMBER: 60/543,296
/ PRIOR FILING DATE: 2004-02-11
/ PRIOR APPLICATION NUMBER: 60/580,347
/ PRIOR FILING DATE: 2004-06-18
/ PRIOR APPLICATION NUMBER: 10/293,418
/ PRIOR FILING DATE: 2002-11-14
/ PRIOR APPLICATION NUMBER: 60/331,469
/ PRIOR FILING DATE: 2001-11-16
/ PRIOR APPLICATION NUMBER: 60/340,817
/ PRIOR FILING DATE: 2001-12-19
/ PRIOR APPLICATION NUMBER: 09/880,748
/ PRIOR FILING DATE: 2001-06-15
/ PRIOR APPLICATION NUMBER: 60/293,499
/ PRIOR FILING DATE: 2001-05-25
/ PRIOR APPLICATION NUMBER: 60/277,379
/ PRIOR FILING DATE: 2001-03-21
/ PRIOR APPLICATION NUMBER: 60/276,248
/ PRIOR FILING DATE: 2001-03-16
/ PRIOR APPLICATION NUMBER: 60/240,816
/ PRIOR FILING DATE: 2000-10-17
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 3247
/ SEQ ID NO 2148
/ LENGTH: 14
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-054-515-2148

Query Match      23.7% Score 27; DB 7; Length 14;
Best Local Similarity 83.3%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      12 PKAPL 17
DB      8 POSPLY 13

RESULT 28
US-11-054-515-2382
/ Sequence 2382, Application US/11054515
/ Publication No. US20050255532A1
/ GENERAL INFORMATION:
/ APPLICANT: Ruben et al.
/ TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
/ FILE REFERENCE: PF523P3
/ CURRENT APPLICATION NUMBER: US/11/054,515
/ PRIOR FILING DATE: 2005-02-10
/ PRIOR APPLICATION NUMBER: 60/543,296
/ PRIOR FILING DATE: 2004-02-11
/ PRIOR APPLICATION NUMBER: 60/580,347
/ PRIOR FILING DATE: 2004-06-18
/ PRIOR APPLICATION NUMBER: 10/293,418
/ PRIOR FILING DATE: 2002-11-14
/ PRIOR APPLICATION NUMBER: 60/331,469
/ PRIOR FILING DATE: 2001-11-16
/ PRIOR APPLICATION NUMBER: 60/340,817
/ PRIOR FILING DATE: 2001-12-19
/ PRIOR APPLICATION NUMBER: 09/880,748
/ PRIOR FILING DATE: 2001-06-15
/ PRIOR APPLICATION NUMBER: 60/293,499
/ PRIOR FILING DATE: 2001-05-25
/ PRIOR APPLICATION NUMBER: 60/277,379
/ PRIOR FILING DATE: 2001-03-21
/ PRIOR APPLICATION NUMBER: 60/276,248
/ PRIOR FILING DATE: 2001-03-16
/ PRIOR APPLICATION NUMBER: 60/240,816
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 3247
/ SEQ ID NO 3282
/ LENGTH: 14
/ TYPE: PRT
/ ORGANISM: Homo sapiens
```

```
US-11-054-515-2382

Query Match      23.7% Score 27; DB 7; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      12 PKAPL 16
DB      8 PKAPL 12

RESULT 29
US-11-054-515-2466
/ Sequence 2466, Application US/11054515
/ Publication No. US20050255532A1
/ GENERAL INFORMATION:
/ APPLICANT: Ruben et al.
/ TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
/ FILE REFERENCE: PF523P3
/ CURRENT APPLICATION NUMBER: US/11/054,515
/ PRIOR FILING DATE: 2005-02-10
/ PRIOR APPLICATION NUMBER: 60/543,296
/ PRIOR FILING DATE: 2004-02-11
/ PRIOR APPLICATION NUMBER: 60/580,347
/ PRIOR FILING DATE: 2004-06-18
/ PRIOR APPLICATION NUMBER: 10/293,418
/ PRIOR FILING DATE: 2002-11-14
/ PRIOR APPLICATION NUMBER: 60/331,469
/ PRIOR FILING DATE: 2001-11-16
/ PRIOR APPLICATION NUMBER: 60/340,817
/ PRIOR FILING DATE: 2001-12-19
/ PRIOR APPLICATION NUMBER: 09/880,748
/ PRIOR FILING DATE: 2001-06-15
/ PRIOR APPLICATION NUMBER: 60/293,499
/ PRIOR FILING DATE: 2001-05-25
/ PRIOR APPLICATION NUMBER: 60/277,379
/ PRIOR FILING DATE: 2001-03-21
/ PRIOR APPLICATION NUMBER: 60/276,248
/ PRIOR FILING DATE: 2001-03-16
/ PRIOR APPLICATION NUMBER: 60/240,816
/ PRIOR FILING DATE: 2000-10-17
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 3247
/ SEQ ID NO 2466
/ LENGTH: 14
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-054-515-2466

Query Match      23.7% Score 27; DB 7; Length 14;
Best Local Similarity 66.7%; Pred. No. 1.3e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      12 PKAPL 17
DB      8 POSPLY 13

RESULT 30
US-11-054-515-2486
/ Sequence 2486, Application US/11054515
/ Publication No. US20050255532A1
/ GENERAL INFORMATION:
/ APPLICANT: Ruben et al.
/ TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
/ FILE REFERENCE: PF523P3
/ CURRENT APPLICATION NUMBER: US/11/054,515
/ PRIOR FILING DATE: 2005-02-10
/ PRIOR APPLICATION NUMBER: 60/543,296
/ PRIOR FILING DATE: 2004-02-11
/ PRIOR APPLICATION NUMBER: 60/580,347
/ PRIOR FILING DATE: 2004-06-18
/ PRIOR APPLICATION NUMBER: 10/293,418
```

```
/ PRIOR FILING DATE: 2002-11-14
/ PRIOR APPLICATION NUMBER: 60/331,469
/ PRIOR FILING DATE: 2001-11-16
/ PRIOR APPLICATION NUMBER: 60/340,817
/ PRIOR FILING DATE: 2001-12-19
/ PRIOR APPLICATION NUMBER: 09/880,748
/ PRIOR FILING DATE: 2001-06-15
/ PRIOR APPLICATION NUMBER: 60/293,499
/ PRIOR FILING DATE: 2001-05-25
/ PRIOR APPLICATION NUMBER: 60/277,379
/ PRIOR FILING DATE: 2001-03-21
/ PRIOR APPLICATION NUMBER: 60/276,248
/ PRIOR FILING DATE: 2001-03-16
/ PRIOR APPLICATION NUMBER: 60/240,816
/ PRIOR FILING DATE: 2000-10-17
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 3247
/ SEQ ID NO 2486
/ LENGTH: 14
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-054-515-2486

Query Match      23.7%; Score 27; DB 7; Length 14;
Best Local Similarity 66.7%; Pred. No. 1.3e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      12 PKAPL 17
Db      8 PKAPL 13

RESULT 31
US-11-054-515-2534
/ Sequence 2534, Application US/11054515
/ Publication No. US20050255532A1
/ GENERAL INFORMATION:
/ APPLICANT: Ruben et al.
/ TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
/ FILE REFERENCE: PF523P3
/ CURRENT APPLICATION NUMBER: US/11/054,515
/ PRIOR FILING DATE: 2005-02-10
/ PRIOR APPLICATION NUMBER: 60/543,296
/ PRIOR FILING DATE: 2004-02-11
/ PRIOR APPLICATION NUMBER: 60/580,347
/ PRIOR FILING DATE: 2004-06-18
/ PRIOR APPLICATION NUMBER: 10/293,418
/ PRIOR FILING DATE: 2002-11-14
/ PRIOR APPLICATION NUMBER: 60/331,469
/ PRIOR FILING DATE: 2001-11-16
/ PRIOR APPLICATION NUMBER: 60/340,817
/ PRIOR FILING DATE: 2001-12-19
/ PRIOR APPLICATION NUMBER: 09/880,748
/ PRIOR FILING DATE: 2001-06-15
/ PRIOR APPLICATION NUMBER: 60/293,499
/ PRIOR FILING DATE: 2001-05-25
/ PRIOR APPLICATION NUMBER: 60/277,379
/ PRIOR FILING DATE: 2001-03-21
/ PRIOR APPLICATION NUMBER: 60/276,248
/ PRIOR FILING DATE: 2001-03-16
/ PRIOR APPLICATION NUMBER: 60/240,816
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 3247
/ SEQ ID NO 2534
/ LENGTH: 14
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-054-515-2534

Query Match      23.7%; Score 27; DB 7; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Qy      12 PKAPL 16
Db      8 PKAPL 12

RESULT 32
US-11-054-515-2544
/ Sequence 2544, Application US/11054515
/ Publication No. US20050255532A1
/ GENERAL INFORMATION:
/ APPLICANT: Ruben et al.
/ TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
/ FILE REFERENCE: PF523P3
/ CURRENT APPLICATION NUMBER: US/11/054,515
/ PRIOR FILING DATE: 2005-02-10
/ PRIOR APPLICATION NUMBER: 60/543,296
/ PRIOR FILING DATE: 2004-02-11
/ PRIOR APPLICATION NUMBER: 60/580,347
/ PRIOR FILING DATE: 2004-06-18
/ PRIOR APPLICATION NUMBER: 10/293,418
/ PRIOR FILING DATE: 2002-11-14
/ PRIOR APPLICATION NUMBER: 60/331,469
/ PRIOR FILING DATE: 2001-11-16
/ PRIOR APPLICATION NUMBER: 60/340,817
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 3247
/ SEQ ID NO 2544
/ LENGTH: 14
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-054-515-2544

Query Match      23.7%; Score 27; DB 7; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      12 PKAPL 16
Db      8 PKAPL 12

RESULT 33
US-11-054-515-2697
/ Sequence 2697, Application US/11054515
/ Publication No. US20050255532A1
/ GENERAL INFORMATION:
/ APPLICANT: Ruben et al.
/ TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
/ FILE REFERENCE: PF523P3
/ CURRENT APPLICATION NUMBER: US/11/054,515
/ PRIOR FILING DATE: 2005-02-10
/ PRIOR APPLICATION NUMBER: 60/543,296
/ PRIOR FILING DATE: 2004-02-11
/ PRIOR APPLICATION NUMBER: 60/580,347
/ PRIOR FILING DATE: 2004-06-18
/ PRIOR APPLICATION NUMBER: 10/293,418
/ PRIOR FILING DATE: 2002-11-14
/ PRIOR APPLICATION NUMBER: 60/331,469
/ PRIOR FILING DATE: 2001-11-16
/ PRIOR APPLICATION NUMBER: 60/340,817
/ PRIOR FILING DATE: 2001-12-19
```

```
/ PRIOR APPLICATION NUMBER: 09/880,748
/ PRIOR FILING DATE: 2001-06-15
/ PRIOR APPLICATION NUMBER: 60/293,499
/ PRIOR FILING DATE: 2001-05-25
/ PRIOR APPLICATION NUMBER: 60/277,379
/ PRIOR FILING DATE: 2001-03-21
/ PRIOR APPLICATION NUMBER: 60/276,248
/ PRIOR FILING DATE: 2001-03-16
/ PRIOR APPLICATION NUMBER: 60/240,816
/ PRIOR FILING DATE: 2000-10-17
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 3247
/ SEQ ID NO 2697
/ LENGTH: 14
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-054-515-2697

Query Match      23.7%; Score 27; DB 7; Length 14;
Best Local Similarity 83.3%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      12 PRAPLY 17
Db      8 PYAPLY 13

RESULT 34
US-10-503-575-271
/ Sequence 271, Application US/10503575
/ Publication No. US20050244823A1
/ GENERAL INFORMATION:
/ APPLICANT: Dijkstra, Jan Wouter
/ APPLICANT: van Veele, Petrus Antonius
/ TITLE OF INVENTION: NOVEL EPITOPES FOR CELLAC DISEASE AND AUTOIMMUNE DISEASES, METHOD
/ TITLE OF INVENTION: DETECTING THOSE AND NOVEL NON-ANTIGENIC FOOD COMPOUNDS
/ FILE REFERENCE: 2799/72843-PC-US
/ CURRENT APPLICATION NUMBER: US/10/503,575
/ CURRENT FILING DATE: 2004-08-04
/ PRIOR APPLICATION NUMBER: PCT/NL03/00077
/ PRIOR FILING DATE: 2003-02-04
/ PRIOR APPLICATION NUMBER: EP 02075456.0
/ PRIOR FILING DATE: 2002-02-04
/ NUMBER OF SEQ ID NOS: 340
/ SOFTWARE: Patent version 3.1
/ SEQ ID NO 271
/ LENGTH: 19
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-503-575-271

Query Match      23.7%; Score 27; DB 6; Length 19;
Best Local Similarity 55.6%; Pred. No. 1.8e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy      7 SRLGNPKAP 15
Db      4 SLUGSGQGP 12

RESULT 35
US-11-105-268-20
/ Sequence 20, Application US/11105268
/ Publication No. US20050260204A1
/ GENERAL INFORMATION:
/ APPLICANT: Allan, Christian
/ TITLE OF INVENTION: ANTI-IL-9 ANTIBODY FORMULATIONS AND USES THEREOF
/ FILE REFERENCE: 10271-126-999
/ CURRENT APPLICATION NUMBER: US/11/105,268
/ PRIOR FILING DATE: 2005-04-12
/ PRIOR APPLICATION NUMBER: 60/561,845
/ PRIOR FILING DATE: 2004-04-12
```

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/ NUMBER OF SEQ ID NOS: 60
/ SOFTWARE: Patent version 3.2
/ SEQ ID NO 20
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-105-268-20

Query Match      22.8%; Score 26; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 5.5e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 YETP 5
Db      4 YETP 7

RESULT 36
US-11-110-274-331
/ Sequence 331, Application US/11110274
/ Publication No. US2005026502A1
/ GENERAL INFORMATION:
/ APPLICANT: Merchere, Pascal G.
/ APPLICANT: Spittaels, Koenraad P. F.
/ TITLE OF INVENTION: Methods, Compositions and Compound Assays for Inhibiting
/ TITLE OF INVENTION: Amyloid-Beta Protein Production
/ FILE REFERENCE: P27,697-A USA
/ CURRENT APPLICATION NUMBER: US/11/110,274
/ CURRENT FILING DATE: 2005-04-20
/ PRIOR APPLICATION NUMBER: US 60/563,661
/ PRIOR FILING DATE: 2004-04-20
/ NUMBER OF SEQ ID NOS: 620
/ SOFTWARE: Patent version 3.3
/ SEQ ID NO 331
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-110-274-331

Query Match      22.8%; Score 26; DB 7; Length 9;
Best Local Similarity 80.0%; Pred. No. 5.5e+04;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 DYETP 5
Db      4 DYETP 8

RESULT 37
US-11-033-365-48
/ Sequence 48, Application US/11033365
/ Publication No. US20050250678A1
/ GENERAL INFORMATION:
/ APPLICANT: Neose Technologies Inc.
/ APPLICANT: Defters, Shawn
/ APPLICANT: Zopf, David
/ APPLICANT: Wang, Zhiguang
/ APPLICANT: Clausen, Henrik
/ TITLE OF INVENTION: O-linked Glycosylation of peptides
/ FILE REFERENCE: 040853-01-5138
/ CURRENT APPLICATION NUMBER: US/11/033,365
/ CURRENT FILING DATE: 2005-01-10
/ PRIOR APPLICATION NUMBER: 60/535,284
/ PRIOR FILING DATE: 2004-01-08
/ PRIOR APPLICATION NUMBER: 60/544,411
/ PRIOR FILING DATE: 2004-02-12
/ PRIOR APPLICATION NUMBER: 60/546,631
/ PRIOR FILING DATE: 2004-02-20
/ PRIOR APPLICATION NUMBER: 60/555,813
/ PRIOR FILING DATE: 2004-03-23
/ PRIOR APPLICATION NUMBER: 60/570,891
/ PRIOR FILING DATE: 2004-05-12
```

/ NUMBER OF SEQ ID NOS: 213  
/ SOFTWARE: PatentIn version 3.2  
/ SEQ ID NO 48  
/ LENGTH: 11  
/ TYPE: PRT  
/ ORGANISM: Homo sapiens  
US-11-033-365-48

Query Match 22.8%; Score 26; DB 7; Length 11;  
Best Local Similarity 62.5%; Pred. No. 1.5e+02;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 9 LGNPKAPL 16  
|||  
1 LGIPQPL 8

RESULT 38  
US-11-033-365-213  
/ Sequence 213, Application US/11033365  
/ Publication No. US20050250678A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Neose Technologies Inc.  
/ APPLICANT: DeFees, Shawn  
/ APPLICANT: Zopf, David  
/ APPLICANT: Wang, ZhiGuang  
/ APPLICANT: Clausen, Henrik  
/ TITLE OF INVENTION: O-linked Glycosylation of peptides  
/ FILE REFERENCE: 040853-01-5138  
/ CURRENT APPLICATION NUMBER: US/11/033,365  
/ CURRENT FILING DATE: 2005-01-10  
/ PRIOR APPLICATION NUMBER: 60/535,284  
/ PRIOR FILING DATE: 2004-01-08  
/ PRIOR APPLICATION NUMBER: 60/544,411  
/ PRIOR FILING DATE: 2004-02-12  
/ PRIOR APPLICATION NUMBER: 60/546,631  
/ PRIOR FILING DATE: 2004-02-20  
/ PRIOR APPLICATION NUMBER: 60/555,813  
/ PRIOR FILING DATE: 2004-03-23  
/ PRIOR APPLICATION NUMBER: 60/570,891  
/ PRIOR FILING DATE: 2004-05-12  
/ NUMBER OF SEQ ID NOS: 213  
/ SOFTWARE: PatentIn version 3.2  
/ SEQ ID NO 213  
/ LENGTH: 11  
/ TYPE: PRT  
/ ORGANISM: Homo sapiens  
US-11-033-365-213

Query Match 22.8%; Score 26; DB 7; Length 11;  
Best Local Similarity 75.0%; Pred. No. 1.5e+02;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 9 LGNPKAPL 16  
|||  
1 LGIPWAPL 8

RESULT 39  
US-11-073-347-150  
/ Sequence 150, Application US/11073347  
/ Publication No. US20050260234A1  
/ GENERAL INFORMATION:  
/ APPLICANT: SIMARD, John J. L.  
/ APPLICANT: DIAMOND, David C.  
/ TITLE OF INVENTION: ANTI-NEOVASCULATURE PREPARATIONS FOR  
/ FILE REFERENCE: MANNK.015C1  
/ CURRENT APPLICATION NUMBER: US/11/073,347  
/ PRIOR FILING DATE: 2005-03-04  
/ PRIOR APPLICATION NUMBER: 10/094,699  
/ PRIOR FILING DATE: 2002-03-07  
/ PRIOR APPLICATION NUMBER: 60/274,063

/ PRIOR FILING DATE: 2001-03-07  
/ NUMBER OF SEQ ID NOS: 159  
/ SOFTWARE: FastSeq for Windows Version 4.0  
/ SEQ ID NO 150  
/ LENGTH: 11  
/ TYPE: PRT  
/ ORGANISM: Homo sapien  
US-11-073-347-150

Query Match 22.8%; Score 26; DB 7; Length 11;  
Best Local Similarity 55.6%; Pred. No. 1.5e+02;  
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 9 LGNPKAPLY 17  
|||  
3 LGLPDRPFY 11

RESULT 40  
US-11-073-347-151  
/ Sequence 151, Application US/11073347  
/ Publication No. US20050260234A1  
/ GENERAL INFORMATION:  
/ APPLICANT: SIMARD, John J. L.  
/ APPLICANT: DIAMOND, David C.  
/ TITLE OF INVENTION: ANTI-NEOVASCULATURE PREPARATIONS FOR  
/ FILE REFERENCE: MANNK.015C1  
/ CURRENT APPLICATION NUMBER: US/11/073,347  
/ CURRENT FILING DATE: 2005-03-04  
/ PRIOR APPLICATION NUMBER: 10/094,699  
/ PRIOR FILING DATE: 2002-03-07  
/ PRIOR APPLICATION NUMBER: 60/274,063  
/ PRIOR FILING DATE: 2001-03-07  
/ NUMBER OF SEQ ID NOS: 159  
/ SOFTWARE: FastSeq for Windows Version 4.0  
/ SEQ ID NO 151  
/ LENGTH: 12  
/ TYPE: PRT  
/ ORGANISM: Homo sapien  
US-11-073-347-151

Query Match 22.8%; Score 26; DB 7; Length 12;  
Best Local Similarity 55.6%; Pred. No. 1.6e+02;  
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 9 LGNPKAPLY 17  
|||  
4 LGLPDRPFY 12

RESULT 41  
US-11-073-347-152  
/ Sequence 152, Application US/11073347  
/ Publication No. US20050260234A1  
/ GENERAL INFORMATION:  
/ APPLICANT: SIMARD, John J. L.  
/ APPLICANT: DIAMOND, David C.  
/ TITLE OF INVENTION: ANTI-NEOVASCULATURE PREPARATIONS FOR  
/ FILE REFERENCE: MANNK.015C1  
/ CURRENT APPLICATION NUMBER: US/11/073,347  
/ CURRENT FILING DATE: 2005-03-04  
/ PRIOR APPLICATION NUMBER: 10/094,699  
/ PRIOR FILING DATE: 2002-03-07  
/ PRIOR APPLICATION NUMBER: 60/274,063  
/ PRIOR FILING DATE: 2001-03-07  
/ NUMBER OF SEQ ID NOS: 159  
/ SOFTWARE: FastSeq for Windows Version 4.0  
/ SEQ ID NO 152  
/ LENGTH: 13  
/ TYPE: PRT  
/ ORGANISM: Homo sapien



US-11-073-347-152

Query Match 22.8%; Score 26; DB 7; Length 13;

Best Local Similarity 55.6%; Pred. No. 1.7e+02; Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 9 LGNPKAPLY 17  
| | | | |  
Db 5 LGLPDRPFY 13

RESULT 42

US-11-054-515-2683

; Sequence 2683, Application US/11054515  
; Publication No. US20050255532A1

; GENERAL INFORMATION:

; APPLICANT: Ruben et al.

; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys

; FILE REFERENCE: PFS23P3

; CURRENT APPLICATION NUMBER: US/11/054,515

; PRIOR FILING DATE: 2005-02-10

; PRIOR APPLICATION NUMBER: 60/543,296

; PRIOR FILING DATE: 2004-02-11

; PRIOR APPLICATION NUMBER: 60/580,347

; PRIOR FILING DATE: 2004-06-18

; PRIOR APPLICATION NUMBER: 10/293,418

; PRIOR FILING DATE: 2002-11-14

; PRIOR APPLICATION NUMBER: 60/331,469

; PRIOR FILING DATE: 2001-11-16

; PRIOR APPLICATION NUMBER: 60/340,817

; PRIOR FILING DATE: 2001-12-19

; PRIOR APPLICATION NUMBER: 09/880,748

; PRIOR FILING DATE: 2001-06-15

; PRIOR APPLICATION NUMBER: 60/293,499

; PRIOR FILING DATE: 2001-05-25

; PRIOR APPLICATION NUMBER: 60/277,379

; PRIOR FILING DATE: 2001-03-21

; PRIOR APPLICATION NUMBER: 60/276,248

; PRIOR FILING DATE: 2001-03-16

; PRIOR APPLICATION NUMBER: 60/240,816

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 3247

; SEQ ID NO 2683

; LENGTH: 14

; TYPE: PRT

; ORGANISM: Homo sapiens

US-11-054-515-2683

Query Match 22.8%; Score 26; DB 7; Length 14;

Best Local Similarity 66.7%; Pred. No. 1.9e+02; Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 12 PKAPLY 17  
| | | | |  
Db 8 PQAPLF 13

RESULT 43

US-11-054-515-2689

; Sequence 2689, Application US/11054515

; Publication No. US20050255532A1

; GENERAL INFORMATION:

; APPLICANT: Ruben et al.

; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys

; FILE REFERENCE: PFS23P3

; CURRENT APPLICATION NUMBER: US/11/054,515

; PRIOR FILING DATE: 2005-02-10

; PRIOR APPLICATION NUMBER: 60/543,296

; PRIOR FILING DATE: 2004-02-11

; PRIOR APPLICATION NUMBER: 60/580,347

; PRIOR FILING DATE: 2004-06-18

; PRIOR APPLICATION NUMBER: 10/293,418

; PRIOR FILING DATE: 2002-11-14

; PRIOR APPLICATION NUMBER: 60/331,469

; PRIOR FILING DATE: 2001-11-16

; PRIOR APPLICATION NUMBER: 60/340,817

; PRIOR FILING DATE: 2001-12-19

; PRIOR APPLICATION NUMBER: 09/880,748

; PRIOR FILING DATE: 2001-06-15

; PRIOR APPLICATION NUMBER: 60/293,499

; PRIOR FILING DATE: 2001-05-25

; PRIOR APPLICATION NUMBER: 60/277,379

; PRIOR FILING DATE: 2001-03-21

; PRIOR APPLICATION NUMBER: 60/276,248

; PRIOR FILING DATE: 2001-03-16

; PRIOR APPLICATION NUMBER: 60/240,816

; PRIOR FILING DATE: 2000-10-17

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 3247

; SEQ ID NO 2689

; LENGTH: 14

; TYPE: PRT

; ORGANISM: Homo sapiens

US-11-054-515-2689

Query Match 22.8%; Score 26; DB 7; Length 14;

Best Local Similarity 66.7%; Pred. No. 1.9e+02; Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 12 PKAPLY 17  
| | | | |  
Db 8 PQAPLF 13

RESULT 44

US-11-054-515-2720

; Sequence 2720, Application US/11054515

; Publication No. US20050255532A1

; GENERAL INFORMATION:

; APPLICANT: Ruben et al.

; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys

; FILE REFERENCE: PFS23P3

; CURRENT APPLICATION NUMBER: US/11/054,515

; PRIOR FILING DATE: 2005-02-10

; PRIOR APPLICATION NUMBER: 60/543,296

; PRIOR FILING DATE: 2004-02-11

; PRIOR APPLICATION NUMBER: 60/580,347

; PRIOR FILING DATE: 2004-06-18

; PRIOR APPLICATION NUMBER: 10/293,418

; PRIOR FILING DATE: 2002-11-14

; PRIOR APPLICATION NUMBER: 60/331,469

; PRIOR FILING DATE: 2001-11-16

; PRIOR APPLICATION NUMBER: 60/340,817

; PRIOR FILING DATE: 2001-12-19

; PRIOR APPLICATION NUMBER: 09/880,748

; PRIOR FILING DATE: 2001-06-15

; PRIOR APPLICATION NUMBER: 60/293,499

; PRIOR FILING DATE: 2001-05-25

; PRIOR APPLICATION NUMBER: 60/277,379

; PRIOR FILING DATE: 2001-03-21

; PRIOR APPLICATION NUMBER: 60/276,248

; PRIOR FILING DATE: 2001-03-16

; PRIOR APPLICATION NUMBER: 60/240,816

; PRIOR FILING DATE: 2000-10-17

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 3247

; SEQ ID NO 2720

; LENGTH: 14

; TYPE: PRT

; ORGANISM: Homo sapiens

US-11-054-515-2720

Query Match 22.8%; Score 26; DB 7; Length 14;

Best Local Similarity 66.7%; Pred. No. 1.9e+02; Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 12 PKAPLY 17  
| | | |  
Db 8 PSSPLY 13

## RESULT 45

US-11-073-347-153  
; Sequence 153, Application US/11073347  
; Publication No. US20050260234A1  
; GENERAL INFORMATION:  
; APPLICANT: SIMARD, John J. L.  
; APPLICANT: DIAMOND, David C.  
; TITLE OF INVENTION: ANTI-NEOVASCULATURE PREPARATIONS FOR  
; FILE REFERENCE: MANNK.015C1  
; CURRENT FILING DATE: 2005-03-04  
; PRIOR FILING DATE: 2002-03-07  
; PRIOR APPLICATION NUMBER: 10/094,699  
; PRIOR FILING DATE: 2001-03-07  
; NUMBER OF SEQ ID NOS: 159  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 153  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-11-073-347-153

Query Match 22.8%; Score 26; DB 7; Length 14;  
Best Local Similarity 55.6%; Pred. No. 1.9e+02;  
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 9 LGNPKAPLY 17  
| | | | |  
Db 6 LGLPDRPFY 14

## RESULT 46

US-11-073-347-154  
; Sequence 154, Application US/11073347  
; Publication No. US20050260234A1  
; GENERAL INFORMATION:  
; APPLICANT: SIMARD, John J. L.  
; APPLICANT: DIAMOND, David C.  
; TITLE OF INVENTION: ANTI-NEOVASCULATURE PREPARATIONS FOR  
; FILE REFERENCE: MANNK.015C1  
; CURRENT FILING DATE: 2005-03-04  
; PRIOR FILING DATE: 2002-03-07  
; PRIOR APPLICATION NUMBER: 10/094,699  
; PRIOR FILING DATE: 2001-03-07  
; NUMBER OF SEQ ID NOS: 159  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 154  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-11-073-347-154

Query Match 22.8%; Score 26; DB 7; Length 15;  
Best Local Similarity 55.6%; Pred. No. 2e+02;  
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 9 LGNPKAPLY 17  
| | | | |  
Db 7 LGLPDRPFY 15

## RESULT 47

US-11-073-347-156  
; Sequence 156, Application US/11073347  
; Publication No. US20050260234A1  
; GENERAL INFORMATION:  
; APPLICANT: SIMARD, John J. L.  
; APPLICANT: DIAMOND, David C.  
; TITLE OF INVENTION: ANTI-NEOVASCULATURE PREPARATIONS FOR  
; FILE REFERENCE: MANNK.015C1  
; CURRENT FILING DATE: 2005-03-04  
; PRIOR FILING DATE: 2002-03-07  
; PRIOR APPLICATION NUMBER: 10/094,699  
; PRIOR FILING DATE: 2001-03-07  
; NUMBER OF SEQ ID NOS: 159  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 156  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-11-073-347-156

Query Match 22.8%; Score 26; DB 7; Length 16;  
Best Local Similarity 55.6%; Pred. No. 2.2e+02;  
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 9 LGNPKAPLY 17  
| | | | |  
Db 8 LGLPDRPFY 16

## RESULT 48

US-11-152-697-55  
; Sequence 55, Application US/11152697  
; Publication No. US2006000367A1  
; GENERAL INFORMATION:  
; APPLICANT: Bristol-Myers Squibb Company  
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING A NOVEL HUMAN KUPFER CELL RECEPTOR  
; FILE REFERENCE: D0242 NP  
; CURRENT FILING DATE: 2005-06-14  
; PRIOR FILING DATE: 2004-06-15  
; NUMBER OF SEQ ID NOS: 63  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 55  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-152-697-55

Query Match 22.8%; Score 26; DB 7; Length 16;  
Best Local Similarity 45.5%; Pred. No. 2.2e+02;  
Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 6 GSRLGNPKAPL 16  
| | | | |  
Db 2 GDHLGNTNADI 12

## RESULT 49

US-11-073-347-158  
; Sequence 158, Application US/11073347  
; Publication No. US20050260234A1  
; GENERAL INFORMATION:  
; APPLICANT: SIMARD, John J. L.  
; APPLICANT: DIAMOND, David C.  
; TITLE OF INVENTION: ANTI-NEOVASCULATURE PREPARATIONS FOR  
; FILE REFERENCE: MANNK.015C1  
; CURRENT FILING DATE: 2005-03-04  
; PRIOR FILING DATE: 2002-03-07  
; PRIOR APPLICATION NUMBER: 10/094,699  
; PRIOR FILING DATE: 2001-03-07  
; NUMBER OF SEQ ID NOS: 159  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 158  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-11-073-347-158

Query Match 22.8%; Score 26; DB 7; Length 16;  
Best Local Similarity 45.5%; Pred. No. 2.2e+02;  
Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

```
/ CURRENT FILING DATE: 2005-03-04
/ PRIOR APPLICATION NUMBER: 10/094,699
/ PRIOR FILING DATE: 2002-03-07
/ PRIOR APPLICATION NUMBER: 60/274,063
/ PRIOR FILING DATE: 2001-03-07
/ NUMBER OF SEQ ID NOS: 159
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 158
/ LENGTH: 17
/ TYPE: PRT
/ ORGANISM: Homo sapien
US-11-073-347-158
```

```
Query Match      22.8%; Score 26; DB 7; Length 17;
Best Local Similarity 55.6%; Pred. No. 2.3e+02;
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
QY      9 LGNPKAPLY 17
      |||||
Db      9 LGLEPDRPFY 17
```

```
RESULT 50
US-11-220-439-4
/ Sequence 4, Application US/11220439
/ Publication No. US20060003938A1
/ GENERAL INFORMATION:
/ APPLICANT: Octavo Jr., Labzlo
/ TITLE OF INVENTION: Novel Pyrrhocoriclin-Derived Peptides, and Methods of
/ FILE REFERENCE: WST91BUSA
/ CURRENT APPLICATION NUMBER: US/11/220,439
/ PRIOR FILING DATE: 2005-09-07
/ PRIOR APPLICATION NUMBER: US/09/980,804
/ PRIOR FILING DATE: 2001-12-03
/ PRIOR APPLICATION NUMBER: 60/140,606
/ PRIOR FILING DATE: 1999-06-23
/ PRIOR APPLICATION NUMBER: 60/154,135
/ PRIOR FILING DATE: 1999-09-15
/ NUMBER OF SEQ ID NOS: 30
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 4
/ LENGTH: 18
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ NAME/KEY: MOD_RES
/ LOCATION: (1)-
/ OTHER INFORMATION: Asp in position 1 is modified by a
/ NAME/KEY: MOD_RES
/ LOCATION: (18)
/ OTHER INFORMATION: 1-aminocyclo-hexane carboxylic acid
/ OTHER INFORMATION: Arg in position 18 is modified by an amino linker
/ FEATURE:
/ OTHER INFORMATION: modification of Pyrrhocoriclin
US-11-220-439-4
```

```
Query Match      22.8%; Score 26; DB 7; Length 18;
Best Local Similarity 50.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      12 PKAPLYKR 19
      |||||
Db      11 PPRPIYKR 18
```

```
RESULT 51
US-11-220-439-22
/ Sequence 22, Application US/11220439
/ Publication No. US20060003938A1
/ GENERAL INFORMATION:
/ APPLICANT: Octavo Jr., Labzlo
```

```
/ TITLE OF INVENTION: Novel Pyrrhocoriclin-Derived Peptides, and Methods of
/ FILE REFERENCE: WST91BUSA
/ CURRENT APPLICATION NUMBER: US/11/220,439
/ PRIOR FILING DATE: 2005-09-07
/ PRIOR APPLICATION NUMBER: US/09/980,804
/ PRIOR FILING DATE: 2001-12-03
/ PRIOR APPLICATION NUMBER: 60/140,606
/ PRIOR FILING DATE: 1999-06-23
/ PRIOR APPLICATION NUMBER: 60/154,135
/ PRIOR FILING DATE: 1999-09-15
/ NUMBER OF SEQ ID NOS: 30
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 22
/ LENGTH: 18
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ NAME/KEY: MOD_RES
/ LOCATION: (1)-
/ OTHER INFORMATION: Asp in position 1 is modified by a
/ NAME/KEY: MOD_RES
/ LOCATION: (18)
/ OTHER INFORMATION: 1-aminocyclo-hexane carboxylic acid group
/ OTHER INFORMATION: Arg in position 18 is modified by a
/ FEATURE:
/ OTHER INFORMATION: beta-acetyl-2,3-diaminopropionic acid group
US-11-220-439-22
```

```
Query Match      22.8%; Score 26; DB 7; Length 18;
Best Local Similarity 50.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      12 PKAPLYKR 19
      |||||
Db      11 PPRPIYKR 18
```

```
RESULT 52
US-11-220-439-24
/ Sequence 24, Application US/11220439
/ Publication No. US20060003938A1
/ GENERAL INFORMATION:
/ APPLICANT: Octavo Jr., Labzlo
/ TITLE OF INVENTION: Novel Pyrrhocoriclin-Derived Peptides, and Methods of
/ FILE REFERENCE: WST91BUSA
/ CURRENT APPLICATION NUMBER: US/11/220,439
/ PRIOR FILING DATE: 2005-09-07
/ PRIOR APPLICATION NUMBER: US/09/980,804
/ PRIOR FILING DATE: 2001-12-03
/ PRIOR APPLICATION NUMBER: 60/140,606
/ PRIOR FILING DATE: 1999-06-23
/ PRIOR APPLICATION NUMBER: 60/154,135
/ PRIOR FILING DATE: 1999-09-15
/ NUMBER OF SEQ ID NOS: 30
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 24
/ LENGTH: 18
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ NAME/KEY: MOD_RES
/ LOCATION: (1)-
/ OTHER INFORMATION: Asp in position 1 is modified by a
/ NAME/KEY: MOD_RES
/ LOCATION: (18)
/ OTHER INFORMATION: 1-aminocyclo-hexane carboxylic acid group
/ OTHER INFORMATION: Arg in position 18 is modified by a
/ FEATURE:
/ OTHER INFORMATION: beta-acetyl-2,3-diamino propionic acid group
/ OTHER INFORMATION: modification of Pyrrhocoriclin
```

US-11-220-439-24

Query Match 22.8%; Score 26; DB 7; Length 18;  
Best Local Similarity 50.0%; Pred. No. 2.5e+02;  
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 12 PKAPLYKR 19  
DB 11 PPRPIYNR 18

RESULT 53

US-11-220-439-10  
; Sequence 10, Application US/11220439  
; Publication No. US20060003938A1  
; GENERAL INFORMATION:  
; APPLICANT: Octos Jr., Laszlo  
; TITLE OF INVENTION: Novel Pyrrhocoricin-Derived Peptides, and Methods of  
; FILE REFERENCE: MST91BUSA  
; CURRENT APPLICATION NUMBER: US/11/220,439  
; PRIOR FILING DATE: 2005-09-07  
; PRIOR APPLICATION NUMBER: 60/140,804  
; PRIOR FILING DATE: 2001-12-03  
; PRIOR APPLICATION NUMBER: 60/140,606  
; PRIOR FILING DATE: 1999-06-23  
; PRIOR APPLICATION NUMBER: 60/154,135  
; PRIOR FILING DATE: 1999-09-15  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 19  
; LENGTH: 19  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: MOD\_RES  
; LOCATION: (1)-  
; OTHER INFORMATION: Asp in position 1 is modified by a  
; OTHER INFORMATION: 1-aminocyclo-hexane carboxylic acid  
; FEATURE:  
; OTHER INFORMATION: modification of Pyrrhocoricin  
US-11-220-439-10

Query Match 22.8%; Score 26; DB 7; Length 19;  
Best Local Similarity 50.0%; Pred. No. 2.6e+02;  
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 12 PKAPLYKR 19  
DB 11 PPRPIYNR 18

RESULT 54

US-11-220-439-25  
; Sequence 25, Application US/11220439  
; Publication No. US20060003938A1  
; GENERAL INFORMATION:  
; APPLICANT: Octos Jr., Laszlo  
; TITLE OF INVENTION: Novel Pyrrhocoricin-Derived Peptides, and Methods of  
; FILE REFERENCE: MST91BUSA  
; CURRENT APPLICATION NUMBER: US/11/220,439  
; PRIOR FILING DATE: 2005-09-07  
; PRIOR APPLICATION NUMBER: 60/140,804  
; PRIOR FILING DATE: 2001-12-03  
; PRIOR APPLICATION NUMBER: 60/140,606  
; PRIOR FILING DATE: 1999-06-23  
; PRIOR APPLICATION NUMBER: 60/154,135  
; PRIOR FILING DATE: 1999-09-15  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 25  
; LENGTH: 19

; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: MOD\_RES  
; LOCATION: (19)  
; OTHER INFORMATION: Arg in position 19 is modified by a  
; OTHER INFORMATION: beta-acetyl-2,3-diamino propionic acid group  
; FEATURE:  
; OTHER INFORMATION: modification of Pyrrhocoricin  
US-11-220-439-25

Query Match 22.8%; Score 26; DB 7; Length 19;  
Best Local Similarity 50.0%; Pred. No. 2.6e+02;  
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 12 PKAPLYKR 19  
DB 12 PPRPIYNR 19

RESULT 55

US-11-133-465A-6  
; Sequence 6, Application US/1133465A  
; Publication No. US20050277593A1  
; GENERAL INFORMATION:  
; APPLICANT: Cross, Anne  
; TITLE OF INVENTION: Dieckgraefe, Brian  
; FILE REFERENCE: 004255,00029  
; CURRENT APPLICATION NUMBER: US/11/133,465A  
; PRIOR FILING DATE: 2005-05-20  
; PRIOR APPLICATION NUMBER: 60/573,340  
; PRIOR FILING DATE: 2004-05-24  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 6  
; LENGTH: 20  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-133-465A-6

Query Match 22.8%; Score 26; DB 7; Length 20;  
Best Local Similarity 45.5%; Pred. No. 2.8e+02;  
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 3 EYPSRLGNPK 13  
DB 6 ELPSARIRCPK 16

RESULT 56

US-11-220-439-2  
; Sequence 2, Application US/11220439  
; Publication No. US20060003938A1  
; GENERAL INFORMATION:  
; APPLICANT: Octos Jr., Laszlo  
; TITLE OF INVENTION: Novel Pyrrhocoricin-Derived Peptides, and Methods of  
; FILE REFERENCE: MST91BUSA  
; CURRENT APPLICATION NUMBER: US/11/220,439  
; PRIOR FILING DATE: 2005-09-07  
; PRIOR APPLICATION NUMBER: 60/140,804  
; PRIOR FILING DATE: 2001-12-03  
; PRIOR APPLICATION NUMBER: 60/140,606  
; PRIOR FILING DATE: 1999-06-23  
; PRIOR APPLICATION NUMBER: 60/154,135  
; PRIOR FILING DATE: 1999-09-15  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 20  
; TYPE: PRT  
; ORGANISM: Pyrrhocoricin

```
/
/ FEATURE:
/ NAME/KEY: MOD_RES
/ LOCATION: (11)
/ OTHER INFORMATION: Thr in position 11 is modified with Gal-GalNAc
US-11-220-439-2

Query Match          22.8%; Score 26; DB 7; Length 20;
Best Local Similarity 50.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      12 PKAPLYR 19
      | | | |
      | | | |
Db      12 PPRPIYR 19

RESULT 57
US-11-220-439-6
/ Sequence 6, Application US/11220439
/ Publication No. US20060003938A1
/ GENERAL INFORMATION:
/ APPLICANT: Oltos Jr., Laszlo
/ TITLE OF INVENTION: Novel Pyrrhocoriclin-Derived Peptides, and Methods of
/ FILE REFERENCE: MST91BUSA
/ CURRENT APPLICATION NUMBER: US/11/220,439
/ CURRENT FILING DATE: 2005-09-07
/ PRIOR APPLICATION NUMBER: US/09/980,804
/ PRIOR FILING DATE: 2001-12-03
/ PRIOR APPLICATION NUMBER: 60/140,606
/ PRIOR FILING DATE: 1999-06-23
/ PRIOR APPLICATION NUMBER: 60/154,135
/ PRIOR FILING DATE: 1999-09-15
/ NUMBER OF SEQ ID NOS: 30
/ SOFTWARE: Patentln Ver. 2.1
/ SEQ ID NO 6
/ LENGTH: 20
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: modification of Pyrrhocoriclin
US-11-220-439-6

Query Match          22.8%; Score 26; DB 7; Length 20;
Best Local Similarity 50.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      12 PKAPLYR 19
      | | | |
      | | | |
Db      12 PPRPIYR 19

RESULT 58
US-11-220-439-11
/ Sequence 11, Application US/11220439
/ Publication No. US20060003938A1
/ GENERAL INFORMATION:
/ APPLICANT: Oltos Jr., Laszlo
/ TITLE OF INVENTION: Novel Pyrrhocoriclin-Derived Peptides, and Methods of
/ FILE REFERENCE: MST91BUSA
/ CURRENT APPLICATION NUMBER: US/11/220,439
/ CURRENT FILING DATE: 2005-09-07
/ PRIOR APPLICATION NUMBER: US/09/980,804
/ PRIOR FILING DATE: 2001-12-03
/ PRIOR APPLICATION NUMBER: 60/140,606
/ PRIOR FILING DATE: 1999-06-23
/ PRIOR APPLICATION NUMBER: 60/154,135
/ PRIOR FILING DATE: 1999-09-15
/ NUMBER OF SEQ ID NOS: 30
/ SOFTWARE: Patentln Ver. 2.1
/ SEQ ID NO 11
/ LENGTH: 20
/ TYPE: PRT
```

```
/
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ NAME/KEY: MOD_RES
/ LOCATION: (1)
/ OTHER INFORMATION: ACETYLATION
/ NAME/KEY: MOD_RES
/ LOCATION: (11)
/ OTHER INFORMATION: Thr in position 11 is modified with Gal-GalNAc
/ FEATURE:
/ OTHER INFORMATION: modification of Pyrrhocoriclin
US-11-220-439-11

Query Match          22.8%; Score 26; DB 7; Length 20;
Best Local Similarity 50.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      12 PKAPLYR 19
      | | | |
      | | | |
Db      12 PPRPIYR 19

RESULT 59
US-11-220-439-12
/ Sequence 12, Application US/11220439
/ Publication No. US20060003938A1
/ GENERAL INFORMATION:
/ APPLICANT: Oltos Jr., Laszlo
/ TITLE OF INVENTION: Novel Pyrrhocoriclin-Derived Peptides, and Methods of
/ FILE REFERENCE: MST91BUSA
/ CURRENT APPLICATION NUMBER: US/11/220,439
/ CURRENT FILING DATE: 2005-09-07
/ PRIOR APPLICATION NUMBER: US/09/980,804
/ PRIOR FILING DATE: 2001-12-03
/ PRIOR APPLICATION NUMBER: 60/140,606
/ PRIOR FILING DATE: 1999-06-23
/ PRIOR APPLICATION NUMBER: 60/154,135
/ PRIOR FILING DATE: 1999-09-15
/ NUMBER OF SEQ ID NOS: 30
/ SOFTWARE: Patentln Ver. 2.1
/ SEQ ID NO 12
/ LENGTH: 20
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ NAME/KEY: MOD_RES
/ LOCATION: (1)
/ OTHER INFORMATION: ACETYLATION
/ NAME/KEY: MOD_RES
/ LOCATION: (20)
/ OTHER INFORMATION: Arg in position 20 is modified by an imide group
/ FEATURE:
/ OTHER INFORMATION: modification of Pyrrhocoriclin
US-11-220-439-12

Query Match          22.8%; Score 26; DB 7; Length 20;
Best Local Similarity 50.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      12 PKAPLYR 19
      | | | |
      | | | |
Db      13 PPRPIYR 20

RESULT 60
US-11-220-439-13
/ Sequence 13, Application US/11220439
/ Publication No. US20060003938A1
/ GENERAL INFORMATION:
/ APPLICANT: Oltos Jr., Laszlo
/ TITLE OF INVENTION: Novel Pyrrhocoriclin-Derived Peptides, and Methods of
/ FILE REFERENCE: MST91BUSA
```

;/ CURRENT APPLICATION NUMBER: US/11/220,439  
;/ CURRENT FILING DATE: 2005-09-07  
;/ PRIOR APPLICATION NUMBER: US/09/980,804  
;/ PRIOR FILING DATE: 2001-12-03  
;/ PRIOR APPLICATION NUMBER: 60/140,606  
;/ PRIOR FILING DATE: 1999-06-23  
;/ PRIOR APPLICATION NUMBER: 60/154,135  
;/ PRIOR FILING DATE: 1999-09-15  
;/ NUMBER OF SEQ ID NOS: 30  
;/ SOFTWARE: PatentIn Ver. 2.1  
;/ SEQ ID NO 13  
;/ LENGTH: 20  
;/ TYPE: PRT  
;/ ORGANISM: Artificial Sequence  
;/ FEATURE:  
;/ NAME/KEY: MOD\_RES  
;/ LOCATION: (1)  
;/ OTHER INFORMATION: ACETYLTATION  
;/ NAME/KEY: MOD\_RES  
;/ LOCATION: (20)  
;/ OTHER INFORMATION: Arg in position 20 is modified by a  
;/ OTHER INFORMATION: beta-acetyl-2,3-diamino propionic acid group  
;/ FEATURE:  
;/ OTHER INFORMATION: modification of Pyrrhocoricin  
;/ US-11-220-439-13

Query Match 22.8%; Score 26; DB 7; Length 20;  
Best Local Similarity 50.0%; Pred. No. 2.8e+02;  
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 12 PKAPLYKR 19  
| | | | |  
Db 13 PPRPLYNR 20

RESULT 61  
US-11-220-439-16  
;/ Sequence 16, Application US/11220439  
;/ Publication No. US20060003938A1  
;/ GENERAL INFORMATION:  
;/ APPLICANT: Ocvos Jr., Laszlo  
;/ TITLE OF INVENTION: Novel Pyrrhocoricin-Derived Peptides, and Methods of  
;/ FILE REFERENCE: WST91BUSA  
;/ CURRENT APPLICATION NUMBER: US/11/220,439  
;/ CURRENT FILING DATE: 2005-09-07  
;/ PRIOR APPLICATION NUMBER: US/09/980,804  
;/ PRIOR FILING DATE: 2001-12-03  
;/ PRIOR APPLICATION NUMBER: 60/140,606  
;/ PRIOR FILING DATE: 1999-06-23  
;/ PRIOR APPLICATION NUMBER: 60/154,135  
;/ PRIOR FILING DATE: 1999-09-15  
;/ NUMBER OF SEQ ID NOS: 30  
;/ SOFTWARE: PatentIn Ver. 2.1  
;/ SEQ ID NO 16  
;/ LENGTH: 20  
;/ TYPE: PRT  
;/ ORGANISM: Artificial Sequence  
;/ FEATURE:  
;/ NAME/KEY: MOD\_RES  
;/ LOCATION: (1)  
;/ OTHER INFORMATION: Val in position 1 is in the D configuration  
;/ NAME/KEY: MOD\_RES  
;/ LOCATION: (20)  
;/ OTHER INFORMATION: Asn in position 20 is in the D configuration  
;/ FEATURE:  
;/ OTHER INFORMATION: modification of Pyrrhocoricin  
;/ US-11-220-439-16

Query Match 22.8%; Score 26; DB 7; Length 20;  
Best Local Similarity 50.0%; Pred. No. 2.8e+02;  
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 12 PKAPLYKR 19  
| | | | |  
Db 12 PPRPLYNR 19

RESULT 62  
US-11-220-439-23  
;/ Sequence 23, Application US/11220439  
;/ Publication No. US20060003938A1  
;/ GENERAL INFORMATION:  
;/ APPLICANT: Ocvos Jr., Laszlo  
;/ TITLE OF INVENTION: Novel Pyrrhocoricin-Derived Peptides, and Methods of  
;/ FILE REFERENCE: WST91BUSA  
;/ CURRENT APPLICATION NUMBER: US/11/220,439  
;/ CURRENT FILING DATE: 2005-09-07  
;/ PRIOR APPLICATION NUMBER: US/09/980,804  
;/ PRIOR FILING DATE: 2001-12-03  
;/ PRIOR APPLICATION NUMBER: 60/140,606  
;/ PRIOR FILING DATE: 1999-06-23  
;/ PRIOR APPLICATION NUMBER: 60/154,135  
;/ PRIOR FILING DATE: 1999-09-15  
;/ NUMBER OF SEQ ID NOS: 30  
;/ SOFTWARE: PatentIn Ver. 2.1  
;/ SEQ ID NO 23  
;/ LENGTH: 20  
;/ TYPE: PRT  
;/ ORGANISM: Artificial Sequence  
;/ FEATURE:  
;/ NAME/KEY: MOD\_RES  
;/ LOCATION: (1)  
;/ OTHER INFORMATION: ACETYLTATION  
;/ NAME/KEY: MOD\_RES  
;/ LOCATION: (20)  
;/ OTHER INFORMATION: Arg in position 20 is modified by a  
;/ OTHER INFORMATION: beta-acetyl-2,3-diamino propionic acid group  
;/ FEATURE:  
;/ OTHER INFORMATION: modification of Pyrrhocoricin  
;/ US-11-220-439-23

Query Match 22.8%; Score 26; DB 7; Length 20;  
Best Local Similarity 50.0%; Pred. No. 2.8e+02;  
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 12 PKAPLYKR 19  
| | | | |  
Db 13 PPRPLYNR 20

RESULT 63  
US-11-220-439-26  
;/ Sequence 26, Application US/11220439  
;/ Publication No. US20060003938A1  
;/ GENERAL INFORMATION:  
;/ APPLICANT: Ocvos Jr., Laszlo  
;/ TITLE OF INVENTION: Novel Pyrrhocoricin-Derived Peptides, and Methods of  
;/ FILE REFERENCE: WST91BUSA  
;/ CURRENT APPLICATION NUMBER: US/11/220,439  
;/ CURRENT FILING DATE: 2005-09-07  
;/ PRIOR APPLICATION NUMBER: US/09/980,804  
;/ PRIOR FILING DATE: 2001-12-03  
;/ PRIOR APPLICATION NUMBER: 60/140,606  
;/ PRIOR FILING DATE: 1999-06-23  
;/ PRIOR APPLICATION NUMBER: 60/154,135  
;/ PRIOR FILING DATE: 1999-09-15  
;/ NUMBER OF SEQ ID NOS: 30  
;/ SOFTWARE: PatentIn Ver. 2.1  
;/ SEQ ID NO 26  
;/ LENGTH: 20  
;/ TYPE: PRT  
;/ ORGANISM: Artificial Sequence  
;/ FEATURE:

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/ NAME/KEY: PEPTIDE
/ LOCATION: (1) ..(20)
/ OTHER INFORMATION: D configuration
/ FEATURE:
/ OTHER INFORMATION: modification of Pyrrhococcin
US-11-220-439-26

Query Match          22.4%; Score 25.5; DB 7; Length 20;
Best Local Similarity 50.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      12 PKAPLYKR 19
Db      12 PPRPIYKR 19

RESULT 64
US-11-022-562-64
/ Sequence 64, Application US/11022562
/ Publication No. US20050249742A1
/ GENERAL INFORMATION:
/ APPLICANT: Ruprecht, Ruth M.
/ APPLICANT: Shisong, Jiansg
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING
/ TITLE OF INVENTION: A CYTOTOXIC T LYMPHOCYTE IMMUNE RESPONSE
/ FILE REFERENCE: DPN-043CN
/ CURRENT APPLICATION NUMBER: US/11/022,562
/ CURRENT FILING DATE: 2004-12-22
/ PRIOR APPLICATION NUMBER: PCT/US03/20322
/ PRIOR FILING DATE: 2003-06-27
/ PRIOR APPLICATION NUMBER: 60/392718
/ PRIOR FILING DATE: 2002-06-27
/ NUMBER OF SEQ ID NOS: 340
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 64
/ LENGTH: 15
/ TYPE: PRT
/ ORGANISM: Human Immunodeficiency Virus
US-11-022-562-64

Query Match          22.4%; Score 25.5; DB 7; Length 15;
Best Local Similarity 50.0%; Pred. No. 2.4e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 3; Gaps 1;

QY      11 NPKAP---LYKR 19
Db      1 NPEIPVGEIYKR 12

RESULT 65
US-11-045-024-13027
/ Sequence 13027, Application US/11045024
/ Publication No. US20050271676A1
/ GENERAL INFORMATION:
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Livingston, Brian
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Baker, Denise Marie
/ APPLICANT: Celis, Basteban
/ APPLICANT: Kubo, Ralph
/ APPLICANT: Grey, Howard M.
/ APPLICANT: BpImmune Inc.
/ TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
/ TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
/ FILE REFERENCE: 2060.0040007
/ CURRENT APPLICATION NUMBER: US/11/045,024
/ CURRENT FILING DATE: 2005-01-28
/ PRIOR APPLICATION NUMBER: US 09/412,863
/ PRIOR FILING DATE: 1999-10-05
/ PRIOR APPLICATION NUMBER: US 08/027,146
/ PRIOR FILING DATE: 1993-03-05
```

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/ PRIOR APPLICATION NUMBER: US 08/073,205
/ PRIOR FILING DATE: 1993-06-04
/ PRIOR APPLICATION NUMBER: US 08/103,396
/ PRIOR FILING DATE: 1993-08-06
/ PRIOR APPLICATION NUMBER: US 08/159,184
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/159,339
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/205,713
/ PRIOR FILING DATE: 1994-03-04
/ PRIOR APPLICATION NUMBER: US 08/347,610
/ PRIOR FILING DATE: 1994-12-01
/ NUMBER OF SEQ ID NOS: 14528
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 13027
/ LENGTH: 15
/ TYPE: PRT
/ ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-13027

Query Match          22.4%; Score 25.5; DB 7; Length 15;
Best Local Similarity 50.0%; Pred. No. 2.4e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 3; Gaps 1;

QY      11 NPKAP---LYKR 19
Db      1 NPEIPVGEIYKR 12

RESULT 66
US-11-045-024-13086
/ Sequence 13086, Application US/11045024
/ Publication No. US20050271676A1
/ GENERAL INFORMATION:
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Livingston, Brian
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Baker, Denise Marie
/ APPLICANT: Celis, Basteban
/ APPLICANT: Kubo, Ralph
/ APPLICANT: Grey, Howard M.
/ APPLICANT: BpImmune Inc.
/ TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
/ TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
/ FILE REFERENCE: 2060.0040007
/ CURRENT APPLICATION NUMBER: US/11/045,024
/ CURRENT FILING DATE: 2005-01-28
/ PRIOR APPLICATION NUMBER: US 09/412,863
/ PRIOR FILING DATE: 1999-10-05
/ PRIOR APPLICATION NUMBER: US 08/027,146
/ PRIOR FILING DATE: 1993-03-05
/ PRIOR APPLICATION NUMBER: US 08/073,205
/ PRIOR FILING DATE: 1993-06-04
/ PRIOR APPLICATION NUMBER: US 08/103,396
/ PRIOR FILING DATE: 1993-08-06
/ PRIOR APPLICATION NUMBER: US 08/159,184
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/159,339
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/205,713
/ PRIOR FILING DATE: 1994-03-04
/ PRIOR APPLICATION NUMBER: US 08/347,610
/ PRIOR FILING DATE: 1994-12-01
/ NUMBER OF SEQ ID NOS: 14528
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 13086
/ LENGTH: 15
/ TYPE: PRT
/ ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-13086
```

Query Match 22.4%; Score 25.5; DB 7; Length 15;  
Best Local Similarity 50.0%; Pred. No. 2.4e+02;  
Matches 6; Conservative 1; Mismatches 2; Indels 3; Gaps 1;

QY 11 NPKAP---LYKR 19  
DB 1 NPIPIVGDIYKR 12

RESULT 67  
US-11-022-562-304  
; Sequence 304, Application US/11022562  
; Publication No. US20050249742A1  
; GENERAL INFORMATION:  
; APPLICANT: Rupprecht, Ruth M.  
; APPLICANT: Shiesong, Jiang  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING  
; TITLE OF INVENTION: A CYTOTOXIC T LYMPHOCYTE IMMUNE RESPONSE  
; FILE REFERENCE: DFN-043CN  
; CURRENT APPLICATION NUMBER: US/11/022,562  
; PRIOR FILING DATE: 2004-12-22  
; PRIOR APPLICATION NUMBER: PCT/US03/20322  
; PRIOR FILING DATE: 2003-06-27  
; PRIOR APPLICATION NUMBER: 60/392718  
; NUMBER OF SEQ ID NOS: 340  
; SOFTWARE: FaastSeq for Windows Version 4.0  
; SEQ ID NO 304  
; LENGTH: 20  
; TYPE: PRT  
; ORGANISM: Human Immunodeficiency Virus  
US-11-022-562-304

Query Match 22.4%; Score 25.5; DB 7; Length 20;  
Best Local Similarity 50.0%; Pred. No. 3.3e+02;  
Matches 6; Conservative 1; Mismatches 2; Indels 3; Gaps 1;

QY 11 NPKAP---LYKR 19  
DB 3 NPIPIVGDIYKR 14

RESULT 68  
US-11-022-562-305  
; Sequence 305, Application US/11022562  
; Publication No. US20050249742A1  
; GENERAL INFORMATION:  
; APPLICANT: Rupprecht, Ruth M.  
; APPLICANT: Shiesong, Jiang  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING  
; TITLE OF INVENTION: A CYTOTOXIC T LYMPHOCYTE IMMUNE RESPONSE  
; FILE REFERENCE: DFN-043CN  
; CURRENT APPLICATION NUMBER: US/11/022,562  
; PRIOR FILING DATE: 2004-12-22  
; PRIOR APPLICATION NUMBER: PCT/US03/20322  
; PRIOR FILING DATE: 2003-06-27  
; PRIOR APPLICATION NUMBER: 60/392718  
; PRIOR FILING DATE: 2002-06-27  
; NUMBER OF SEQ ID NOS: 340  
; SOFTWARE: FaastSeq for Windows Version 4.0  
; SEQ ID NO 305  
; LENGTH: 20  
; TYPE: PRT  
; ORGANISM: Human Immunodeficiency Virus  
US-11-022-562-305

Query Match 22.4%; Score 25.5; DB 7; Length 20;  
Best Local Similarity 50.0%; Pred. No. 3.3e+02;  
Matches 6; Conservative 1; Mismatches 2; Indels 3; Gaps 1;

QY 11 NPKAP---LYKR 19  
DB 3 NPIPIVGDIYKR 14

RESULT 69  
US-10-859-643-418  
; Sequence 418, Application US/10859643  
; Publication No. US2006000293A1  
; GENERAL INFORMATION:  
; APPLICANT: Chailita-Eld, Pia M.  
; APPLICANT: Raitano, Arthur B.  
; APPLICANT: Paris, Mary  
; APPLICANT: Hubert, Rene S.  
; APPLICANT: Morrison, Karen Jane Meyrick  
; APPLICANT: Jakobovits, Aya  
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein  
; TITLE OF INVENTION: Engineered 161p2p10B Useful in Treatment and Detection of  
; FILE REFERENCE: 511582006203  
; CURRENT APPLICATION NUMBER: US/10/859,643  
; PRIOR FILING DATE: 2004-06-02  
; PRIOR APPLICATION NUMBER: US 10/005,480  
; PRIOR FILING DATE: 2001-11-07  
; NUMBER OF SEQ ID NOS: 765  
; SOFTWARE: FaastSeq for Windows Version 4.0  
; SEQ ID NO 418  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-859-643-418

Query Match 21.9%; Score 25; DB 6; Length 10;  
Best Local Similarity 66.7%; Pred. No. 1.9e+02;  
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 DYEYRG 6  
DB 3 DYNIDG 8

RESULT 70  
US-10-859-643-429  
; Sequence 429, Application US/10859643  
; Publication No. US2006000293A1  
; GENERAL INFORMATION:  
; APPLICANT: Chailita-Eld, Pia M.  
; APPLICANT: Raitano, Arthur B.  
; APPLICANT: Paris, Mary  
; APPLICANT: Hubert, Rene S.  
; APPLICANT: Morrison, Karen Jane Meyrick  
; APPLICANT: Jakobovits, Aya  
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein  
; TITLE OF INVENTION: Engineered 161p2p10B Useful in Treatment and Detection of  
; FILE REFERENCE: 511582006203  
; CURRENT APPLICATION NUMBER: US/10/859,643  
; PRIOR FILING DATE: 2004-06-02  
; PRIOR APPLICATION NUMBER: US 10/005,480  
; PRIOR FILING DATE: 2001-11-07  
; NUMBER OF SEQ ID NOS: 765  
; SOFTWARE: FaastSeq for Windows Version 4.0  
; SEQ ID NO 429  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-859-643-429

Query Match 21.9%; Score 25; DB 6; Length 10;  
Best Local Similarity 66.7%; Pred. No. 1.9e+02;  
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 DYEYRG 6  
DB 1 DYNIDG 6



## RESULT 71

US-11-097-864-418  
Sequence 418, Application US/11097864  
Publication No. US200502659241  
GENERAL INFORMATION:  
APPLICANT: Challita-Bid, Pia M.  
APPLICANT: Raitano, Arthur B.  
APPLICANT: Fairis, Mary  
APPLICANT: Hubert, Rene S.  
APPLICANT: Morrison, Karen Jane Meyrick  
APPLICANT: Jakobovits, Aya  
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 161P2F10B  
FILE REFERENCE: 511582006205  
CURRENT APPLICATION NUMBER: US/11/097,864  
CURRENT FILING DATE: 2005-04-01  
PRIOR APPLICATION NUMBER: US 10/062,109  
PRIOR FILING DATE: 2002-01-31  
PRIOR APPLICATION NUMBER: US 10/005,480  
PRIOR FILING DATE: 2001-11-07  
NUMBER OF SEQ ID NOS: 765  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 418  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Homo Sapien  
US-11-097-864-418

## Query Match

Best Local Similarity 21.9%; Score 25; DB 7; Length 10;  
Pred. No. 1.9e+02;  
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DYEYPG 6  
Db 3 DYNVYG 8

## RESULT 72

US-11-097-864-429  
Sequence 429, Application US/11097864  
Publication No. US200502659241  
GENERAL INFORMATION:  
APPLICANT: Challita-Bid, Pia M.  
APPLICANT: Raitano, Arthur B.  
APPLICANT: Fairis, Mary  
APPLICANT: Hubert, Rene S.  
APPLICANT: Morrison, Karen Jane Meyrick  
APPLICANT: Jakobovits, Aya  
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 161P2F10B  
FILE REFERENCE: 511582006205  
CURRENT APPLICATION NUMBER: US/11/097,864  
CURRENT FILING DATE: 2005-04-01  
PRIOR APPLICATION NUMBER: US 10/062,109  
PRIOR FILING DATE: 2002-01-31  
PRIOR APPLICATION NUMBER: US 10/005,480  
PRIOR FILING DATE: 2001-11-07  
NUMBER OF SEQ ID NOS: 765  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 429  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Homo Sapien  
US-11-097-864-429

## Query Match

Best Local Similarity 21.9%; Score 25; DB 7; Length 10;  
Pred. No. 1.9e+02;  
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DYEYPG 6  
Db 1 DYNVYG 6

## RESULT 73

US-11-097-912-418  
Sequence 418, Application US/11097912  
Publication No. US20050265921A1  
GENERAL INFORMATION:  
APPLICANT: Challita-Bid, Pia M.  
APPLICANT: Raitano, Arthur B.  
APPLICANT: Fairis, Mary  
APPLICANT: Hubert, Rene S.  
APPLICANT: Morrison, Karen Jane Meyrick  
APPLICANT: Jakobovits, Aya  
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 161P2F10B  
FILE REFERENCE: 511582006204  
CURRENT APPLICATION NUMBER: US/11/097,912  
CURRENT FILING DATE: 2005-04-01  
PRIOR APPLICATION NUMBER: US 10/062,109  
PRIOR FILING DATE: 2002-01-31  
PRIOR APPLICATION NUMBER: US 10/005,480  
PRIOR FILING DATE: 2001-11-07  
NUMBER OF SEQ ID NOS: 765  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 418  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Homo Sapien  
US-11-097-912-418

## Query Match

Best Local Similarity 21.9%; Score 25; DB 7; Length 10;  
Pred. No. 1.9e+02;  
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DYEYPG 6  
Db 3 DYNVYG 8

## RESULT 74

US-11-097-912-429  
Sequence 429, Application US/11097912  
Publication No. US20050265921A1  
GENERAL INFORMATION:  
APPLICANT: Challita-Bid, Pia M.  
APPLICANT: Raitano, Arthur B.  
APPLICANT: Fairis, Mary  
APPLICANT: Hubert, Rene S.  
APPLICANT: Morrison, Karen Jane Meyrick  
APPLICANT: Jakobovits, Aya  
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 161P2F10B  
FILE REFERENCE: 511582006204  
CURRENT APPLICATION NUMBER: US/11/097,912  
CURRENT FILING DATE: 2005-04-01  
PRIOR APPLICATION NUMBER: US 10/062,109  
PRIOR FILING DATE: 2002-01-31  
PRIOR APPLICATION NUMBER: US 10/005,480  
PRIOR FILING DATE: 2001-11-07  
NUMBER OF SEQ ID NOS: 765  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 429  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Homo Sapien  
US-11-097-912-429

## Query Match

Best Local Similarity 21.9%; Score 25; DB 7; Length 10;  
Pred. No. 1.9e+02;  
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DYEYPG 6  
Db 1 DYNVYG 6

Db 1 DYNVDG 6

RESULT 75

US-11-156-843-119

/ Sequence 119, Application US/11156843

/ Publication No. US20050267035A1

/ GENERAL INFORMATION:

/ APPLICANT: West, Robert R.

/ APPLICANT: Sheppard, Paul O.

/ APPLICANT: Fox, Brian

/ TITLE OF INVENTION: Peptide and Polypeptide Inhibitors of

/ FILE REFERENCE: 00-33

/ CURRENT APPLICATION NUMBER: US/11/156,843

/ PRIOR FILING DATE: 2005-06-20

/ PRIOR FILING DATE: 2001-06-18

/ NUMBER OF SEQ ID NOS: 140

/ SOFTWARE: FastSeq for Windows Version 4.0

/ SEQ ID NO 119

/ LENGTH: 10

/ TYPE: PRT

/ ORGANISM: Artificial Sequence

/ FEATURE:

/ OTHER INFORMATION: C1s exosite binding moiety

US-11-156-843-119

Query Match 21.9%; Score 25; DB 7; Length 10;

Best Local Similarity 100.0%; Pred. No. 1.9e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYEY 4

Db 6 DYEY 9

RESULT 76

US-11-045-024-2015

/ Sequence 2015, Application US/11045024

/ Publication No. US20050271676A1

/ GENERAL INFORMATION:

/ APPLICANT: Sette, Alessandro

/ APPLICANT: Sidney, John

/ APPLICANT: Southwood, Scott

/ APPLICANT: Livingston, Brian

/ APPLICANT: Chesnut, Robert

/ APPLICANT: Baker, Denise Marie

/ APPLICANT: Cells, Stephen

/ APPLICANT: Kubo, Ralph

/ APPLICANT: Grey, Howard M.

/ APPLICANT: Epimmune Inc.

/ TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency

/ FILE REFERENCE: 2060.0040007

/ CURRENT APPLICATION NUMBER: US/11/045,024

/ PRIOR FILING DATE: 2005-01-28

/ PRIOR APPLICATION NUMBER: US 09/412,863

/ PRIOR FILING DATE: 1999-10-05

/ PRIOR APPLICATION NUMBER: US 08/027,146

/ PRIOR FILING DATE: 1993-03-05

/ PRIOR APPLICATION NUMBER: US 08/073,205

/ PRIOR FILING DATE: 1993-06-04

/ PRIOR APPLICATION NUMBER: US 08/103,396

/ PRIOR FILING DATE: 1993-08-06

/ PRIOR APPLICATION NUMBER: US 08/159,184

/ PRIOR FILING DATE: 1993-11-29

/ PRIOR APPLICATION NUMBER: US 08/159,339

/ PRIOR FILING DATE: 1993-11-29

/ PRIOR APPLICATION NUMBER: US 08/205,713

/ PRIOR FILING DATE: 1994-03-04

/ PRIOR APPLICATION NUMBER: US 08/347,610

/ PRIOR FILING DATE: 1994-12-01

/ NUMBER OF SEQ ID NOS: 14528

/ SOFTWARE: FastSeq for Windows Version 4.0

/ SEQ ID NO 2015

/ LENGTH: 10

/ TYPE: PRT

/ ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS

US-11-045-024-2015

Query Match 21.9%; Score 25; DB 7; Length 10;

Best Local Similarity 44.4%; Pred. No. 2.1e+02;

Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 12 PKAPYKRP 20

Db 1 PQTLMQRP 9

RESULT 77

US-11-033-365-49

/ Sequence 49, Application US/11033365

/ Publication No. US20050250678A1

/ GENERAL INFORMATION:

/ APPLICANT: Neose Technologies Inc.

/ APPLICANT: Defrees, Shawn

/ APPLICANT: Zopf, David

/ APPLICANT: Wang, ZhiGuang

/ APPLICANT: Clausen, Henrik

/ TITLE OF INVENTION: O-linked Glycosylation of peptides

/ FILE REFERENCE: 040853-01-5138

/ CURRENT APPLICATION NUMBER: US/11/033,365

/ PRIOR FILING DATE: 2005-01-10

/ PRIOR APPLICATION NUMBER: 60/535,284

/ PRIOR FILING DATE: 2004-01-08

/ PRIOR APPLICATION NUMBER: 60/544,411

/ PRIOR FILING DATE: 2004-02-12

/ PRIOR APPLICATION NUMBER: 60/546,631

/ PRIOR FILING DATE: 2004-02-20

/ PRIOR APPLICATION NUMBER: 60/555,813

/ PRIOR FILING DATE: 2004-03-23

/ PRIOR APPLICATION NUMBER: 60/570,891

/ PRIOR FILING DATE: 2004-05-12

/ NUMBER OF SEQ ID NOS: 213

/ SOFTWARE: PatentIn version 3.2

/ SEQ ID NO 49

/ LENGTH: 11

/ TYPE: PRT

/ ORGANISM: Homo sapiens

US-11-033-365-49

Query Match 21.9%; Score 25; DB 7; Length 11;

Best Local Similarity 62.5%; Pred. No. 2.1e+02;

Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 9 LGNPKAPL 16

Db 1 LGIPKSP 8

RESULT 78

US-11-156-843-28

/ Sequence 28, Application US/11156843

/ Publication No. US20050267035A1

/ GENERAL INFORMATION:

/ APPLICANT: West, Robert R.

/ APPLICANT: Sheppard, Paul O.

/ APPLICANT: Fox, Brian

/ TITLE OF INVENTION: Peptide and Polypeptide Inhibitors of

/ FILE REFERENCE: 00-33

/ CURRENT APPLICATION NUMBER: US/11/156,843

/ PRIOR FILING DATE: 2005-06-20

/ PRIOR APPLICATION NUMBER: US/09/883,727

/ PRIOR FILING DATE: 2001-06-18

```
/ NUMBER OF SEQ ID NOS: 140
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 28
/ LENGTH: 11
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: C1s exosite binding moiety
/ NAME/KEY: MUTAGEN
/ LOCATION: (5)...(5)
/ OTHER INFORMATION: Xaa = Phe-(p-CH2)SO3H
US-11-156-843-28

Query Match          21.9%; Score 25; DB 7; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DYEV 4
        ||||
Db       7 DYEV 10

RESULT 79
US-11-156-843-35
/ Sequence 35, Application US/11156843
/ Publication NO. US20050267035A1
/ GENERAL INFORMATION:
/ APPLICANT: West, Robert R.
/ APPLICANT: Sheppard, Paul O.
/ APPLICANT: Fox, Brian
/ TITLE OF INVENTION: Peptide and Polypeptide Inhibitors of
/ TITLE OF INVENTION: Complement C1s
/ FILE REFERENCE: 00-33
/ CURRENT APPLICATION NUMBER: US/11/156,843
/ CURRENT FILING DATE: 2005-06-20
/ PRIOR APPLICATION NUMBER: US/09/883,727
/ PRIOR FILING DATE: 2001-06-18
/ NUMBER OF SEQ ID NOS: 140
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 35
/ LENGTH: 11
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: C1s exosite binding moiety
/ NAME/KEY: MUTAGEN
/ LOCATION: (5)...(5)
/ OTHER INFORMATION: Xaa = sulfated tyrosine
US-11-156-843-35

Query Match          21.9%; Score 25; DB 7; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DYEV 4
        ||||
Db       7 DYEV 10

RESULT 80
US-11-045-024-2247
/ Sequence 2247, Application US/11045024
/ Publication NO. US20050271676A1
/ GENERAL INFORMATION:
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Livingston, Brian
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Baker, Denise Marie
/ APPLICANT: Celis, Bateban
```

```
/ APPLICANT: Kubo, Ralph
/ APPLICANT: Grey, Howard M.
/ APPLICANT: Eptimmune Inc.
/ TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
/ TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
/ FILE REFERENCE: 2060.0040007
/ CURRENT APPLICATION NUMBER: US/11/045,024
/ CURRENT FILING DATE: 2005-01-28
/ PRIOR APPLICATION NUMBER: US 09/412,863
/ PRIOR FILING DATE: 1999-10-05
/ PRIOR APPLICATION NUMBER: US 08/027,146
/ PRIOR FILING DATE: 1993-03-05
/ PRIOR APPLICATION NUMBER: US 08/073,205
/ PRIOR FILING DATE: 1993-06-04
/ PRIOR APPLICATION NUMBER: US 08/103,396
/ PRIOR FILING DATE: 1993-08-06
/ PRIOR APPLICATION NUMBER: US 08/159,184
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/159,339
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/205,713
/ PRIOR FILING DATE: 1994-03-04
/ PRIOR APPLICATION NUMBER: US 08/347,610
/ PRIOR FILING DATE: 1994-12-01
/ NUMBER OF SEQ ID NOS: 14528
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 2247
/ LENGTH: 11
/ TYPE: PRT
/ ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-2247
```

```
Query Match          21.9%; Score 25; DB 7; Length 11;
Best Local Similarity 44.4%; Pred. No. 2.1e+02;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY      12 PRAPLYKRP 20
        |::|||
Db       1 POTTWQRP 9

RESULT 81
US-11-045-024-5380
/ Sequence 5380, Application US/11045024
/ Publication NO. US20050271676A1
/ GENERAL INFORMATION:
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Livingston, Brian
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Baker, Denise Marie
/ APPLICANT: Celis, Bateban
/ APPLICANT: Kubo, Ralph
/ APPLICANT: Grey, Howard M.
/ APPLICANT: Eptimmune Inc.
/ TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
/ TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
/ FILE REFERENCE: 2060.0040007
/ CURRENT APPLICATION NUMBER: US/11/045,024
/ CURRENT FILING DATE: 2005-01-28
/ PRIOR APPLICATION NUMBER: US 09/412,863
/ PRIOR FILING DATE: 1999-10-05
/ PRIOR APPLICATION NUMBER: US 08/027,146
/ PRIOR FILING DATE: 1993-03-05
/ PRIOR APPLICATION NUMBER: US 08/073,205
/ PRIOR FILING DATE: 1993-06-04
/ PRIOR APPLICATION NUMBER: US 08/103,396
/ PRIOR FILING DATE: 1993-08-06
/ PRIOR APPLICATION NUMBER: US 08/159,184
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/159,339
/ PRIOR FILING DATE: 1993-11-29
```

PRIOR APPLICATION NUMBER: US 08/205,713  
PRIOR FILING DATE: 1994-03-04  
PRIOR APPLICATION NUMBER: US 08/247,610  
PRIOR FILING DATE: 1994-12-01  
NUMBER OF SEQ ID NOS: 14528  
SOFTWARE: FastSeq for windows Version 4.0  
SEQ ID NO 5380  
LENGTH: 11  
TYPE: PRT  
ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS  
US-11-045-024-5380

Query Match 21.9%; Score 25; DB 7; Length 11;  
Best Local Similarity 44.4%; Pred. No. 2.1e+02;  
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 12 PKAPLYKRP 20  
|:|:|  
DB 2 POTTLMQRP 10

RESULT 82  
US-11-045-024-7847  
Sequence 7847, Application US/11045024  
Publication No. US2005021676A1  
GENERAL INFORMATION:  
APPLICANT: Sette, Alessandro  
APPLICANT: Sidney, John  
APPLICANT: Southwood, Scott  
APPLICANT: Livingston, Brian  
APPLICANT: Chesnut, Robert  
APPLICANT: Baker, Denise Marie  
APPLICANT: Celis, Betteban  
APPLICANT: Kubo, Ralph  
APPLICANT: Grey, Howard M.  
APPLICANT: Epimmune Inc.  
TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency  
FILE REFERENCE: 2060.0040007  
CURRENT APPLICATION NUMBER: US/11/045,024  
CURRENT FILING DATE: 2005-01-28  
PRIOR APPLICATION NUMBER: US 09/412,863  
PRIOR FILING DATE: 1999-10-05  
PRIOR APPLICATION NUMBER: US 08/027,146  
PRIOR FILING DATE: 1993-03-05  
PRIOR APPLICATION NUMBER: US 08/073,205  
PRIOR FILING DATE: 1993-06-04  
PRIOR APPLICATION NUMBER: US 08/103,396  
PRIOR FILING DATE: 1993-08-06  
PRIOR APPLICATION NUMBER: US 08/159,184  
PRIOR FILING DATE: 1993-11-29  
PRIOR APPLICATION NUMBER: US 08/159,339  
PRIOR FILING DATE: 1993-11-29  
PRIOR APPLICATION NUMBER: US 08/205,713  
PRIOR FILING DATE: 1994-03-04  
PRIOR APPLICATION NUMBER: US 08/247,610  
PRIOR FILING DATE: 1994-12-01  
NUMBER OF SEQ ID NOS: 14528  
SOFTWARE: FastSeq for windows Version 4.0  
SEQ ID NO 7847  
LENGTH: 11  
TYPE: PRT  
ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS  
US-11-045-024-7847

Query Match 21.9%; Score 25; DB 7; Length 11;  
Best Local Similarity 44.4%; Pred. No. 2.1e+02;  
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 12 PKAPLYKRP 20  
|:|:|  
DB 1 POTTLMQRP 9

RESULT 83  
US-10-511-559-464  
Sequence 464, Application US/10511559  
Publication No. US20050256304A1  
GENERAL INFORMATION:  
APPLICANT: JONES, Tim  
APPLICANT: BAKER, Matthew  
APPLICANT: CARR, Francis, J.  
TITLE OF INVENTION: MODIFIED FACTOR VIII  
FILE REFERENCE: MER-133  
CURRENT APPLICATION NUMBER: US/10/511,559  
CURRENT FILING DATE: 2004-10-15  
PRIOR APPLICATION NUMBER: PCT/EP03/04063  
PRIOR FILING DATE: 2003-04-17  
PRIOR APPLICATION NUMBER: EP 02008712.8  
PRIOR FILING DATE: 2002-04-18  
PRIOR APPLICATION NUMBER: EP 03006554.4  
PRIOR FILING DATE: 2003-03-24  
NUMBER OF SEQ ID NOS: 1147  
SOFTWARE: FastSeq for windows Version 4.0  
SEQ ID NO 464  
LENGTH: 13  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Potential Epitope of human Factor VIII  
US-10-511-559-464

Query Match 21.9%; Score 25; DB 6; Length 13;  
Best Local Similarity 50.0%; Pred. No. 2.5e+02;  
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 7 SRLGNPKAPL 16  
|:|:|:|  
DB 4 SLLGPPSMPV 13

RESULT 84  
US-11-054-515-2470  
Sequence 2470, Application US/11054515  
Publication No. US20050255532A1  
GENERAL INFORMATION:  
APPLICANT: Ruben et al.  
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BlyS  
FILE REFERENCE: PFS2393  
CURRENT APPLICATION NUMBER: US/11/054,515  
CURRENT FILING DATE: 2005-02-10  
PRIOR APPLICATION NUMBER: 60/543,296  
PRIOR FILING DATE: 2004-02-11  
PRIOR APPLICATION NUMBER: 60/580,347  
PRIOR FILING DATE: 2004-06-18  
PRIOR APPLICATION NUMBER: 10/293,418  
PRIOR FILING DATE: 2002-11-14  
PRIOR APPLICATION NUMBER: 60/331,469  
PRIOR FILING DATE: 2001-11-16  
PRIOR APPLICATION NUMBER: 60/340,817  
PRIOR FILING DATE: 2001-12-19  
PRIOR APPLICATION NUMBER: 09/880,748  
PRIOR FILING DATE: 2001-06-15  
PRIOR APPLICATION NUMBER: 60/293,499  
PRIOR FILING DATE: 2001-05-25  
PRIOR APPLICATION NUMBER: 60/277,379  
PRIOR FILING DATE: 2001-03-21  
PRIOR APPLICATION NUMBER: 60/276,248  
PRIOR FILING DATE: 2001-03-16  
PRIOR APPLICATION NUMBER: 60/240,816  
PRIOR FILING DATE: 2000-10-17  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 3247  
SEQ ID NO 2470  
LENGTH: 13  
TYPE: PRT

ORGANISM: Homo sapiens  
US-11-054-515-2470

Query Match 21.9%; Score 25; DB 7; Length 13;  
Best Local Similarity 66.7%; Pred. No. 2.5e+02;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 12 PKAPLY 17  
| : |||  
DB 8 PHSPLY 13

RESULT 85

US-11-006-119-35  
Sequence 35, Application US/11006119  
Publication No. US20050260691A1  
GENERAL INFORMATION:  
APPLICANT: Ndao, Momar  
APPLICANT: Ward, Brian  
APPLICANT: Caffrey, Rebecca  
APPLICANT: Spithill, Terry  
APPLICANT: Li, Hongshean  
APPLICANT: Poduel, Vladimir  
APPLICANT: Perichon, Regis  
APPLICANT: CIPHERGEN Biosystems, Inc.  
TITLE OF INVENTION: Serum biomarkers for Chagas Disease  
FILE REFERENCE: 016866-012130US  
CURRENT APPLICATION NUMBER: US/11/006,119  
CURRENT FILING DATE: 2004-12-06  
PRIOR APPLICATION NUMBER: US 60/527,153  
PRIOR FILING DATE: 2003-12-05  
PRIOR APPLICATION NUMBER: US 60/565,093  
PRIOR FILING DATE: 2004-04-22  
PRIOR APPLICATION NUMBER: US 60/625,519  
PRIOR FILING DATE: 2004-11-06  
NUMBER OF SEQ ID NOS: 38  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 35  
LENGTH: 13  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:C-terminal  
OTHER INFORMATION: truncation 24.7 kDa fragment of Apolipoprotein A-I  
OTHER INFORMATION: (ApoA-I) Chagas disease biomarker tryptic digest  
US-11-006-119-35

Query Match 21.9%; Score 25; DB 7; Length 13;  
Best Local Similarity 50.0%; Pred. No. 2.5e+02;  
Matches 6; Conservative 2; Mismatches 2; Indels 2; Gaps 1;

QY 1 DY--EYGSRLG 10  
| : |||  
DB 1 DYVSQEGSGALG 12

RESULT 86

US-10-983-174-6  
Sequence 6, Application US/10983174  
Publication No. US20050261307A1  
GENERAL INFORMATION:  
APPLICANT: CAI, SHAOPEI  
APPLICANT: CHOU, JOYCE  
APPLICANT: HARWOOD, ERIC  
APPLICANT: HEISE, CARLA C.  
APPLICANT: MACHALBSKI, TIMOTHY D.  
APPLICANT: RYCKMAN, DAVID  
APPLICANT: SHANG, XIAO  
APPLICANT: WIESMANN, MARION  
APPLICANT: ZHU, SHUGUANG  
TITLE OF INVENTION: INHIBITION OF FGFR3 AND TREATMENT OF MULTIPLE MYELOMA  
FILE REFERENCE: 072121-0445

CURRENT APPLICATION NUMBER: US/10/983,174  
CURRENT FILING DATE: 2004-11-05  
PRIOR APPLICATION NUMBER: 60/546,017  
PRIOR FILING DATE: 2004-02-19  
PRIOR APPLICATION NUMBER: 60/526,425  
PRIOR FILING DATE: 2003-12-02  
PRIOR APPLICATION NUMBER: 60/526,426  
PRIOR FILING DATE: 2003-12-02  
PRIOR APPLICATION NUMBER: 60/517,915  
PRIOR FILING DATE: 2003-11-07  
PRIOR APPLICATION NUMBER: 10/644,055  
PRIOR FILING DATE: 2003-08-19  
PRIOR APPLICATION NUMBER: 60/405,729  
PRIOR FILING DATE: 2002-08-23  
PRIOR APPLICATION NUMBER: 60/428,210  
PRIOR FILING DATE: 2002-11-21  
PRIOR APPLICATION NUMBER: 60/484,048  
PRIOR FILING DATE: 2003-07-01  
PRIOR APPLICATION NUMBER: 60/426,282  
PRIOR FILING DATE: 2002-11-13  
PRIOR APPLICATION NUMBER: 60/460,493  
PRIOR FILING DATE: 2003-04-03  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 7  
SOFTWARE: PatentIn Ver. 3.2  
SEQ ID NO 6  
LENGTH: 14  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-10-983-174-6

Query Match 21.9%; Score 25; DB 6; Length 14;  
Best Local Similarity 66.7%; Pred. No. 2.7e+02;  
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 10 GNPXAP 15  
| : |||  
DB 3 GGEKTP 8

RESULT 87

US-10-719-150-1  
Sequence 1, Application US/10719150  
Publication No. US20040120953A1  
GENERAL INFORMATION:  
APPLICANT: Kevin J. Tracey  
APPLICANT: Hachao Wang  
TITLE OF INVENTION: ANTAGONISTS OF HMGI FOR TREATING  
TITLE OF INVENTION: INFLAMMATORY CONDITIONS  
FILE REFERENCE: 3268.1000-011  
CURRENT APPLICATION NUMBER: US/10/719,150  
CURRENT FILING DATE: 2003-11-21  
PRIOR APPLICATION NUMBER: US/10/300,068  
PRIOR FILING DATE: 2002-11-20  
PRIOR APPLICATION NUMBER: US 10/210,747  
PRIOR FILING DATE: 2002-07-31  
PRIOR APPLICATION NUMBER: US 09/503,632  
PRIOR FILING DATE: 2000-02-14  
PRIOR APPLICATION NUMBER: US 09/248,574  
PRIOR FILING DATE: 1999-02-11  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1  
LENGTH: 14  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-719-150-1

Query Match 21.9%; Score 25; DB 6; Length 14;  
Best Local Similarity 66.7%; Pred. No. 2.7e+02;

Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 10 GNPAP 15

Db 3 GNPAP 8

RESULT 88  
US-11-054-515-2529

; Sequence 2529, Application US/11054515  
; Publication No. US2005025532A1

; GENERAL INFORMATION:

; APPLICANT: Ruben et al.

; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys

; FILE REFERENCE: PF523P3

; CURRENT APPLICATION NUMBER: US/11/054,515

; CURRENT FILING DATE: 2005-02-10

; PRIOR APPLICATION NUMBER: 60/543,296

; PRIOR FILING DATE: 2004-02-11

; PRIOR APPLICATION NUMBER: 60/580,347

; PRIOR FILING DATE: 2004-06-18

; PRIOR APPLICATION NUMBER: 10/293,418

; PRIOR FILING DATE: 2002-11-14

; PRIOR APPLICATION NUMBER: 60/331,469

; PRIOR FILING DATE: 2001-11-16

; PRIOR APPLICATION NUMBER: 60/340,817

; PRIOR FILING DATE: 2001-12-19

; PRIOR APPLICATION NUMBER: 09/880,748

; PRIOR FILING DATE: 2001-06-15

; PRIOR APPLICATION NUMBER: 60/293,499

; PRIOR FILING DATE: 2001-05-25

; PRIOR APPLICATION NUMBER: 60/277,379

; PRIOR FILING DATE: 2001-03-21

; PRIOR APPLICATION NUMBER: 60/276,248

; PRIOR FILING DATE: 2001-03-16

; PRIOR APPLICATION NUMBER: 60/240,816

; PRIOR FILING DATE: 2000-10-17

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 3247

; SEQ ID NO 2529

; LENGTH: 14

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-11-054-515-2529

Query Match

Best Local Similarity 21.9%; Score 25; DB 7; Length 14;

Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 12 PNPAP 18

Db 8 PNPAP 14

RESULT 89

US-11-054-515-2691

; Sequence 2691, Application US/11054515

; Publication No. US2005025532A1

; GENERAL INFORMATION:

; APPLICANT: Ruben et al.

; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys

; FILE REFERENCE: PF523P3

; CURRENT APPLICATION NUMBER: US/11/054,515

; CURRENT FILING DATE: 2005-02-10

; PRIOR APPLICATION NUMBER: 60/543,296

; PRIOR FILING DATE: 2004-02-11

; PRIOR APPLICATION NUMBER: 60/580,347

; PRIOR FILING DATE: 2004-06-18

; PRIOR APPLICATION NUMBER: 10/293,418

; PRIOR FILING DATE: 2002-11-14

; PRIOR APPLICATION NUMBER: 60/331,469

; PRIOR FILING DATE: 2001-11-16

; PRIOR APPLICATION NUMBER: 60/340,817

; PRIOR FILING DATE: 2001-12-19

; PRIOR APPLICATION NUMBER: 09/880,748

; PRIOR FILING DATE: 2001-06-15

; PRIOR APPLICATION NUMBER: 60/293,499

; PRIOR FILING DATE: 2001-05-25

; PRIOR APPLICATION NUMBER: 60/277,379

; PRIOR FILING DATE: 2001-03-21

; PRIOR APPLICATION NUMBER: 60/276,248

; PRIOR FILING DATE: 2001-03-16

; PRIOR APPLICATION NUMBER: 60/240,816

; PRIOR FILING DATE: 2000-10-17

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 3247

; SEQ ID NO 2691

; LENGTH: 14

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-11-054-515-2691

Query Match

Best Local Similarity 21.9%; Score 25; DB 7; Length 14;

Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 12 PNPAP 17

Db 8 PNPAP 13

RESULT 90

US-10-719-150-4

; Sequence 4, Application US/10719150

; Publication No. US20040120953A1

; GENERAL INFORMATION:

; APPLICANT: Kevin J. Tracey

; TITLE OF INVENTION: ANTAGONISTS OF HMGI FOR TREATING

; FILE REFERENCE: 3268.1000-011

; CURRENT APPLICATION NUMBER: US/10/719,150

; CURRENT FILING DATE: 2003-11-21

; PRIOR APPLICATION NUMBER: US/10/300,068

; PRIOR FILING DATE: 2002-11-20

; PRIOR APPLICATION NUMBER: US 10/210,747

; PRIOR FILING DATE: 2002-07-31

; PRIOR APPLICATION NUMBER: US 09/503,632

; PRIOR FILING DATE: 2000-02-14

; PRIOR APPLICATION NUMBER: US 09/248,574

; PRIOR FILING DATE: 1999-02-11

; NUMBER OF SEQ ID NOS: 6

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 4

; LENGTH: 15

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: antigen

; US-10-719-150-4

Query Match

Best Local Similarity 21.9%; Score 25; DB 6; Length 15;

Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 10 GNPAP 15

Db 3 GNPAP 8

RESULT 91

US-11-045-024-13167

; Sequence 13167, Application US/11045024

; Publication No. US20050271676A1

; GENERAL INFORMATION:

; APPLICANT: Sette, Alessandro

```
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
APPLICANT: Livingston, Brian
APPLICANT: Chesnut, Robert
APPLICANT: Baker, Denise Marie
APPLICANT: Cella, Esteban
APPLICANT: Kubo, Ralph
APPLICANT: Grey, Howard M.
APPLICANT: EpiImmune Inc.
TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
FILE REFERENCE: 2060.0040007
CURRENT APPLICATION NUMBER: US/11/045,024
CURRENT FILING DATE: 2005-01-28
PRIOR APPLICATION NUMBER: US 09/412,863
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: US 08/027,146
PRIOR FILING DATE: 1993-03-05
PRIOR APPLICATION NUMBER: US 08/073,205
PRIOR FILING DATE: 1993-06-04
PRIOR APPLICATION NUMBER: US 08/103,396
PRIOR FILING DATE: 1993-08-06
PRIOR APPLICATION NUMBER: US 08/159,184
PRIOR FILING DATE: 1993-11-29
PRIOR APPLICATION NUMBER: US 08/159,339
PRIOR FILING DATE: 1993-11-29
PRIOR APPLICATION NUMBER: US 08/205,713
PRIOR FILING DATE: 1994-03-04
PRIOR APPLICATION NUMBER: US 08/347,610
PRIOR FILING DATE: 1994-12-01
NUMBER OF SEQ ID NOS: 14528
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 13167
LENGTH: 15
TYPE: PRT
ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-13167

Query Match      21.9%; Score 25; DB 7; Length 15;
Best Local Similarity 44.4%; Pred. No. 2.9e+02;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
```

```
APPLICANT: Southwood, Scott
APPLICANT: Livingston, Brian
APPLICANT: Chesnut, Robert
APPLICANT: Baker, Denise Marie
APPLICANT: Cella, Esteban
APPLICANT: Kubo, Ralph
APPLICANT: Grey, Howard M.
APPLICANT: EpiImmune Inc.
TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
FILE REFERENCE: 2060.0040007
CURRENT APPLICATION NUMBER: US/11/045,024
CURRENT FILING DATE: 2005-01-28
PRIOR APPLICATION NUMBER: US 09/412,863
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: US 08/027,146
PRIOR FILING DATE: 1993-03-05
PRIOR APPLICATION NUMBER: US 08/073,205
PRIOR FILING DATE: 1993-06-04
PRIOR APPLICATION NUMBER: US 08/103,396
PRIOR FILING DATE: 1993-08-06
PRIOR APPLICATION NUMBER: US 08/159,184
PRIOR FILING DATE: 1993-11-29
PRIOR APPLICATION NUMBER: US 08/159,339
PRIOR FILING DATE: 1993-11-29
PRIOR APPLICATION NUMBER: US 08/205,713
PRIOR FILING DATE: 1994-03-04
PRIOR APPLICATION NUMBER: US 08/347,610
PRIOR FILING DATE: 1994-12-01
NUMBER OF SEQ ID NOS: 14528
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 13283
LENGTH: 15
TYPE: PRT
ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-13283

Query Match      21.9%; Score 25; DB 7; Length 15;
Best Local Similarity 44.4%; Pred. No. 2.9e+02;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
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Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
QY 12 PKAPLYRKP 20  
|:|:|  
Db 7 PQTLMWRP 15

RESULT 94  
US-10-201-525-23  
; Sequence 23, Application US/10201525  
; Publication No. US2006009631A1  
; GENERAL INFORMATION:  
; APPLICANT: Board of Regents of the University of Oklahoma  
; TITLE OF INVENTION: TYROSYLPROTEIN SULFOTRANSFERASES AND METHODS OF USE THEREOF  
; FILE REFERENCE: 5827,005  
; CURRENT APPLICATION NUMBER: US/10/201,525  
; CURRENT FILING DATE: 2002-07-22  
; PRIOR APPLICATION NUMBER: 09/785,343  
; PRIOR FILING DATE: 2001-02-16  
; PRIOR APPLICATION NUMBER: PCT/US99/16750  
; PRIOR FILING DATE: 1999-07-23  
; NUMBER OF SEQ ID NOS: 45  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 23  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-201-525-23

Query Match 21.9%; Score 25; DB 6; Length 17;  
Best Local Similarity 100.0%; Pred. No. 3.3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYEX 4  
| | | |  
Db 8 DYEX 11

RESULT 95  
US-11-006-119-38  
; Sequence 38, Application US/11006119  
; Publication No. US20050260691A1  
; GENERAL INFORMATION:  
; APPLICANT: Ndao, Momar  
; APPLICANT: Ward, Brian  
; APPLICANT: Caffrey, Rebecca  
; APPLICANT: Spithill, Terry  
; APPLICANT: Li, Hongshan  
; APPLICANT: Poduet, Vladimir  
; APPLICANT: Perichon, Regis  
; APPLICANT: CIPHERGEN Biosystems, Inc.  
; TITLE OF INVENTION: Serum Biomarkers for Chagas Disease  
; FILE REFERENCE: 01666-012130US  
; CURRENT APPLICATION NUMBER: US/11/006,119  
; CURRENT FILING DATE: 2004-12-06  
; PRIOR APPLICATION NUMBER: US 60/527,153  
; PRIOR FILING DATE: 2003-12-05  
; PRIOR FILING DATE: 2004-04-22  
; PRIOR FILING DATE: 2004-04-22  
; PRIOR APPLICATION NUMBER: US 60/625,519  
; PRIOR FILING DATE: 2004-11-06  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 38  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:C-terminal  
; OTHER INFORMATION: truncation 24.7 kDa fragment of Apolipoprotein A-1  
; OTHER INFORMATION: ApoA-I) Chagas disease biomarker cryptic digest  
US-11-006-119-38

Query Match 21.9%; Score 25; DB 7; Length 17;  
Best Local Similarity 50.0%; Pred. No. 3.3e+02;  
Matches 6; Conservative 2; Mismatches 2; Indels 2; Gaps 1;

QY 1 DY--EYPSRLG 10  
| | : | | |  
Db 5 DYVSQFEGSALG 16

RESULT 96  
US-11-128-059-11  
; Sequence 11, Application US/11128059  
; Publication No. US20050287638A1  
; GENERAL INFORMATION:  
; APPLICANT: WEIGEL, PAUL H  
; APPLICANT: WEIGEL, JANET A  
; TITLE OF INVENTION: HYALURONAN RECEPTOR FOR ENDOCYTOSIS, VARIANTS THEREOF, AND  
; FILE REFERENCE: 5864,033  
; CURRENT APPLICATION NUMBER: US/11/128,059  
; CURRENT FILING DATE: 2005-05-12  
; PRIOR APPLICATION NUMBER: 60/570,915  
; PRIOR FILING DATE: 2004-05-13  
; PRIOR APPLICATION NUMBER: 10/133,172  
; PRIOR FILING DATE: 2002-04-25  
; PRIOR APPLICATION NUMBER: 60/286,468  
; PRIOR FILING DATE: 2001-04-25  
; PRIOR APPLICATION NUMBER: 09/842,930  
; PRIOR FILING DATE: 2001-04-25  
; NUMBER OF SEQ ID NOS: 100  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 11  
; LENGTH: 19  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-128-059-11

Query Match 21.9%; Score 25; DB 7; Length 19;  
Best Local Similarity 50.0%; Pred. No. 3.7e+02;  
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 10 GNPAPLYR 19  
| | | | | | | | | |  
Db 7 GGPDAFCNRR 16

RESULT 97  
US-10-623-155-493  
; Sequence 493, Application US/10623155  
; Publication No. US20050261166A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Tonglong  
; APPLICANT: Peckham, David W.  
; APPLICANT: Retter, Marc W.  
; APPLICANT: Fanger, Gary R.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; FILE REFERENCE: 210121.455C20  
; CURRENT APPLICATION NUMBER: US/10/623,155  
; CURRENT FILING DATE: 2003-07-17  
; NUMBER OF SEQ ID NOS: 560  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 493  
; LENGTH: 20  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-623-155-493

Query Match 21.9%; Score 25; DB 6; Length 20;  
Best Local Similarity 50.0%; Pred. No. 3.9e+02;  
Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;



QY 5 PGSRLGNP 12  
DB 7 PGNFLONRPEPTAP 14

RESULT 98  
US-11-045-024-13091

/ Sequence 13091, Application US/11045024  
/ Publication No. US20050271676A1

/ GENERAL INFORMATION:

/ APPLICANT: Sette, Alessandro

/ APPLICANT: Sidney, John

/ APPLICANT: Southwood, Scott

/ APPLICANT: Livingston, Brian

/ APPLICANT: Chesnut, Robert

/ APPLICANT: Baker, Denise Marie

/ APPLICANT: Celis, Esceban

/ APPLICANT: Kubo, Ralph

/ APPLICANT: Grey, Howard M.

/ APPLICANT: Epiimmune Inc.

/ TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency  
/ TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions

/ FILE REFERENCE: 2060.0040007

/ CURRENT APPLICATION NUMBER: US/11/045,024

/ CURRENT FILING DATE: 2005-01-28

/ PRIOR APPLICATION NUMBER: US 09/412,863

/ PRIOR FILING DATE: 1999-10-05

/ PRIOR APPLICATION NUMBER: US 08/027,146

/ PRIOR FILING DATE: 1993-03-05

/ PRIOR APPLICATION NUMBER: US 08/073,205

/ PRIOR FILING DATE: 1993-06-04

/ PRIOR APPLICATION NUMBER: US 08/103,396

/ PRIOR FILING DATE: 1993-08-06

/ PRIOR APPLICATION NUMBER: US 08/159,184

/ PRIOR FILING DATE: 1993-11-29

/ PRIOR APPLICATION NUMBER: US 08/159,339

/ PRIOR FILING DATE: 1993-11-29

/ PRIOR APPLICATION NUMBER: US 08/205,713

/ PRIOR FILING DATE: 1994-03-04

/ PRIOR APPLICATION NUMBER: US 08/347,610

/ PRIOR FILING DATE: 1994-12-01

/ NUMBER OF SEQ ID NOS: 14528

/ SOFTWARE: FastSeq for Windows Version 4.0

/ SEQ ID NO 13091

/ LENGTH: 15

/ TYPE: PRT

/ ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS

/ US-11-045-024-13091

/ Query Match

/ Best Local Similarity 21.5%; Score 24.5; DB 7; Length 15;

/ Matches 7; Conservative 1; Mismatches 3; Indels 3; Gaps 1;

/ QY 5 PGSRLGNP 15

/ DB 1 PGNFLONRPEPTAP 14

/ RESULT 99

/ US-11-105-708-25

/ Sequence 25, Application US/11105708

/ Publication No. US20050281821A1

/ GENERAL INFORMATION:

/ APPLICANT: Pernaas, Flavia

/ APPLICANT: Freimark, Bruce

/ APPLICANT: Van Epps, Dennis

/ APPLICANT: Brooks, Peter C

/ TITLE OF INVENTION: Method and Composition for Angiogenesis Inhibition

/ FILE REFERENCE: 30797-704.501

/ CURRENT APPLICATION NUMBER: US/11/105,708

/ CURRENT FILING DATE: 2005-04-13

/ PRIOR APPLICATION NUMBER: 09/478,977

/ PRIOR FILING DATE: 2000-01-06

/ PRIOR APPLICATION NUMBER: 60/152,496  
/ PRIOR FILING DATE: 1999-09-02  
/ PRIOR APPLICATION NUMBER: 60/143,534  
/ PRIOR FILING DATE: 1999-09-02  
/ PRIOR APPLICATION NUMBER: 60/114,878  
/ PRIOR FILING DATE: 1999-01-06  
/ PRIOR APPLICATION NUMBER: 60/114,877  
/ PRIOR FILING DATE: 1999-01-06  
/ NUMBER OF SEQ ID NOS: 25  
/ SOFTWARE: PatentIn version 3.2  
/ SEQ ID NO 25  
/ LENGTH: 9  
/ TYPE: PRT  
/ ORGANISM: Artificial  
/ FEATURE:  
/ OTHER INFORMATION: Synthetic peptide  
/ US-11-105-708-25

Query Match  
Best Local Similarity 21.1%; Score 24; DB 7; Length 9;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKYP 5  
DB 3 DHQYP 7

RESULT 100  
US-10-859-643-448

/ Sequence 448, Application US/10859643

/ Publication No. US20060002993A1

/ GENERAL INFORMATION:

/ APPLICANT: Challita-Eid, Pia M.

/ APPLICANT: Raitano, Arthur B.

/ APPLICANT: Fails, Mary

/ APPLICANT: Hubert, Rene S.

/ APPLICANT: Morlison, Karen Jane Meyrick

/ TITLE OF INVENTION: Nucleic Acid and Corresponding Protein

/ TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of

/ FILE REFERENCE: 511582006203

/ CURRENT APPLICATION NUMBER: US/10/859,643

/ CURRENT FILING DATE: 2004-06-02

/ PRIOR APPLICATION NUMBER: US 10/005,480

/ PRIOR FILING DATE: 2001-11-07

/ NUMBER OF SEQ ID NOS: 765

/ SOFTWARE: FastSeq for Windows Version 4.0

/ SEQ ID NO 448

/ LENGTH: 10

/ TYPE: PRT

/ ORGANISM: Homo Sapien

/ US-10-859-643-448

/ Query Match

/ Best Local Similarity 21.1%; Score 24; DB 6; Length 10;

/ Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 YKYPGSL 9  
DB 1 YKYPGSL 8

Search completed: January 20, 2006, 19:46:28  
Job time : 9.07692 secs

**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using SW model

Run on: January 20, 2006, 18:55:50 : Search time 11.3462 Seconds  
(without alignment)  
169.602 Million cell updates/sec

Title: US-09-662-293-2

Perfect score: 114  
Sequence: 1 DYEPGSRGNPKAPLYKRP 20

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 3886

Minimum DB seq length: 0  
Maximum DB seq length: 20

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 100 summaries

Database :

1: PIR 80: \*  
2: p1r1: \*  
3: p1r2: \*  
4: p1r3: \*  
5: p1r4: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	33	28.9	18	2	S36120
2	29	25.4	16	2	PH0137
3	29	25.4	19	2	S59485
4	27	23.7	15	2	A08416
5	26	22.8	13	2	IS0173
6	26	22.8	20	2	S44465
7	25.5	22.4	16	2	PT0224
8	25.5	22.4	18	2	PQ0072
9	25	21.9	9	2	S70332
10	25	21.9	11	2	PT0217
11	25	21.9	16	2	PH1302
12	25	21.9	16	2	B28587
13	24	21.1	10	2	S62880
14	24	21.1	15	2	D28587
15	24	21.1	15	2	F28587
16	24	21.1	15	2	PH0772
17	24	21.1	15	2	A49255
18	24	21.1	16	2	F53284
19	24	21.1	19	2	A05505
20	23	20.2	14	2	S62374
21	23	20.2	15	2	S27248
22	23	20.2	15	2	PN0665
23	23	20.2	15	2	PT0097
24	23	20.2	16	2	PH0749
25	23	20.2	16	2	S10678
26	23	20.2	17	2	G85956
27	23	20.2	20	2	PQ0046
28	22.5	19.7	14	2	S23369
29	22	19.3	11	2	S04875

30	22	19.3	11	4	I54081	retinoic acid rece
31	22	19.3	15	2	S21238	hydrogen sulfite re
32	22	19.3	17	2	S58660	H+-transporting tw
33	22	19.3	18	1	A58589	alpha-conotoxin EI
34	22	19.3	18	2	S56715	hydroxymethylgluta
35	22	19.3	18	2	A29558	pigment-dispersing
36	22	19.3	20	2	G61491	seed protein wa-25
37	22	19.3	20	2	A49142	hyaluronidase (EC
38	22	19.3	20	2	A34859	heliothermine (Mex
39	21.5	18.9	10	1	XASNPC	angiotensin-conver
40	21	18.4	11	2	I33098	173k exoantigen -
41	21	18.4	14	2	BSTD	bombesin - fire-fl
42	21	18.4	14	2	PH1322	Ig heavy chain DJ
43	21	18.4	14	2	PN0666	dystrophin-associ
44	21	18.4	15	2	PQ0195	Sfil1-glycoprotein
45	21	18.4	15	2	S29485	GTP-binding protei
46	21	18.4	15	2	S51735	T-cell receptor be
47	21	18.4	15	2	I53284	T-cell receptor be
48	21	18.4	15	2	PT0091	H+-transporting tw
49	21	18.4	16	2	PH1580	Ig H chain V-D-J r
50	21	18.4	16	2	H35141	T-cell receptor de
51	21	18.4	18	1	MTROB	melanotropin beta
52	21	18.4	18	1	DRUPD	pigment-dispersing
53	21	18.4	18	2	A45590	beta-pigment-dispe
54	21	18.4	19	2	PH1609	Ig H chain V-D-J r
55	21	18.4	20	2	S72501	protein kinase C 1
56	21	18.4	20	2	S19240	histone H2B (clone
57	21	18.4	20	2	B53592	H+-exporting ATPas
58	20.5	18.0	13	2	PH0756	T-cell receptor be
59	20.5	18.0	20	2	B59326	ribosomal protein
60	20	17.5	4	2	PT0240	Ig heavy chain CRD
61	20	17.5	7	2	A38081	amine oxidase (cop
62	20	17.5	8	2	A41117	acetylcholinestera
63	20	17.5	10	1	A61126	gonadolibertin - sp
64	20	17.5	10	1	RHA02	gonadolibertin II -
65	20	17.5	10	2	S24190	cryptase (EC 3.4.2
66	20	17.5	10	2	B46030	gonadolibertin II -
67	20	17.5	11	2	B41476	probable antigen 5
68	20	17.5	11	2	S07207	Crln1a-angiotensin
69	20	17.5	12	2	S74196	3-hydroxy-3-methyl
70	20	17.5	12	2	PN0663	dystrophin-associ
71	20	17.5	12	2	C20907	Ig kappa-1 chain J
72	20	17.5	12	2	A61503	sterol carrier pro
73	20	17.5	13	2	S63492	dissimilatory sulf
74	20	17.5	13	2	C53275	Ig kappa-1 chain J
75	20	17.5	13	2	S33800	chaperone, TCP1-re
76	20	17.5	14	2	S60353	amylopullulanase -
77	20	17.5	14	2	B60683	maize dehydratase
78	20	17.5	15	2	S24159	leukocyte elastase
79	20	17.5	15	2	S59492	formate dehydrogen
80	20	17.5	15	2	PA0002	phocovsystem II oxy
81	20	17.5	15	2	PL0143	carbon-monoxide de
82	20	17.5	15	2	S36896	ribosomal protein
83	20	17.5	15	2	S04586	NADH2 dehydrogenas
84	20	17.5	16	2	B54877	alpha-conotoxin Pn
85	20	17.5	16	2	T37075	hypothetical prote
86	20	17.5	16	2	G24304	ribosomal protein
87	20	17.5	16	2	PT0237	Ig heavy chain CDR
88	20	17.5	16	2	A42291	tail fiber protein
89	20	17.5	16	2	JT0609	leukocyte chemotac
90	20	17.5	17	2	B61334	lysozyme (EC 3.4.21
91	20	17.5	17	2	I49593	cystic fibrosis tr
92	20	17.5	17	2	I84733	gene CFRP protein
93	20	17.5	17	2	B25348	glycogen (starch) a
94	20	17.5	18	2	S47196	T-cell receptor J-
95	20	17.5	18	2	B44239	amine oxidase (cop
96	20	17.5	19	2	S25715	hypothetical prote
97	20	17.5	19	2	S43045	translation elonga
98	20	17.5	20	2	JP0059	ribosomal protein
99	20	17.5	20	2	B46174	RNA-binding protei
100	19.5	17.1	16	2	S38292	30k allergen - rye

## ALIGNMENTS

## RESULT 1

S36120  
 lectin - Euphorbia marginata (fragment)  
 C|Species: Euphorbia marginata  
 C|Date: 19-Mar-1997 #sequence\_revision 06-Jun-1997 #text\_change 09-Jul-2004  
 C|Accession: S36120  
 R|Stipe, F.; Licastrero, F.; Morill, M.C.; Parente, A.; Savino, G.; Abbondanza, A.; Bolog  
 Blochtm. Biophys. Acta 1158, 33-39, 1993  
 A|Title: Purification and partial characterization of a mitogenic lectin from the latex  
 A|Reference number: S36120; PMID:93537266; PMID:8353129  
 A|Accession: S36120  
 A|Molecule type: protein  
 A|Residues: 1-18 <SRI>  
 A|Cross-references: UNIPROT:P33889; UNIPARC:UPI00001256C1  
 C|Keywords: lectin

## Query Match

Best Local Similarity 28.9%; Score 33; DB 2; Length 18;  
 Pred. No. 88;  
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 YPGSRLGNP 12  
 |||||  
 Db 2 YPGSHISGP 10

## RESULT 2

PH0137  
 T-cell receptor beta chain V-D-J region M320 - human (fragment)  
 C|Species: Homo sapiens (man)  
 C|Date: 23-Nov-1991 #sequence\_revision 23-Nov-1991 #text\_change 30-May-1997  
 C|Accession: PH0137  
 R|Martin, R.; Howell, M.D.; Uraquemada, D.; Fierlage, M.; Richert, J.; Brostoff, S.; Lo  
 J. Exp. Med. 173, 19-24, 1991  
 A|Title: A myelin basic protein peptide is recognized by cytotoxic T cells in the contex  
 A|Reference number: PH0135; PMID:91086843; PMID:1702137  
 A|Accession: PH0137  
 A|Molecule type: mRNA  
 A|Residues: 1-16 <MAR>  
 A|Cross-references: UNIPARC:UPI000017C3AF  
 C|Keywords: T-cell receptor

## Query Match

Best Local Similarity 25.4%; Score 29; DB 2; Length 16;  
 Pred. No. 33e+02;  
 Matches 6; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 2 YEPGSRGNPKAPLY 17  
 |||||  
 Db 1 YFCASRRKDSPPSPPLH 16

## RESULT 3

S59485  
 hyroxyproline-rich cell wall glycoprotein (42k and others) - kidney bean (fragment)  
 C|Species: Phaseolus vulgaris (kidney bean)  
 C|Date: 27-Apr-1996 #sequence\_revision 26-Jul-1996 #text\_change 09-Jul-2004  
 C|Accession: S59485; S59485; S59483  
 R|Mojlaszek, P.; Trethowan, J.; Bolwell, G.P.  
 Plant Mol. Biol. 28, 1075-1087, 1995  
 A|Title: Specificity in the immobilization of cell wall proteins in response to differen  
 A|Reference number: S59481; PMID:96011753; PMID:7548825  
 A|Accession: S59485  
 A|Molecule type: protein  
 A|Residues: 1-19 <WOJ>  
 A|Cross-references: UNIPROT:Q7M1M8; UNIPARC:UPI0000177E5D  
 A|Note: hyroxyproline-rich cell wall glycoprotein, 42k  
 A|Accession: S59484  
 A|Molecule type: protein  
 A|Residues: 1-15 <WOW>  
 A|Cross-references: UNIPARC:UPI0000177E5E  
 A|Note: hyroxyproline-rich cell wall glycoprotein, 84k

A|Accession: S59483

A|Molecule type: protein

A|Residues: 1-14 <WOF>

A|Cross-references: UNIPARC:UPI0000177E5P

A|Note: hyroxyproline-rich cell wall glycoprotein, 136k, minor component

C|Superfamily: proline-rich protein 3

C|Keywords: glycoprotein; hydroxyproline

F,6,11,16/Modified site: hydroxyproline (Pro) #status experimental

## Query Match

Best Local Similarity 25.4%; Score 29; DB 2; Length 19;  
 Pred. No. 4e+02;  
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 13 KAPLYKRP 20  
 |||||  
 Db 9 KPVYIKRP 16

## RESULT 4

A08416  
 lombriclike kinase (EC 2.7.3.5) - earthworm (lumbicus terrestris) (fragment)  
 C|Species: Lumbicus terrestris (common earthworm)  
 C|Date: 21-May-1988 #sequence\_revision 21-May-1988 #text\_change 09-Jul-2004  
 C|Accession: A08416  
 R|der Terrosian, B.; Deevages, G.; Pradel, L.A.; Kassab, R.; van Thoai, N.  
 Eur. J. Biochem. 22, 585-592, 1971  
 A|Title: Comparative structural studies of the active site of ATP: guanidine phosphotran  
 A|Reference number: A08416; PMID:72066544; PMID:5128744  
 A|Accession: A08416  
 A|Molecule type: protein  
 A|Residues: 1-15 <DER>  
 A|Cross-references: UNIPROT:P11918; UNIPARC:UPI000012DEBE  
 C|Keywords: phosphotransferase

## Query Match

Best Local Similarity 23.7%; Score 27; DB 2; Length 15;  
 Pred. No. 6.4e+02;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 PGSRLG 10  
 |||||  
 Db 7 PGSNLG 12

## RESULT 5

I50173  
 alpha-2 collagen - chicken (fragment)  
 C|Species: Gallus gallus (chicken)  
 C|Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 09-Jul-2004  
 C|Accession: I50173  
 R|Arvedimenco, B.V.; Vogel, G.; Yamada, Y.; Matzel, J.V.  
 Cell 21, 689-696, 1980  
 A|Title: Correlation between splicing sites within an intron and their sequence compleme  
 A|Reference number: I50172; PMID:81064671; PMID:6159982  
 A|Accession: I50173  
 A|Status: preliminary; translated from GB/EMBL/DBJ  
 A|Molecule type: DNA  
 A|Residues: 1-13 <AV>  
 A|Cross-references: UNIPROT:P02467; UNIPARC:UPI00001712AB; GB:M10540; NID:9211324; PIDN  
 C|Genetics:  
 A|introns: 12/3

## Query Match

Best Local Similarity 22.8%; Score 26; DB 2; Length 13;  
 Pred. No. 7.8e+02;  
 Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 5 PGSRLGNPKAP 15  
 |||||  
 Db 2 PGSRLGNPKAP 12

## RESULT 6

S44465  
 pyrrhocoricin - Pyrrhocoris apterus

C/Species: Pyrrhocoris apterus  
C/Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 09-Jul-2004  
C/Accession: S44465

R/Cocciandich, S.; Dupont, A.; Hegy, G.; Lanot, R.; Holder, F.; Hetru, C.; Hoffmann, J.A.

Biochem. J. 300, 567-575, 1994

A/Title: Novel inducible antibacterial peptides from a hemipteran insect, the sap-sucking

A/Reference number: S44463; PMID:8002963

A/Accession: S44465

A/Molecule type: protein

A/Residues: 1-20 <COC>

A/Cross-references: UNIPROT:P37362; UNIPARC:UPI0000132E13

C/Function: antibacterial protein

A/Description: active against Gram-negative bacteria

C/Keywords: antibacterial; hemolymph; immune response

Query Match 22.8%; Score 26; DB 2; Length 20;

Best Local Similarity 50.0%; Pred. No. 1.2e+03;

Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 12 PKAPLYKR 19

DB 12 PPRPIYNR 19

RESULT 7

PT0224

Ig heavy chain CDR3 region (clone 1-91) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996

C/Accession: PT0224

R/Yamada, M.; Masserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.

J. Exp. Med. 173, 395-407, 1991

A/Title: Preferential utilization of specific immunoglobulin heavy chain diversity and

A/Reference number: PT0222; PMID:9108337; PMID:1899102

A/Accession: PT0224

A/Molecule type: DNA

A/Residues: 1-16 <YAM>

A/Cross-references: UNIPARC:UPI000017C1D6

A/Experimental source: B lymphocyte

A/Note: the authors translated the stop codon for residue 9 as X

C/Keywords: heterotrimer; immunoglobulin

Query Match 22.4%; Score 25.5; DB 2; Length 16;

Best Local Similarity 57.1%; Pred. No. 1.2e+03;

Matches 8; Conservative 0; Mismatches 3; Indels 3; Gaps 2;

QY 1 DYEYPSRL--GNP 12

DB 4 DYSY-GXLLGPNP 16

RESULT 8

PQ0072

T-cell receptor beta chain (BTB98) - bovine (fragment)

C/Species: Bos primigenius taurus (cattle)

C/Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 20-Feb-1995

C/Accession: PQ0072

R/Tanaka, A.; Ishiguro, N.; Shingawa, M.

submitted to JIPD, May 1990

A/Description: Sequence analysis of bovine T-cell receptor beta chain genes.

A/Reference number: JQ0472

A/Accession: PQ0072

A/Molecule type: mRNA

A/Residues: 1-18 <TAN>

A/Cross-references: UNIPARC:UPI000011D064

A/Experimental source: T cell

C/Genetics:

A/Gene: BTB98

C/Keywords: receptor

Query Match 22.4%; Score 25.5; DB 2; Length 16;

Best Local Similarity 50.0%; Pred. No. 1.3e+03;

Matches 5; Conservative 3; Mismatches 1; Indels 1; Gaps 1;

QY 1 DYEYPSRL 9

DB 6 DYHGPETKL 15

RESULT 9

S70332

endosperm protein, 10K - rye (fragment)

C/Species: Secale cereale (rye)

C/Date: 19-Mar-1998 #sequence\_revision 17-Apr-1998 #text\_change 17-Apr-1998

C/Accession: S70332

R/Rocher, A.; Calero, M.; Soriano, F.; Mendez, E.

Biochim. Biophys. Acta 1295, 13-22, 1996

A/Title: Identification of major rye secalins as coeliac immunoreactive proteins.

A/Reference number: S70327; PMID:8679669

A/Accession: S70332

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-9 <ROC>

A/Cross-references: UNIPARC:UPI000017B132

Query Match 21.9%; Score 25; DB 2; Length 9;

Best Local Similarity 66.7%; Pred. No. 2.8e+05;

Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 YEYRGS 7

DB 4 YEYAGN 9

RESULT 10

PT0217

T-cell receptor beta chain V-J region (4-1-E-2) - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 31-Dec-1991 #sequence\_revision 31-Dec-1991 #text\_change 30-May-1997

C/Accession: PT0217

R/Nakano, N.; Kikutan, H.; Nishimoto, H.; Kishimoto, T.

J. Exp. Med. 173, 1091-1097, 1991

A/Title: T cell receptor V gene usage of fetal beta cell-reactive T cells is not restri

A/Reference number: PT0209; PMID:91217621; PMID:1902501

A/Accession: PT0217

A/Molecule type: mRNA

A/Residues: 1-11 <NAK>

A/Cross-references: UNIPARC:UPI000017C851

C/Keywords: T-cell receptor

Query Match 21.9%; Score 25; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 9.4e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 SRLGN 11

DB 3 SRLGN 7

RESULT 11

PH1302

Ig heavy chain DJ region (clone C76-105) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999

C/Accession: PH1302

R/Masserman, R.; Gallil, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.

J. Exp. Med. 176, 1577-1581, 1992

A/Title: Predominance of fetal type DJH joining in young children with B precursor lymph

A/Reference number: PH1302; PMID:93094761; PMID:1460419

A/Accession: PH1302

A/Molecule type: DNA

A/Residues: 1-16 <WAS>

A/Cross-references: UNIPARC:UPI000017C24C

C/Keywords: heterotrimer; immunoglobulin

Query Match 21.9%; Score 25; DB 2; Length 16;  
Best Local Similarity 46.2%; Pred. No. 1.4e+03;  
Matches 6; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 3 YEPGSLGNPKAP 15  
| | | | |  
| | | | |  
Db 1 EYISGLVRLGP 13

RESULT 12  
B28587  
T-cell receptor beta-2 chain J-B2.3 segment - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 16-Aug-1988 #sequence\_revision 16-Aug-1988 #text\_change 05-Nov-1999  
C/Accession: B28587  
R/Toyonaga, B.; Yoshikai, Y.; Vadasz, V.; Chin, B.; Mak, T.W.  
Proc. Natl. Acad. Sci. U.S.A. 82, 8624-8628, 1985  
A/Title: Organization and sequences of the diversity, joining, and constant region genes  
A/Reference number: A94081; MUID:86094276; PMID:3866244  
A/Accession: B28587  
A/Molecule type: DNA  
A/Residues: 1-16 <TOY>  
A/Cross-references: UNIPARC:UPI000002FDD6; GB:M14159; NID:G338852; PIDN:AAA60677.1; PID:  
C/Keywords: T-cell receptor

Query Match 21.9%; Score 25; DB 2; Length 16;  
Best Local Similarity 54.5%; Pred. No. 1.4e+03;  
Matches 6; Conservative 2; Mismatches 1; Indels 2; Gaps 1;

QY 1 DYEX--PGSRL 9  
| | | | |  
| | | | |  
Db 3 DTQYFGPGTRL 13

RESULT 13  
S62880  
polygalacturonase (EC 3.2.1.15) IV - Aspergillus sp. (fragment)  
C/Species: Aspergillus sp.  
C/Date: 28-Oct-1996 #sequence\_revision 13-Mar-1997 #text\_change 09-Jul-2004  
C/Accession: S62880  
R/Stratillova, E.; Dzurova, M.; Markovic, O.; Joernvall, H.  
FEBS Lett. 382, 164-166, 1996  
A/Title: An essential tyrosine residue of Aspergillus polygalacturonase.  
A/Reference number: S62880; MUID:96196586; PMID:8612742  
A/Accession: S62880  
A/Molecule type: protein  
A/Residues: 1-10 <STR>  
A/Cross-references: UNIPROT:Q7M500; UNIPARC:UPI000017B3DA  
A/Keywords: glycosidase; hydrolase  
F/4/Active site: Tyr #status predicted

Query Match 21.1%; Score 24; DB 2; Length 10;  
Best Local Similarity 66.7%; Pred. No. 1.2e+03;  
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 DYEYFG 6  
| | | | |  
| | | | |  
Db 1 DYAYTG 6

RESULT 14  
D28587  
T-cell receptor beta-2 chain J-B2.5 segment - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 16-Aug-1988 #sequence\_revision 16-Aug-1988 #text\_change 05-Nov-1999  
C/Accession: D28587  
R/Toyonaga, B.; Yoshikai, Y.; Vadasz, V.; Chin, B.; Mak, T.W.  
Proc. Natl. Acad. Sci. U.S.A. 82, 8624-8628, 1985  
A/Title: Organization and sequences of the diversity, joining, and constant region genes  
A/Reference number: A94081; MUID:86094276; PMID:3866244  
A/Accession: D28587  
A/Molecule type: DNA  
A/Residues: 1-15 <TOY>

A/Cross-references: UNIPARC:UPI0000113C7C; GB:M14159; NID:G338852; PIDN:AAA60679.1; PID:  
C/Keywords: T-cell receptor

Query Match 21.1%; Score 24; DB 2; Length 15;  
Best Local Similarity 62.5%; Pred. No. 1.9e+03;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 YEPGSL 9  
| | | | |  
| | | | |  
Db 5 YRPGGTRL 12

RESULT 15  
F28587  
T-cell receptor beta-2 chain J-B2.7 segment - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 16-Aug-1988 #sequence\_revision 16-Aug-1988 #text\_change 05-Nov-1999  
C/Accession: F28587  
R/Toyonaga, B.; Yoshikai, Y.; Vadasz, V.; Chin, B.; Mak, T.W.  
Proc. Natl. Acad. Sci. U.S.A. 82, 8624-8628, 1985  
A/Title: Organization and sequences of the diversity, joining, and constant region genes  
A/Reference number: A94081; MUID:86094276; PMID:3866244  
A/Accession: F28587  
A/Molecule type: DNA  
A/Residues: 1-15 <TOY>  
A/Cross-references: UNIPARC:UPI0000113C7E; GB:M14159; NID:G338852; PIDN:AAA60681.1; PID:  
C/Keywords: T-cell receptor

Query Match 21.1%; Score 24; DB 2; Length 15;  
Best Local Similarity 62.5%; Pred. No. 1.9e+03;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 YEPGSL 9  
| | | | |  
| | | | |  
Db 5 YRPGGTRL 12

RESULT 16  
PH0772  
T-cell receptor beta chain (I4) - mouse (fragment)  
C/Species: Mus musculus (house mouse)  
C/Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 05-Nov-1999  
C/Accession: PH0772  
R/Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.  
J. Exp. Med. 174, 1371-1383, 1991  
A/Title: T cell receptor genes in a series of class I major histocompatibility complex-1  
allelic exclusion and antigen-specific repertoire.  
A/Reference number: PH0746; MUID:92078846; PMID:1836010  
A/Accession: PH0772  
A/Molecule type: mRNA  
A/Residues: 1-15 <CAS>  
A/Cross-references: UNIPARC:UPI0000115PBF; EMBL:X60866; NID:G52749; PIDN:CAA43256.1; PIC:  
A/Experimental source: T lymphocyte  
C/Keywords: T-cell receptor

Query Match 21.1%; Score 24; DB 2; Length 15;  
Best Local Similarity 45.5%; Pred. No. 1.9e+03;  
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 7 SRLGNPKAPLY 17  
| | | | |  
| | | | |  
Db 4 SRDRDQAPLF 14

RESULT 17  
A42255  
T-cell receptor beta chain V-D-J-C region (V beta 7, J beta 1.6) - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 21-Jan-1994 #sequence\_revision 18-Nov-1994 #text\_change 30-May-1997  
C/Accession: A42255  
R/Rosenberg, W.W.; Moss, P.A.; Bell, J.I.  
Eur. J. Immunol. 22, 541-549, 1992  
A/Title: Variation in human T cell receptor V beta and J beta repertoire: analysis using

A/Reference number: A49039; MUID:92164737; PMID:1311263  
 A/Accession: A49255  
 A/Status: preliminary; not compared with conceptual translation  
 A/Molecule type: nucleic acid  
 A/Residues: 1-16 <ROS>  
 A/Cross-references: UNIPARC:UPI000017C3B9  
 A/Note: sequence extracted from NCBI backbone (NCBIF:90722)  
 C/Keywords: T-cell receptor

Query Match 21.1%; Score 24; DB 2; Length 16;  
 Best Local Similarity 35.7%; Pred. No. 2e+03;  
 Matches 5; Conservative 4; Mismatches 1; Indels 4; Gaps 1;

QY 4 YPGSR LGNPKAPY 17  
 |||: |||:  
 Db 5 YPGTQ---NSPLH 14

## RESULT 18

F53284

T-cell receptor beta 2 chain J region, Dbeta2.3 - rabbit

C/Species: Oryctolagus cuniculus (domestic rabbit)

C/Date: 02-May-1994 #sequence\_revision 18-Nov-1994 #text\_change 05-Nov-1999

C/Accession: F53284

R/Harindranath, N.; Alexander, C.B.; Mage, R.G.

Mol. Immunol. 28, 881-888, 1991

A/Title: Evolutionarily conserved organization and sequences of germline diversity and

A/Reference number: A53284; MUID:91342695; PMID:1678859

A/Accession: F53284

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-16 &lt;HAR&gt;

A/Cross-references: UNIPARC:UPI0000115415; GB:S60737; NID:g233916; PIDN:AA19522.1; PID:

A/Note: sequence extracted from NCBI backbone (NCBIN:60737; NCBIF:60744)

C/Keywords: T-cell receptor

Query Match 21.1%; Score 24; DB 2; Length 16;  
 Best Local Similarity 62.5%; Pred. No. 2e+03;  
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 YBPGSRL 9  
 | |||:  
 Db 6 YBPGTRL 13

## RESULT 19

A05305

hemoglobin beta-2 chain - Indian spiny-tailed lizard (fragment)

C/Species: Uromastyx hardwickii (Indian spiny-tailed lizard)

C/Date: 05-Jun-1987 #sequence\_revision 05-Jun-1987 #text\_change 09-Jul-2004

C/Accession: A05305

R/Nagy, S.; Zaidi, Z.H.; von Bahr-Lindstrom, H.; Carlquist, M.; Jernvall, H.

FEBS Lett. 162, 290-295, 1983

A/Reference number: A91314; MUID:84029159; PMID:6628672

A/Accession: A05305

A/Molecule type: protein

A/Residues: 1-19 &lt;NMQ&gt;

A/Cross-references: UNIPROT:P18992; UNIPARC:UPI000012C204

C/Keywords: erythrocyte; oxygen carrier

Query Match 21.1%; Score 24; DB 2; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 2.4e+03;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GNPX 13  
 |||:  
 Db 16 GNPX 19

## RESULT 20

S62374

alpha-1-antichymotrypsin - human (fragment)

C/Date: 24-Aug-1996 #sequence\_revision 13-Mar-1997 #text\_change 31-Dec-2004

C/Accession: S62374

R/Tsuda, M.; Sei, Y.; Ohkubo, T.; Yamamura, M.; Kamiguchi, H.; Akatsuka, A.; Tsuda, T.;

Eur. J. Biochem. 235, 821-827, 1996

A/Title: The defective secretion of a naturally occurring alpha-1-antichymotrypsin vari

A/Reference number: S62374; MUID:96184564; PMID:8654434

A/Accession: S62374

A/Status: preliminary; not compared with conceptual translation

A/Molecule type: mRNA

A/Residues: 1-14 &lt;TSU&gt;

A/Cross-references: UNIPROT:Q9UNU9; UNIPROT:Q96DW8; UNIPROT:Q8N177; UNIPARC:UPI000017C0

C/Superfamily: serpin

Query Match 20.2%; Score 23; DB 2; Length 14;  
 Best Local Similarity 57.1%; Pred. No. 2.5e+03;  
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

## RESULT 21

S27248

pseudogermpl - wheat

C/Species: Triticum aestivum (common wheat)

C/Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 29-Aug-1997

C/Accession: S27248

R/Lane, B.G.; Cumling, A.C.; Peregau, J.; Carlita, N.C.; Hurkman, W.J.; Bernier, F.; Dra

Bur. J. Biochem. 209, 961-969, 1992

A/Title: Germpl isoforms are discrete temporal markers of wheat development. Pseudogerm

ated embryos, it is incorporated into cell walls.

A/Reference number: S27247; MUID:93049354; PMID:1425703

A/Accession: S27248

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-15 &lt;LAN&gt;

A/Cross-references: UNIPARC:UPI000017B14D

Query Match 20.2%; Score 23; DB 2; Length 15;  
 Best Local Similarity 30.8%; Pred. No. 2.7e+03;  
 Matches 4; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 3 EYPSRLGNPKAP 15  
 : |||:  
 Db 3 DYXPXNPXTXPXP 15

## RESULT 22

PN0665

dystrophin-associated glycoprotein A3a-IV - rabbit (fragment)

C/Species: Oryctolagus cuniculus (domestic rabbit)

C/Date: 19-May-1994 #sequence\_revision 19-May-1994 #text\_change 07-May-1999

C/Accession: PN0665

R/Yoshida, M.; Mizuno, Y.; Nonaka, I.; Ozawa, E.

J. Biochem. 114, 634-639, 1993

A/Title: A dystrophin-associated glycoprotein, A3a (one of 43DAG doublet), is retained

A/Reference number: PN0662; MUID:94156881; PMID:8113213

A/Accession: PN0665

A/Molecule type: protein

A/Residues: 1-15 &lt;YOS&gt;

A/Cross-references: UNIPARC:UPI000017C5C4

C/Comment: This protein is retained in Duchenne type muscular dystrophy muscle.

C/Keywords: glycoprotein; skeletal muscle

Query Match 20.2%; Score 23; DB 2; Length 15;  
 Best Local Similarity 57.1%; Pred. No. 2.7e+03;  
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 12 PRAPLYK 18  
 |||:  
 Db 9 PNAAPYQ 15

## RESULT 23

P00097

glutathione peroxidase, non-selenium containing - mouse (fragment)

N:Alternate names: antioxidant protein 2

C:Species: Mus musculus (house mouse)

C:Date: 21-Aug-1998 #sequence\_revision 21-Aug-1998 #text\_change 24-Nov-1999

C:Accession: P00097

R:Kawakami, T.; Uchida, T.; Sakai, T.; Kamo, M.; Morimasa, T.; Tsugita, A.

submitted to JIPI, July 1998

A:Description: Proteome analysis of mouse brain.

A:Reference number: P00091

A:Accession: P00097

A:Molecule type: protein

A:Residues: 1-15 &lt;KAW&gt;

A:Cross-references: UNIPARC:UPI000017C66B

A:Experimental source: brain, striatum

## Query Match

Best Local Similarity 20.2%; Score 23; DB 2; Length 15;

Matches 5; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 5 PGSRLLGNPKAPLYK 18

DB 1 PGGLLGLGXBPSPF 14

## RESULT 24

PH0749

T-cell receptor beta chain (883) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 05-Nov-1999

C:Accession: PH0749

R:Casanova, J.L.; Romero, P.; Widmann, C.; Koutlikky, P.; Maryanski, J.L.

J. Exp. Med. 174, 1371-1383, 1991

A:Title: T cell receptor genes in a series of class I major histocompatibility complex-  
allelic exclusion and antigen-specific repertoire.

A:Reference number: PH0746; MUID:9207846; PMID:1836010

A:Accession: PH0749

A:Molecule type: mRNA

A:Residues: 1-16 &lt;CAS&gt;

A:Cross-references: UNIPARC:UPI0000115FA8; EMBL:X60840; NID:G50116; PIDD:CAA43233.1; PIDD

A:Experimental source: T lymphocyte

C:Keywords: T-cell receptor

## Query Match

Best Local Similarity 20.2%; Score 23; DB 2; Length 16;

Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 11 NPKAPLY 17

DB 9 NNQAPLYF 15

## RESULT 25

S10678

aldehyde dehydrogenase (EC 1.-.-.-) - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 21-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 09-Jul-2004

C:Accession: S10678

R:Abbe, T.; Takada, K.; Ohkawa, K.; Matsuda, M.

Biochem. J. 269, 25-29, 1990

A:Title: Purification and characterization of a rat brain aldehyde dehydrogenase able to

A:Reference number: S10678; MUID:90328980; PMID:2375753

A:Accession: S10678

A:Molecule type: protein

A:Residues: 1-16 &lt;ABB&gt;

A:Cross-references: UNIPROT:Q7M053; UNIPARC:UPI000017C8AE

C:Keywords: oxidoreductase

## Query Match

Best Local Similarity 20.2%; Score 23; DB 2; Length 16;

Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 10 GNPAPLY 17

DB 3 GZPTAVMY 10

## RESULT 26

G85956

hypothetical protein 24331 [imported] - Escherichia coli (strain O157:H7, substrain EDL9

C:Species: Escherichia coli

C:Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 09-Jul-2004

C:Accession: G85956

R:Perma, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glaeser, J.D.; Rose, D.J.; Mayhew

Iller, L.; Grobeck, B.J.; Davis, N.W.; Lam, A.; Dimalanta, E.; Potamousis, K.; Apodaca,

Nature 409, 529-533, 2001

A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.

A:Reference number: A85480; MUID:21074935; PMID:11206551

A:Accession: G85956

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-17 &lt;STO&gt;

A:Cross-references: UNIPROT:Q8X4A4; UNIPARC:UPI00000D081B; GB:AE005174; NID:G12517539; P

A:Experimental source: strain O157:H7, substrain EDL933

C:Genetics:

A:Gene: 24331

## Query Match

Best Local Similarity 20.2%; Score 23; DB 2; Length 17;

Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 YPGSRLLG 10

DB 7 PFGKRYG 13

## RESULT 27

P00046

citrate (61)-synthase (EC 4.1.3.7) - Streptomyces hygroscopicus (fragment)

N:Alternate names: citrate condensing enzyme; citrogenase; condensing enzyme; oxaloaceta

C:Species: Streptomyces hygroscopicus

C:Date: 31-Dec-1990 #sequence\_revision 31-Dec-1990 #text\_change 09-Jul-2004

C:Accession: P00046

R:Shimotohno, K.W.; Imai, S.; Murakami, T.; Seto, H.

Agric. Biol. Chem. 54, 463-470, 1990

A:Title: Purification and characterization of citrate synthase from Streptomyces hygrosc

A:Reference number: P00106; MUID:90334852; PMID:1366511

A:Accession: P00046

A:Molecule type: protein

A:Residues: 1-20 &lt;SHI&gt;

A:Cross-references: UNIPROT:P20903; UNIPARC:UPI0000127A2B

A:Experimental source: strain SF-1293

C:Comment: This enzyme catalyzes the synthesis of citric acid.

C:Keywords: carbon-carbon lyase; coenzyme A; oxo-acid-lyase; tricarboxylic acid cycle

## Query Match

Best Local Similarity 20.2%; Score 23; DB 2; Length 20;

Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKYP 5

DB 13 EYSYP 17

## RESULT 28

S23369

T-cell receptor alpha chain J region - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 22-Nov-1993 #sequence\_revision 26-May-1995 #text\_change 17-Mar-1999

C:Accession: S23369

R:Pluschke, G.; Ricken, G.; Taube, H.; Kroninger, S.; Melchers, I.; Peter, H.H.; Eichmair

Eur. J. Immunol. 21, 2749-2754, 1991

A:Title: Biased T cell receptor V(alpha) region repertoire in the synovial fluid of rhe

A:Reference number: S23364; MUID:92037820; PMID:1657615



A/Accession: S23369  
 A/Status: preliminary; translation not shown  
 A/Molecule type: mRNA  
 A/Residues: 1-14 <PIV>  
 A/Cross-references: UNIPARC:UPI000017C390, EMBL:X58163  
 C/Keywords: T-cell receptor

Query Match 19.7%; Score 22.5; DB 2; Length 14;  
 Best Local Similarity 66.7%; Pred. No. 3e+03;  
 Matches 6; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

OY 3 EYPGSRIGN 11  
 |||  
 Db 4 EYGSQ-GN 11

RESULT 29  
 S04875  
 nifs protein - Bradyrhizobium japonicum (fragment)  
 C/Species: Bradyrhizobium japonicum  
 C/Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 09-Jul-2004  
 C/Accession: S04875  
 R/Beijing, S.  
 submitted to the EMBL Data Library, December 1988  
 A/Reference number: S04873  
 A/Accession: S04875  
 A/Molecule type: DNA  
 A/Residues: 1-11 <EBR>  
 A/Cross-references: UNIPROT:P37030, UNIPARC:UPI000016E719, EMBL:X13691, NID:G39544; PIDN  
 C/Genetics:  
 A/Status: nifs  
 A/Start codon: GTG

Query Match 19.3%; Score 22; DB 2; Length 11;  
 Best Local Similarity 60.0%; Pred. No. 2.8e+03;  
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 13 KAPLY 17  
 |||  
 Db 5 KAPLY 9

RESULT 30  
 I54081  
 retinoic acid receptor alpha, exon 3 (mistranslated) - human (fragment)  
 C/Species: Homo sapiens (man)  
 C/Date: 04-Jun-1999 #sequence\_revision 04-Jun-1999 #text\_change 09-Jul-2004  
 C/Accession: I54081  
 R/Dong, S.; Geng, J.P.; Tong, J.H.; Wu, Y.; Cai, J.R.; Sun, G.L.; Chen, S.R.; Wang, Z.Y.  
 Genes Chromosomes Cancer 6: 133-139, 1993  
 A/Title: Breakpoint clusters of the PML gene in acute promyelocytic leukemia: primary st  
 A/Reference number: I54081; MUID:93222087; PMID:7682097  
 A/Accession: I54081  
 A/Status: translated from GB/EMBL/DBJ  
 A/Molecule type: DNA  
 A/Residues: 1-11 <DON>  
 A/Cross-references: UNIPROT:Q1597, UNIPARC:UPI000065E17, GB:S57794, NID:G299073; PIDN  
 A/Note: the translation is from an incorrect reading frame  
 C/Genetics:  
 A/Status: GDB:RARA  
 A/Cross-references: GDB:120337, OMIM:180240  
 A/Map position: 17q12-17q12

Query Match 19.3%; Score 22; DB 4; Length 11;  
 Best Local Similarity 50.0%; Pred. No. 2.8e+03;  
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 12 PKAPLYR 19  
 |||  
 Db 4 PRAAVLRK 11

RESULT 31

S21238

hydrogensulfite reductase (EC 1.8.99.3) beta chain - Desulfovibrio vulgaris (fragment)  
 N/Alternate names: Bisulfite reductase; desulfotubercidin; desulfotubidin; desulfovibridi  
 C/Species: Desulfovibrio vulgaris  
 C/Date: 19-Mar-1997 #sequence\_revision 11-Jun-1999 #text\_change 11-Jun-1999  
 C/Accession: S21238  
 R/Pierik, A.J.; Duyvis, M.G.; van Helvoort, J.M.L.M.; Wolbert, R.B.G.; Hagen, W.R.  
 Eur. J. Biochem. 205: 111-115, 1992  
 A/Title: The third subunit of desulfovibridin-type dissimilatory sulfite reductases.  
 A/Reference number: S21197; MUID:92209491; PMID:1555572  
 A/Accession: S21238  
 A/Molecule type: protein  
 A/Residues: 1-15 <PIR>  
 A/Cross-references: UNIPARC:UPI000017AB71  
 A/Experimental source: strain Hildenborough  
 C/Genetics:  
 A/Status: dsrb  
 C/Complex: heterohexamer; two alpha, two beta and two gamma chains  
 C/Function:  
 A/Description: catalyzes the six-electron reduction of sulfite to sulfide  
 A/Pathway: the terminal oxidase in the sulfate-reduction pathway  
 C/Keywords: heterohexamer; oxidoreductase

Query Match 19.3%; Score 22; DB 2; Length 15;  
 Best Local Similarity 50.0%; Pred. No. 3.9e+03;  
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 11 NPRAPL 16  
 |||  
 Db 8 NPKEPM 13

RESULT 32  
 S58660  
 H+-transporting two-sector ATPase (EC 3.6.3.14) chain c - mouse (fragments)  
 C/Species: Mus musculus (house mouse)  
 C/Date: 15-Feb-1996 #sequence\_revision 01-Mar-1996 #text\_change 03-Jun-2002  
 C/Accession: S58660  
 R/Katz, M.L.; Gao, C.L.; Tompkins, J.A.; Bronson, R.T.; Chin, D.T.  
 Biochem. J. 310, 887-892, 1995  
 A/Title: Mitochondrial ATP synthase subunit c stored in hereditary ceroid-lipofusinosi  
 A/Reference number: S58658; MUID:96033188; PMID:7575423  
 A/Accession: S58660  
 A/Molecule type: protein  
 A/Residues: 1-10; 11-17 <KAT>  
 A/Cross-references: UNIPARC:UPI0000172E45; UNIPARC:UPI000017CD8E  
 C/Genetics:  
 A/Status: nifs  
 A/Keywords: hydrolase; mitochondrion

Query Match 19.3%; Score 22; DB 2; Length 17;  
 Best Local Similarity 33.3%; Pred. No. 4.9e+03;  
 Matches 4; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

OY 1 DYEPGSRIGN 12  
 |||  
 Db 1 DIDTAARFIGNP 12

RESULT 33  
 A58589  
 alpha-conotoxin EI - cone shell (Conus ermineus)  
 C/Species: Conus ermineus (ermine cone)  
 C/Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004  
 C/Accession: A58589  
 R/Martinez, J.S.; Oliveira, B.M.; Gray, W.R.; Craig, A.G.; Groebe, D.R.; Abramson, S.N.;  
 Biochemistry 34, 14519-14526, 1995  
 A/Title: alpha-Conotoxin EI, a new nicotinic acetylcholine receptor antagonist with nov  
 A/Reference number: A58589; MUID:96062516; PMID:7578057  
 A/Accession: A58589  
 A/Molecule type: protein  
 A/Residues: 1-18 <MAR>  
 A/Cross-references: UNIPROT:P50982, UNIPARC:UPI00001287C0

A/Note: sequence confirmed by chemical synthesis

C/Comment: This alpha-conotoxin, as an acetylcholine receptor inhibitor, is a postsynaptic

C/Superfamily: alpha-conotoxin

C/Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; hydroxyproline; post

F/3/Modified site: 4-hydroxyproline (Pro) #status experimental

F/4-10,5-18/disulfide bonds: #status experimental

F/18/Modified site: amidated carboxyl end (Cys) #status experimental

Query Match 19.3%; Score 22; DB 1; Length 18;

Best Local Similarity 30.0%; Pred. No. 4.7e+03; Mismatches 4; Indels 0; Gaps 0;

Matches 3; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 4 YPGSRGPNK 13

DB 7 HPRGNMNPQ 16

#### RESULT 34

556715

hydroxymethylglutaryl-CoA reductase (NADPH2) (EC 1.1.1.34) (clone hmg3.2) - potato (frag

C/Species: Solanum tuberosum (potato)

C/Date: 06-Dec-1996 #sequence\_revision 13-Mar-1997 #text\_change 09-Jul-2004

C/Accession: S56715

R/hatctacharya, M.K.; Patya, N.L.; Dixon, R.A.; Korth, K.L.; Sterner, B.A.

Plant Mol. Biol. 28, 1-15, 1995

A/Title: Features of the hmg 1 subfamily of genes encoding HMG-CoA reductase in potato.

A/Reference number: 556710; PMID:95306778; PMID:7787174

A/Accession: S56715

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-18 <BHA>

A/Cross-references: UNIPROT:Q41458; UNIPARC:UPI00000A2ED5; EMBL:L34830; NID:G529524; PDI

C/Keywords: coenzyme A; oxidoreductase

Query Match 19.3%; Score 22; DB 2; Length 18;

Best Local Similarity 66.7%; Pred. No. 4.7e+03; Mismatches 2; Indels 0; Gaps 0;

Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 12 PKAPLY 17

DB 7 PVKPLY 12

#### RESULT 35

A29558

pigment-dispersing hormone - eastern lubber grasshopper

C/Species: Romalea guttata (eastern lubber grasshopper)

C/Date: 05-Jun-1988 #sequence\_revision 05-Jun-1988 #text\_change 09-Jul-2004

C/Accession: A29558

R/Rao, K.R.; Mohr, C.J.; Riehm, J.P.; Zahow, C.A.; Norton, S.; Johnson, L.; Tarr, C.

J. Biol. Chem. 262, 2672-2675, 1987

A/Title: Primary structure of an analog of crustacean pigment-dispersing hormone from th

A/Reference number: A29558; PMID:87137516; PMID:3818616

A/Accession: A29558

A/Molecule type: protein

A/Residues: 1-18 <RAO>

A/Cross-references: UNIPROT:P09923; UNIPARC:UPI000017BE28

Query Match 19.3%; Score 22; DB 2; Length 18;

Best Local Similarity 54.5%; Pred. No. 4.7e+03; Mismatches 5; Indels 0; Gaps 0;

Matches 6; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 EYPSRLGNPK 13

DB 3 EITNSLGLPK 13

#### RESULT 36

G61491

seed protein ws-25 - winged bean (fragment)

C/Species: Psophocarpus tetragonolobus (winged bean)

C/Date: 07-Oct-1994 #sequence\_revision 07-Oct-1994 #text\_change 09-Jul-2004

C/Accession: G61491

R/Hirano, H.

J. Protein Chem. 8, 115-130, 1989

A/Title: Microsequence analysis of winged bean seed proteins electrophoretically separated from two dif

A/Reference number: A61491; PMID:89351606; PMID:2765119

A/Accession: G61491

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-20 <HIR>

A/Cross-references: UNIPROT:Q7M1P6; UNIPARC:UPI00001763B6

C/Superfamily: plant Kunitz-type proteinase inhibitor

C/Keywords: glycoprotein; seed

Query Match 19.3%; Score 22; DB 2; Length 20;

Best Local Similarity 40.0%; Pred. No. 5.2e+03; Mismatches 3; Indels 0; Gaps 0;

Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 YEPGSRGPN 11

DB 6 YDADGNKLVN 15

#### RESULT 37

A49142

hyaluronidase (EC 3.2.1.-) - stonefish (fragment)

C/Species: Synanceia horrida (stonefish)

C/Date: 19-Dec-1993 #sequence\_revision 11-Apr-1997 #text\_change 20-Jun-2000

C/Accession: A49142

R/Pho, C.H.; Yuen, R.; Chung, M.C.; Khoo, H.E.

Comp. Biochem. Physiol. B 101, 159-163, 1992

A/Title: Purification and partial characterization of hyaluronidase from stonefish (Syna

A/Reference number: A49142; PMID:92362165; PMID:1499262

A/Accession: A49142

A/Molecule type: protein

A/Residues: 1-20 <POH>

A/Cross-references: UNIPARC:UPI000017BF6B

A/Note: sequence extracted from NCBI Backbone (NCBI:111141)

C/Comment: This venom protein is produced by venom glands attached to the spines of the

C/Keywords: glycoprotein; glycosidase; hydrolase; venom

Query Match 19.3%; Score 22; DB 2; Length 20;

Best Local Similarity 50.0%; Pred. No. 5.2e+03; Mismatches 5; Indels 0; Gaps 0;

Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5 PGSRGPNK 14

DB 2 PSXDEGNKKA 11

#### RESULT 38

A34859

heliothermine - Mexican beaded lizard (fragment)

C/Species: Heloderma horridum (Mexican beaded lizard)

C/Date: 20-Jul-1990 #sequence\_revision 20-Jul-1990 #text\_change 09-Jul-2004

C/Accession: A34859

R/Mochizuki-Morales, J.; Martin, B.M.; Possant, L.D.

Toxicol. 28, 299-309, 1990

A/Title: Isolation and characterization of heliothermine, a novel toxin from Heloderma h

A/Reference number: A34859; PMID:90260878; PMID:1693019

A/Accession: A34859

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-20 <MOC>

A/Cross-references: UNIPROT:Q91055; UNIPARC:UPI000017BF68

Query Match 19.3%; Score 22; DB 2; Length 20;

Best Local Similarity 50.0%; Pred. No. 5.2e+03; Mismatches 4; Indels 0; Gaps 0;

Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 PGSRGPN 12

DB 7 PDLMTSNP 14

## RESULT 39

XASNPC

angiotensin-converting enzyme inhibitor - aspic viper

C/Species: Viper aaspis (aspic viper)

C/Date: 31-Mar-1993 #sequence\_revision 31-Mar-1993 #text\_change 09-Jul-2004

C/Accession: A60377

R/Komori, Y.; Sugihara, H.

Int. J. Biochem. 22, 767-771, 1990

A/Title: Characterization of a new inhibitor for angiotensin converting enzyme from the

A/Reference number: A60377; MUID:90382616; PMID:2169439

A/Accession: A60377

A/Molecule type: protein

A/Residues: 1-10 &lt;KOM&gt;

A/Cross-references: UNIPROT:P31351; UNIPARC:UPI0000126497

C/Superfamily: bradykinin-potentiating peptide

C/Keywords: angiotensin-converting enzyme inhibitor; pyroglutamic acid

P/1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match

Best Local Similarity 18.4%; Score 21.5; DB 1; Length 10;

Matches 5; Conservative 1; Mismatches 1; Indels 5; Gaps 1;

QY 4 YPGSRGNPKAP 15

Db 3 WPG----PKVP 9

## RESULT 40

I33098

173K exoantigen - malaria parasite (Plasmodium falciparum) (fragments)

C/Species: Plasmodium falciparum

C/Date: 24-Aug-1990 #sequence\_revision 24-Aug-1990 #text\_change 09-Jun-2000

C/Accession: I33098

R/Michols, J.H.; Hager, L.P.

Submitted to the Protein Sequence Database, May 1990

A/Reference number: A33098

A/Accession: I33098

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-11 &lt;NIC&gt;

A/Cross-references: UNIPARC:UPI0000178581

Query Match

Best Local Similarity 18.4%; Score 21; DB 2; Length 11;

Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 12 PKAPLY 17

Db 4 PKAPLY 9

## RESULT 41

B87D

bombesin - fire-bellied toad

C/Species: Bombina bombina (fire-bellied toad)

C/Date: 13-Jul-1981 #sequence\_revision 13-Jul-1981 #text\_change 31-Dec-2004

C/Accession: A01564

R/Anaetani, A.; Brzopamer, V.; Buccil, M.

Arch. Biochem. Biophys. 148, 443-446, 1972

A/Title: Isolation and amino acid sequences of alytesin and bombesin, two analogous acti

A/Reference number: A01564; MUID:72163516; PMID:4557042

A/Accession: A01564

A/Molecule type: protein

A/Residues: 1-14 &lt;ANA&gt;

A/Cross-references: UNIPROT:P01296; UNIPARC:UPI0000173523

C/Keywords: amidated carboxyl end; cutaneous gland; hormone; neuropeptide; pyroglutamic

P/1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

P/14/Modified site: amidated carboxyl end (Met) #status experimental

Query Match

Best Local Similarity 18.4%; Score 21; DB 1; Length 14;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 RLGN 11

Db 3 RLGN 6

## RESULT 42

PH1322

Ig heavy chain DJ region (clone C344-99) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999

C/Accession: PH1322

R/Wasserman, R.; Gallil, N.; Ito, Y.; Retchard, B.A.; Shane, S.; Rovera, G.

J. Exp. Med. 176, 1577-1581, 1992

A/Title: Predominance of fetal type DJH joining in young children with B precursor lym

A/Reference number: PH1302; MUID:93094761; PMID:1460419

A/Accession: PH1322

A/Molecule type: DNA

A/Residues: 1-14 &lt;MAS&gt;

A/Cross-references: UNIPARC:UPI000017C23C

C/Keywords: heterotrimer; immunoglobulin

Query Match

Best Local Similarity 18.4%; Score 21; DB 2; Length 14;

Matches 5; Conservative 2; Mismatches 2; Indels 2; Gaps 1;

QY 2 YRPGSRGNP 12

Db 6 WDYWGQ--GNP 14

## RESULT 43

PN0666

dystrophin-associated glycoprotein A3a-V - rabbit (fragment)

C/Species: Oryctolagus cuniculus (domestic rabbit)

C/Date: 19-May-1994 #sequence\_revision 19-May-1994 #text\_change 07-May-1999

C/Accession: PN0666

R/Yoshida, M.; Mizuno, Y.; Nonaka, I.; Ozawa, E.

J. Biochem. 114, 634-639, 1993

A/Title: A dystrophin-associated glycoprotein, A3a (one of 43DAG doublets), is retained

A/Reference number: PN0662; MUID:94156881; PMID:8113213

A/Accession: PN0666

A/Molecule type: protein

A/Residues: 1-14 &lt;TOS&gt;

A/Cross-references: UNIPARC:UPI000017C5C5

C/Comment: This protein is retained in Duchenne type muscular dystrophy muscle.

C/Keywords: glycoprotein; skeletal muscle

Query Match

Best Local Similarity 18.4%; Score 21; DB 2; Length 14;

Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 12 PKAPLY 17

Db 9 PKAPLY 14

## RESULT 44

PQ0195

Sf11-glycoprotein - Persian tobacco (fragment)

N/Alternate names: Sf1-glycoprotein

C/Species: Nicotiana glauca (Persian tobacco)

C/Date: 23-Nov-1991 #sequence\_revision 23-Nov-1991 #text\_change 31-Dec-2004

C/Accession: PQ0195; PQ0173

R/Mau, S.L.; Williams, E.G.; Atkinson, A.; Anderson, M.A.; Cornish, E.C.; Grego, B.; Shi

Planta 169, 184-191, 1986

A/Title: Style proteins of a wild tomato (Lycopersicon peruvianum) associated with expr

A/Reference number: PQ0192

A/Accession: PQ0195

A/Molecule type: protein

A/Residues: 1-15 &lt;MAU&gt;

A/Cross-references: UNIPROT:Q9S8X0; UNIPARC:UPI000009FDA3

A/Experimental source: style

R./Jahnen, W.; Batterham, M.P.; Clarke, A.E.; Moritz, R.L.; Simpson, R.  
Plant Cell 1, 493-499, 1989  
A>Title: Identification, isolation, and N-terminal sequencing of style glycoproteins and  
A/Reference number: P00173; PMID:92404717; PMID:2535548  
A/Accession: P00173  
A/Molecule type: protein  
R/Residues: 1-15 <JAH>  
A/Cross-references: UNIPARC:UPI000009FDA3  
A/Experimental source: style  
C/Comment: This protein is involved in self-incompatibility of flowering plants.  
C/Superfamily: RNases  
C/Keywords: glycoprotein

Query Match 18.4%; Score 21; DB 2; Length 15;  
Best Local Similarity 75.0%; Pred. No. 5.5e+03;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVEY 4  
|:|:  
Db 1 DPEY 4

RESULT 45  
S29485  
GTP-binding protein o-ral - Pacific electric ray (fragment)  
C/Species: Torpedo californica (Pacific electric ray)  
C/Date: 22-Nov-1993 #sequence\_revision 27-Feb-1997 #text\_change 13-Mar-1997  
C/Accession: S29485  
R/Volkhardt, W.; Pevsner, J.; Elferink, L.A.; Scheller, R.H.  
FEBS Lett. 317, 53-56, 1993  
A/Title: Association of three small GTP-binding proteins with cholinergic synaptic vesicle  
A/Reference number: S29485; PMID:93154521; PMID:8428634  
A/Accession: S29485  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-15 <VOL>  
A/Cross-references: UNIPARC:UPI000017BF33

Query Match 18.4%; Score 21; DB 2; Length 15;  
Best Local Similarity 57.1%; Pred. No. 5.5e+03;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DVEYPS 7  
|:|:  
Db 8 DVEPTGA 14

RESULT 46  
S51735  
T-cell receptor beta-chain joining region - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 07-May-1995 #sequence\_revision 01-Sep-1995 #text\_change 05-Nov-1999  
C/Accession: S51735  
R/Burthovic-Bello, I.; Steinle, A.; Ziegler, A.G.; Schendel, D.J.  
submitted to the EMBL Data Library, November 1993  
A/Reference number: S51732  
A/Accession: S51735  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-15 <DOR>  
A/Cross-references: UNIPARC:UPI00001165DF; EMBL:Z28344; NID:G607122; PIDN:CAA82198.1; PI  
C/Keywords: T-cell receptor

Query Match 18.4%; Score 21; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 5.5e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 RLGN 11  
|:|:  
Db 7 RLGN 10

RESULT 47

I53284  
T-cell receptor beta 2 chain J region, Jbeta2.7 - rabbit  
C/Species: Oryctolagus cuniculus (domestic rabbit)  
C/Date: 02-May-1994 #sequence\_revision 18-Nov-1994 #text\_change 05-Nov-1999  
C/Accession: I53284  
R/Haridranath, N.; Alexander, C.B.; Mage, R.G.  
Mol. Immunol. 28, 881-888, 1991  
A/Title: Evolutionarily conserved organization and sequences of germ-line diversity and J  
A/Reference number: A53284; PMID:91342695; PMID:1678859  
A/Accession: I53284  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-15 <HAR>  
A/Cross-references: UNIPARC:UPI0000115418; GB:S60737; NID:9233916; PIDN:AA319525.1; PID  
A/Note: sequence extracted from NCBI backbone (NCBIN:60737, NCBIIP:60747)  
C/Keywords: T-cell receptor

Query Match 18.4%; Score 21; DB 2; Length 15;  
Best Local Similarity 50.0%; Pred. No. 5.5e+03;  
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 YEPGSR 9  
|:|:  
Db 5 YEPGPKL 12

RESULT 48  
PT0091  
H+-transporting two-sector ATPase (EC 3.6.3.14) alpha chain - mouse (fragment)  
C/Species: Mus musculus (house mouse)  
C/Date: 21-Aug-1998 #sequence\_revision 21-Aug-1998 #text\_change 03-Jun-2002  
C/Accession: PT0091  
R/Kawakami, T.; Uchida, T.; Sakai, T.; Kamo, M.; Morimasa, T.; Tsugita, A.  
submitted to JIPID, July 1998  
A/Description: Proteome analysis of mouse brain.  
A/Reference number: PT0091  
A/Accession: PT0091  
A/Molecule type: protein  
A/Residues: 1-15 <KAW>  
A/Cross-references: UNIPARC:UPI000017CD8D  
A/Experimental source: brain, striatum  
C/Keywords: hydrolase

Query Match 18.4%; Score 21; DB 2; Length 15;  
Best Local Similarity 75.0%; Pred. No. 5.5e+03;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 YPGS 7  
|:|:  
Db 9 YPGN 12

RESULT 49  
PH1580  
Ig H chain V-D-J region (wild-type clone 3) - mouse (fragment)  
C/Species: Mus musculus (house mouse)  
C/Date: 02-Jun-1994 #sequence\_revision 02-Jun-1994 #text\_change 17-Mar-1999  
C/Accession: PH1580  
R/Levinson, D.A.; Campos-Torres, J.; Leder, P.  
J. Exp. Med. 178, 317-329, 1993  
A/Title: Molecular characterization of transgene-induced immunodeficiency in B-1ess m/cr  
A/Reference number: PH1580; PMID:93301609; PMID:8315387  
A/Accession: PH1580  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-16 <LEV>  
A/Cross-references: UNIPARC:UPI000017CGB8  
A/Experimental source: bone marrow pre-B lymphocyte  
C/Keywords: immunoglobulin

Query Match 18.4%; Score 21; DB 2; Length 16;  
Best Local Similarity 45.5%; Pred. No. 5.9e+03;  
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 7 SRLGNPKAPLV 17  
: ||| : |||  
Db 2 ARLGADARAFY 12

## RESULT 50

T-cell receptor delta chain V region (105.23) - mouse (fragment)  
C/Species: Mus musculus (house mouse)  
C/Date: 31-Aug-1990 #sequence\_revision 31-Aug-1990 #text\_change 30-May-1997  
C/Accession: H35141  
R/Sim, G.R.; Augustin, A.  
Cell 61, 397-405, 1990  
A/Title: Dominantly inherited expression of BID, an invariant undiversified T cell recep  
A/Reference number: A35141; MUID:90242386; PMID:2110506  
A/Accession: H35141  
A/Status: preliminary; not compared with conceptual translation  
A/Molecule type: mRNA  
A/Residues: 1-16 <SIM>  
A/Cross-references: UNIPARC:UPI000017C859  
C/Keywords: T-cell receptor

Query Match 18.4%; Score 21; DB 2; Length 16;  
Best Local Similarity 50.0%; Pred. No. 5.9e+03;  
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 6 GSRLGNPKAP 15  
: ||| : |||  
Db 4 GYLGGIRAP 13

## RESULT 51

MELANO  
melanotropin beta - horse  
C/Species: Equus caballus (domestic horse)  
C/Date: 13-Jul-1981 #sequence\_revision 13-Jul-1981 #text\_change 09-Jul-2004  
C/Accession: A01467  
R/Dixon, J.S.; Li, C.H.  
Gen. Comp. Endocrinol. 1, 161-169, 1961  
A/Title: The isolation and structure of beta-melanocyte-stimulating hormone from horse  
A/Reference number: A01467  
A/Accession: A01467  
A/Molecule type: protein  
A/Residues: 1-18 <DIX>  
A/Cross-references: UNIPROT:P01202; UNIPARC:UPI000012P1C0  
C/Suprafamily: corticotropin-11pocropin  
C/Keywords: hormone

Query Match 18.4%; Score 21; DB 1; Length 18;  
Best Local Similarity 33.3%; Pred. No. 6.7e+03;  
Matches 4; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 2 YEPGSRGNPK 13  
: ||| : |||  
Db 5 YKMEHPRWGSFR 16

## RESULT 52

DRUPD  
pysment-dispersing hormone - Atlantic sand fiddler crab  
N/Alternate names: PDH  
C/Species: Uca pugnator (Atlantic sand fiddler crab)  
C/Date: 31-Dec-1988 #sequence\_revision 31-Dec-1988 #text\_change 09-Jul-2004  
C/Accession: A25144  
R/Nao, K.R.; Riehm, J.P.; Zahnow, C.A.; Kleinholz, L.H.; Tarr, G.E.; Johnson, L.; Norton  
Proc. Natl. Acad. Sci. U.S.A. 82, 5319-5322, 1985  
A/Title: Characterization of a pigment-dispersing hormone in eyestalks of the fiddler cr  
A/Reference number: A25144  
A/Accession: A25144  
A/Molecule type: protein  
A/Residues: 1-18 <RAO>  
A/Cross-references: UNIPROT:P08871; UNIPARC:UPI000012989A  
C/Suprafamily: pigment-dispersing hormone

C/Keywords: amidated carboxyl end; neuropeptide  
F16/Modified site: amidated carboxyl end (ala) #status experimental

Query Match 18.4%; Score 21; DB 1; Length 18;  
Best Local Similarity 54.5%; Pred. No. 6.7e+03;  
Matches 6; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 EYPSRLGNPK 13  
: ||| : |||  
Db 3 ELINSLGLPK 13

## RESULT 53

A45590  
beta-pigment-dispersing hormone analog - red swamp crayfish  
C/Species: Procambarus clarkii (red swamp crayfish)  
C/Date: 22-Apr-1993 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004  
C/Accession: A45590  
R/McCallum, M.L.; Rao, K.R.; Riehm, J.P.; Mohrheer, C.J.; Morgan, W.T.  
Pigment Cell Res. 4, 201-208, 1991  
A/Title: Primary structure and relative potency of an analog of beta-PDH (pigment-dispe  
A/Reference number: A45590; MUID:93390305; PMID:1823925  
A/Status: preliminary; not compared with conceptual translation  
A/Molecule type: nucleic acid  
A/Residues: 1-18 <MCC>  
A/Cross-references: UNIPROT:Q9TWM7; UNIPARC:UPI000007D639  
A/Experimental source: eyestalk  
A/Note: sequence extracted from NCBI backbone (NCBIP:112439)

Query Match 18.4%; Score 21; DB 2; Length 18;  
Best Local Similarity 54.5%; Pred. No. 6.7e+03;  
Matches 6; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 EYPSRLGNPK 13  
: ||| : |||  
Db 3 ELINSLGLPK 13

## RESULT 54

PH1609  
Ig H chain V-D-J region (wild-type clone 336) - mouse (fragment)  
C/Species: Mus musculus (house mouse)  
C/Date: 02-Jun-1994 #sequence\_revision 02-Jun-1994 #text\_change 17-Mar-1999  
C/Accession: PH1609  
R/Levinson, D.A.; Campos-Torres, J.; Leder, P.  
J. Exp. Med. 178, 317-329, 1993  
A/Title: Molecular characterization of transgene-induced immunodeficiency in B-less mic  
A/Reference number: PH1580; MUID:93301609; PMID:8315387  
A/Accession: PH1609  
A/Molecule type: DNA  
A/Residues: 1-19 <LEV>  
A/Cross-references: UNIPARC:UPI000017C6C3  
A/Experimental source: bone marrow pre-B lymphocyte  
C/Keywords: immunoglobulin

Query Match 18.4%; Score 21; DB 2; Length 19;  
Best Local Similarity 66.7%; Pred. No. 7.1e+03;  
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 YEPGSR 7  
: ||| : |||  
Db 6 YYDDGS 11

## RESULT 55

S72501  
protein kinase C inhibitor - human (fragment)  
N/Alternate names: histidine triad nucleotide-binding protein  
C/Species: Homo sapiens (man)  
C/Date: 15-Feb-1997 #sequence\_revision 13-Mar-1997 #text\_change 31-Dec-2004  
C/Accession: S72501; S62623  
R/Maines, M.D.; Traakshel, G.M.

Arch. Biochem. Biophys. 300, 320-326, 1993  
A>Title: Purification and characterization of human biliverdin reductase.  
A'Reference number: S29736; MUID:93143333; PMID:842466  
A'Accession: S72501  
A:Molecule type: protein  
A'Residuals: 1-20 <MAI>  
A'Cross-references: UNIPARC:UPI00001756B0  
A'Note: this protein was identified as biliverdin reductase; the identification is questionable.  
R'Maines, M.D.; Polveda, B.V.; Huang, T.J.; McCoubrey Jr., W.K.  
Eur. J. Biochem. 235, 372-381, 1996  
A>Title: Human biliverdin IX-alpha reductase is a zinc-metalloprotein. Characterization  
A'Reference number: S62622; MUID:96202961; PMID:8631357  
A'Accession: S62623  
A:Molecule type: protein  
A'Residuals: 1-20 <MAV>  
A'Cross-references: UNIPARC:UPI00001756B0  
A'Superfamily: histidine triad hydrolase; histidine triad homology  
C'Keywords: homodimer; protein kinase inhibitor; zinc

Query Match 18.4%; Score 21; DB 2; Length 20;  
Best Local Similarity 42.9%; Pred. No. 7.5e+03;  
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 11 NPKAPLY 17  
:|:|:|:  
Db 8 SPQAPTH 14

RESULT 56  
S19240  
histone H2B (clone pCH1.0ER) - chicken (fragment)  
C'Species: Gallus gallus (chicken)  
C'Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 09-Jul-2004  
C'Accession: I50648; S19240  
R'Sturm, R.A.; Dalton, S.; Wells, J.R.  
Nucleic Acids Res. 16, 8571-8586, 1988  
A>Title: Conservation of histone H2A/H2B intergene regions: a role for the H2B specific  
A'Reference number: I50647; MUID:88355608; PMID:3267232  
A'Accession: I50648  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A'Residuals: 1-20 <ST2>  
A'Cross-references: UNIPROT:Q90859; UNIPARC:UPI00000FD2CA; EMBL:X07765; NID:963429; PIDN:  
C'Superfamily: histone H2B  
C'Keywords: chromosomal protein; nucleosome core

Query Match 18.4%; Score 21; DB 2; Length 20;  
Best Local Similarity 40.0%; Pred. No. 7.5e+03;  
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 5 PGSRLGNPKA 14  
|:|:|:|:  
Db 9 PAKKGSKKA 18

RESULT 57  
B53592  
H+-exporting ATPase (EC 3.6.3.6) 38k chain - Thermus aquaticus (fragment)  
C'Species: Thermus aquaticus  
C'Date: 01-Dec-1995 #sequence\_revision 01-Dec-1995 #text\_change 09-Jul-2004  
C'Accession: B53592  
R'Yokoyama, K.; Akabane, Y.; Ishii, N.; Yoshida, M.  
J. Biol. Chem. 269, 12248-12253, 1994  
A>Title: Isolation of prokaryotic V-0V-1-ATPase from a thermophilic eubacterium Thermus  
A'Reference number: A53592; MUID:94216345; PMID:8163530  
A'Accession: B53592  
A>Status: preliminary  
A:Molecule type: protein  
A'Residuals: 1-20 <YOK>  
A'Cross-references: UNIPROT:Q7M195; UNIPARC:UPI000017CDB1  
C'Keywords: hydrolase

Query Match 18.4%; Score 21; DB 2; Length 20;

Best Local Similarity 27.8%; Pred. No. 7.5e+03;  
Matches 5; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

QY 1 DYEYGSRLGNPKAPLYK 18  
|:|:|:|:  
Db 3 DFAYLNARVRVRGTLTK 20

RESULT 58  
PH0756  
T-cell receptor beta chain (17) - mouse (fragment)  
C'Species: Mus musculus (house mouse)  
C'Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 05-Nov-1999  
C'Accession: PH0756  
R'Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.  
J. Exp. Med. 174, 1371-1383, 1991  
A>Title: T cell receptor genes in a series of class I major histocompatibility complex-  
allelic exclusion and antigen-specific repertoire.  
A'Reference number: PH0746; MUID:92078846; PMID:1836010  
A'Accession: PH0756  
A:Molecule type: mRNA  
A'Residuals: 1-13 <CAS>  
A'Cross-references: UNIPARC:UPI0000115FB0; EMBL:X60850; NID:951482; PIDN:CAA43241.1; PID  
C'Experimental source: T lymphocyte  
C'Keywords: T-cell receptor

Query Match 18.0%; Score 20.5; DB 2; Length 13;  
Best Local Similarity 62.5%; Pred. No. 5.7e+03;  
Matches 5; Conservative 2; Mismatches 0; Indels 1; Gaps 1;

QY 10 GNPKAPLYK 17  
|:|:|:|:  
Db 6 GN-QAPLF 12

RESULT 59  
B59326  
ribosomal protein S8, mitochondrial (imported) - bovine (fragment)  
C'Species: Bos primigenius taurus (cattle)  
C'Date: 31-Dec-2001 #sequence\_revision 31-Dec-2001 #text\_change 31-Dec-2001  
C'Accession: B59326  
R'O'Brien, T.  
submitted to the Protein Sequence Database, July 2000  
A'Description: Mammalian mitochondrial ribosomal proteins (3): Identification of novel p  
A'Reference number: A59326  
A'Accession: B59326  
A>Status: preliminary  
A:Molecule type: protein  
A'Residuals: 1-20 <OBR>  
A'Cross-references: UNIPARC:UPI000017CBBF  
A'Note: amino terminal of the mature form  
C'Keywords: mitochondrion; protein biosynthesis; ribosome

Query Match 18.0%; Score 20.5; DB 2; Length 20;  
Best Local Similarity 45.5%; Pred. No. 9e+03;  
Matches 5; Conservative 2; Mismatches 1; Indels 3; Gaps 1;

QY 10 GNPKAPLYKRP 20  
|:|:|:|:  
Db 7 GSPK--IKKP 14

RESULT 60  
PT0240  
Ig heavy chain CRD3 region (clone 2-100B) - human (fragment)  
C'Species: Homo sapiens (man)  
C'Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996  
C'Accession: PT0240  
R'Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.  
J. Exp. Med. 173, 395-407, 1991  
A>Title: Preferential utilization of specific immunoglobulin heavy chain diversity and J  
A'Reference number: PT0222; MUID:91108337; PMID:1899102  
A'Accession: PT0240

A:Molecule type: DNA  
A:Residues: 1-4 <YAM>  
A:Cross-references: UNIPARC:UPI000017C1E2  
A:Experimental source: B lymphocyte  
C:Keywords: heterotetramer; immunoglobulin

Query Match 17.5%; Score 20; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YPG 6  
|||  
DB 1 YPG 3

RESULT 61  
A38081  
amine oxidase (copper-containing) (EC 1.4.3.6) - yeast (*Pichia angusta*) (fragment)  
C/Species: *Pichia angusta*  
C/Date: 31-Dec-1993 #sequence\_revision 03-Feb-1994 #text\_change 20-Apr-2000  
C/Accession: A38081  
R/Mu, D.; Jansen, S.M.; Smith, A.J.; Brown, D.E.; Dooley, D.M.; Kliman, J.P.  
J. Biol. Chem. 267, 7979-7982, 1992  
A/Title: Tyrosine codon corresponds to topa quinone at the active site of copper amine  
A/Reference number: A38081; PMID:9235001; PMID:1569055  
A/Accession: A38081  
A:Molecule type: protein  
A:Residues: 1-7 <MO>  
A:Cross-references: UNIPARC:UPI000017CA48  
C/Species: copper; oxidoreductase; quinoprotein; topaquinone  
C/Keywords: copper; oxidoreductase; quinoprotein; topaquinone  
P/1/Modified site: topaquinone (Tyr) #status experimental

Query Match 17.5%; Score 20; DB 2; Length 7;  
Best Local Similarity 75.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYEX 4  
|||  
DB 3 NYEX 6

RESULT 62  
A41117  
acetylcholinesterase (EC 3.1.1.7), venom - Asian cobra (fragment)  
C/Species: *Naja naja oxiana* (Asian cobra, Oxus cobra)  
C/Date: 27-Mar-1992 #sequence\_revision 27-Mar-1992 #text\_change 09-Jul-2004  
C/Accession: A41117  
R/Kreienkamp, H.J.; Weise, C.; Rada, R.; Aavikaar, A.; Hucho, F.  
Proc. Natl. Acad. Sci. U.S.A. 88, 6117-6121, 1991  
A/Title: Anticodon subites of the catalytic center of acetylcholinesterase from Torpedo  
A/Reference number: A41117; PMID:91296772; PMID:2068091  
A/Accession: A41117  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-8 <KRR>  
A:Cross-references: UNIPROT:Q7L227; UNIPARC:UPI000017BFC2  
C/Keywords: carboxylic ester hydrolase

Query Match 17.5%; Score 20; DB 2; Length 8;  
Best Local Similarity 42.9%; Pred. No. 2.8e+05;  
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 6 GSRKMP 12  
|||  
DB 1 GAEWMP 7

RESULT 63  
A61126  
gonadolibertin - spotted rattfish  
N/Alternate names: gonadotropin-releasing hormone  
C/Species: *Hydrolagus colliei* (spotted rattfish)  
C/Date: 26-May-1994 #sequence\_revision 26-May-1994 #text\_change 09-Jul-2004

C/Accession: A61126  
R/Lovejoy, D.A.; Sherwood, N.M.; Fischer, W.H.; Jackson, B.C.; Rivier, J.E.; Lee, T.  
Gen. Comp. Endocrinol. 82, 152-161, 1991  
A/Title: Primary structure of gonadotropin-releasing hormone from the brain of a holocoe  
A/Reference number: A61126; PMID:91340067; PMID:1678723  
A/Accession: A61126

A:Molecule type: protein  
A:Residues: 1-10 <LOV>  
A:Cross-references: UNIPROT:P37043; UNIPARC:UPI000012B8F8  
A:Experimental source: brain  
C/Superfamily: gonadolibertin  
C/Keywords: amidated carboxyl end; brain; hormone; pyroglutamic acid  
P/1/Modified site: pyroglutamate carboxylic acid (Gln) #status experimental  
P/10/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 17.5%; Score 20; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 5.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YPG 6  
|||  
DB 8 YPG 10

RESULT 64  
RHAD2  
gonadolibertin II - American alligator  
N/Alternate names: gonadotropin-releasing hormone II  
C/Species: Alligator mississippiensis (American alligator)  
C/Date: 31-Mar-1993 #sequence\_revision 31-Mar-1993 #text\_change 09-Jul-2004  
C/Accession: B60066  
R/Lovejoy, D.A.; Fischer, W.H.; Parker, D.B.; McRory, J.E.; Park, M.; Lance, V.; Swanson  
Regul. Pept. 33, 105-116, 1991  
A/Title: Primary structure of two forms of gonadotropin-releasing hormone from brains o  
A/Reference number: A60066; PMID:91352338; PMID:1882082  
A/Accession: B60066  
A:Molecule type: protein  
A:Residues: 1-10 <LOV>  
A:Cross-references: UNIPROT:P37043; UNIPARC:UPI000012B8F8  
C/Superfamily: gonadolibertin  
C/Keywords: amidated carboxyl end; hormone; hypothalamus; pyroglutamic acid  
P/1/Modified site: pyroglutamate carboxylic acid (Gln) #status experimental  
P/10/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 17.5%; Score 20; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 5.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YPG 6  
|||  
DB 8 YPG 10

RESULT 65  
S24190  
trypsin (EC 3.4.21.59) - bovine (fragment)  
C/Species: *Bos primigenius taurus* (cattle)  
C/Date: 19-Mar-1997 #sequence\_revision 18-Aug-2000 #text\_change 09-Jul-2004  
C/Accession: S24190  
R/Piorucci, L.; Brba, F.; Ascoli, F.  
Biol. Chem. Hoppe-Seyler 373, 483-490, 1992  
A/Title: Bovine trypsin: purification and characterization.  
A/Reference number: S24190; PMID:92384956; PMID:1515079  
A/Accession: S24190  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-10 <RIO>  
A:Cross-references: UNIPROT:Q8HYJ2; UNIPARC:UPI0000175C26  
C/Superfamily: trypsin; trypsin homology  
C/Keywords: hydrolase; serine proteinase; zymogen

Query Match 17.5%; Score 20; DB 2; Length 10;  
Best Local Similarity 80.0%; Pred. No. 5.1e+03;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 EYRGS 7  
| | | |  
Db 6 EAPGS 10

RESULT 66  
B46030  
gonadoliberin II - epiny dogfish

NAlternate names: gonadotropin-releasing hormone  
C:Species: Squalus acanthias (spiny dogfish)

C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 09-Jul-2004

C:Accession: B46030

R:Lovejoy, D.A.; Fischer, W.H.; Ngamwongchon, S.; Craig, A.G.; Nahorniak, C.S.; Peter, R.

Proc. Natl. Acad. Sci. U.S.A. 89, 6373-6377, 1992

A:Title: Distinct sequence of gonadotropin-releasing hormone (GNRH) in dogfish brain pro

A:Reference number: A46030; MUID:9235300; PMID:1631133

A:Accession: B46030

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-10 <LOV>

A:Cross-references: UNIPROT:P37043, UNIPARC:UPI000012B8F8

C:Superfamily: gonadoliberin

C:Keywords: hormone; pyroglutamic acid

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 17.5%; Score 20; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 5.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YPG 6  
| | | |  
Db 8 YPG 10

RESULT 67

E41476

probable antigen 5 - Mycobacterium leprae (fragment)

C:Species: Mycobacterium leprae

C:Date: 10-Apr-1992 #sequence\_revision 10-Apr-1992 #text\_change 18-Jun-1993

C:Accession: E41476

R:Hartshoer, R.A.; van Rens, R.M.; Stabel, L.F.B.M.; de Wit, M.Y.L.; Klatter, P.R.

Infect. Immun. 58, 2821-2827, 1990

A:Title: Selection and characterization of recombinant clones that produce Mycobacterium

A:Reference number: A41476; MUID:90354041; PMID:1696331

A:Accession: E41476

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 1-11 <HAR>

A:Cross-references: UNIPARC:UPI000017AD58

Query Match 17.5%; Score 20; DB 2; Length 11;  
Best Local Similarity 50.0%; Pred. No. 5.7e+03;  
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 6 GSRIGNPKAP 15  
| | | | | |  
Db 1 GSOLPRVGAP 10

RESULT 68

S07207

Crinia-angiotensin, skin - frog (Crinia georgiana)

C:Species: Crinia georgiana

C:Date: 12-Feb-1993 #sequence\_revision 12-Feb-1993 #text\_change 16-Aug-2004

C:Accession: S07207

R:Brigamer, V.; Melchiorri, P.; Nakajima, T.; Yasuhara, T.; Endean, R.

Experientia 35, 1133-1133, 1979

A:Title: Amino acid composition and sequence of crinia-angiotensin, an angiotensin II-1

A:Reference number: S07207; MUID:80024575; PMID:488254

A:Accession: S07207

A:Molecule type: protein

A:Residues: 1-11 <ERS>  
A:Cross-references: UNIPROT:P09037; UNIPARC:UPI000003525C

Query Match 17.5%; Score 20; DB 2; Length 11;  
Best Local Similarity 60.0%; Pred. No. 5.7e+03;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 PGSRL 9  
| | | |  
Db 2 PGDRI 6

RESULT 69

S74196

3-hydroxy-3-methylglutaryl CoA synthase homolog - bovine (fragment)

C:Species: Bos primigenius taurus (cattle)

C:Date: 14-Apr-1998 #sequence\_revision 24-Apr-1998 #text\_change 01-May-1998

C:Accession: S74196

R:Takeuchi, S.; Yoshinaga, T.; Furukawa, T.; Kohno, H.; Tokunaga, R.; Mishimura, K.; Ino

Eur. J. Biochem. 230, 760-765, 1995

A:Title: Induction of terminal enzymes for heme biosynthesis during differentiation of m

A:Reference number: S65629; MUID:9533315; PMID:7607249

A:Accession: S74196

A:Molecule type: protein

A:Residues: 1-12 <YAK>

A:Cross-references: UNIPARC:UPI000017C48E

A:Experimental source: liver

Query Match 17.5%; Score 20; DB 2; Length 12;  
Best Local Similarity 57.1%; Pred. No. 6.2e+03;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 12 PKAPLYK 18  
| | | | | |  
Db 4 PAVPLAK 10

RESULT 70

PN0663

dystrophin-associated glycoprotein A3a-II - rabbit (fragment)

C:Species: Oryctolagus cuniculus (domestic rabbit)

C:Date: 19-May-1994 #sequence\_revision 19-May-1994 #text\_change 07-May-1999

C:Accession: PN0663

R:Yoshida, M.; Mizuno, Y.; Nonaka, I.; Ozawa, E.

J. Biochem. 114, 634-639, 1993

A:Title: A dystrophin-associated glycoprotein, A3a (one of 43DAG doublets), is retained

A:Reference number: PN0662; MUID:9415681; PMID:8113213

A:Accession: PN0663

A:Molecule type: protein

A:Residues: 1-12 <YOS>

A:Cross-references: UNIPARC:UPI000017C5C2

C:Comment: This protein is retained in Duchenne type muscular dystrophy muscle.

Query Match 17.5%; Score 20; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 6.2e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 KAPL 16  
| | | | | |  
Db 1 KAPL 4

RESULT 71

C20907

Ig kappa-1 chain J3 region - rabbit

C:Species: Oryctolagus cuniculus (domestic rabbit)

C:Date: 10-Aug-1990 #sequence\_revision 10-Aug-1990 #text\_change 16-Aug-1996

C:Accession: C20907

R:Morine, D.; Max, B.B.

Nucleic Acids Res. 11, 8877-8890, 1983

A:Title: Structural analysis of a rabbit immunoglobulin kappa2 J-C locus reveals multipl

A:Reference number: A20907; MUID:84169523; PMID:6324107



A/Accession: C20907  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-12 <EMO>  
 A/Cross-references: UNIPARC:UPI000017C5CP  
 C/Keywords: heterotrimer; immunoglobulin

Query Match 17.5%; Score 20; DB 2; Length 12;  
 Best Local Similarity 60.0%; Pred. No. 6.2e+03;  
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 PGSRL 9  
 DB 5 PGTKL 9

## RESULT 72

A61503  
 sterol carrier protein-2-like protein - chicken (fragment)

C/Species: Gallus gallus (chicken)

C/Date: 15-Oct-1994 #sequence\_revision 15-Oct-1994 #text\_change 09-Jul-2004

C/Accession: A61503

R/Reinart, M.P.; Avarit, S.J.; Foglia, T.

Comp. Biochem. Physiol. B 100, 243-248, 1991

A/Title: Purification, characterization and comparison with mammalian SCP-2 of a chicken

A/Reference number: A61503; PMID:92191564; PMID:1799965

A/Accession: A61503

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-12 <RSI>

A/Cross-references: UNIPROT:Q7LZ19; UNIPARC:UPI000017C037

Query Match 17.5%; Score 20; DB 2; Length 12;  
 Best Local Similarity 42.9%; Pred. No. 6.2e+03;  
 Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 13 KAPLYR 19  
 DB 1 ZTPLYPK 7

## RESULT 73

S63492

disulfoglucosyl sulfite reductase beta chain, soluble - Desulfovibrio desulfuricans (fragm

C/Species: Desulfovibrio desulfuricans

C/Date: 28-Oct-1996 #sequence\_revision 13-Mar-1997 #text\_change 17-Mar-1999

C/Accession: S63492

R/Staubert, J.; Arendsen, A.F.; Hagen, W.R.; Kroneck, P.M.H.

Eur. J. Biochem. 233, 873-879, 1995

A/Title: Molecular properties of the disulfoglucosyl sulfite reductase from Desulfovibrio

A/Reference number: S63489; PMID:96085152; PMID:8521853

A/Accession: S63492

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-13 <STG>

A/Cross-references: UNIPARC:UPI000017AB66

Query Match 17.5%; Score 20; DB 2; Length 13;  
 Best Local Similarity 50.0%; Pred. No. 6.8e+03;  
 Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 11 NPKAPL 16  
 DB 8 NPKXPM 13

## RESULT 74

C53275

19 kappa-1 chain J3 segment b95 allotype - rabbit (fragment)

C/Species: Oryctolagus cuniculus (domestic rabbit)

C/Date: 02-May-1994 #sequence\_revision 18-Nov-1994 #text\_change 16-Aug-1996

C/Accession: C53275

R/Ayadi, H.; Marche, P.N.; Cazeneuve, P.A.

Immunogenetics 34, 201-207, 1991

A/Title: Evolution of the rabbit immunoglobulin kappa chain genes.

A/Reference number: A53275; PMID:91372868; PMID:1909995

A/Accession: C53275

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-13 <AVA>

A/Cross-references: UNIPARC:UPI000017C5D0

A/Note: sequence extracted from NCBI backbone (NCBIN:56069, NCBI:P:56164)

C/Comment: This J3 segment may not be functional because of substitutions in the 7 mer

C/Keywords: heterotrimer; immunoglobulin

Query Match 17.5%; Score 20; DB 2; Length 13;  
 Best Local Similarity 60.0%; Pred. No. 6.8e+03;  
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 PGSRL 9  
 DB 5 PGTKL 9

## RESULT 75

S33800

chaperone, TCP1-related - oat

C/Species: Avena sativa (oat)

C/Date: 02-Dec-1993 #sequence\_revision 27-Feb-1997 #text\_change 09-Jul-2004

C/Accession: S33800

R/Mummeit, E.; Grimm, R.; Spehl, V.; Eckerskorn, C.; Schiltz, E.; Gatenby, A.A.; Schaefer

Nature 363, 644-648, 1993

A/Title: A TCP1-related molecular chaperone from plants refolds phytochrome to its photo

A/Reference number: S33800; PMID:93286140; PMID:8099715

A/Accession: S33800

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-13 <MDM>

A/Cross-references: UNIPROT:Q7M1G8; UNIPARC:UPI000017B0D5

Query Match 17.5%; Score 20; DB 2; Length 13;  
 Best Local Similarity 75.0%; Pred. No. 6.8e+03;  
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 10 GNPX 13  
 DB 8 GNPB 11

## RESULT 76

S60353

amylopullulanase - Bacillus sp. (strain KSM-1378) (fragment)

C/Species: Bacillus sp.

A/Variety: strain KSM-1378

C/Date: 24-Aug-1996 #sequence\_revision 13-Mar-1997 #text\_change 31-Dec-2004

C/Accession: S60353

R/Alra, K.; Saeki, K.; Igarashi, K.; Takaiwa, M.; Uemura, T.; Hagihara, H.; Kawai, S.; It

Biochim. Biophys. Acta 1243, 315-324, 1995

A/Title: Purification and characterization of an alkaline amylopullulanase with both al

A/Reference number: S60353; PMID:95244580; PMID:7727505

A/Accession: S60353

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-14 <ARA>

A/Cross-references: UNIPROT:P70983; UNIPARC:UPI000015219C

C/Superfamily: pullulanase type debranching enzyme

Query Match 17.5%; Score 20; DB 2; Length 14;  
 Best Local Similarity 75.0%; Pred. No. 7.4e+03;  
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 17 YKRP 20  
 DB 11 YERP 14

RESULT 77  
B60683  
malate dehydrogenase (decarboxylating) (EC 1.1.1.39) - millet (fragment)  
C:Species: Panicum sp. (millet)  
C:Date: 24-Feb-1994 #sequence\_revision 24-Feb-1994 #text\_change 09-Jul-2004  
C:Accession: B60683  
R:Murata, T.; Ikeda, J.; Takano, M.; Ohgaki, R.  
Plant Cell Physiol. 30, 429-437, 1989  
A:Title: Comparative studies of NAD-malic enzyme from leaves of various C-4 plants.  
A:Reference number: A60683  
A:Accession: B60683  
A:Molecule type: protein  
A:Residues: 1-14 <MUR>  
A:Cross-references: UNIPROT:Q7MT9; UNIPARC:UPI000017B12P  
C:Keywords: oxidoreductase; photosynthesis

Query Match 17.5%; Score 20; DB 2; Length 14;  
Best Local Similarity 80.0%; Pred. No. 7.4e+03;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 PKAPL 16  
DB 6 GGRAPL 10

RESULT 78  
S24159  
leukocyte elastase (EC 3.4.21.37) - sheep (fragment)  
N:Alternate names: neutrophil elastase  
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)  
C:Date: 22-Nov-1993 #sequence\_revision 27-Feb-1997 #text\_change 09-Jul-2004  
C:Accession: S24159  
R:Junger, W.G.; Hallstroem, S.; Liu, F.C.; Redl, H.; Schlag, G.  
Biol. Chem. Hoppe-Seyler 373, 691-698, 1992  
A:Title: The enzymatic and release characteristics of sheep neutrophil elastase: a comparison of the enzyme from sheep and human neutrophils  
A:Reference number: S24159; PMID:93039751; PMID:1418684  
A:Accession: S24159  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-15 <JUN>  
A:Cross-references: UNIPROT:Q9TRJ3; UNIPARC:UPI0000086FEA  
C:Superfamily: trypsin; trypsin homology  
C:Keywords: hydrolase; serine protease

Query Match 17.5%; Score 20; DB 2; Length 15;  
Best Local Similarity 44.4%; Pred. No. 7.9e+03;  
Matches 4; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 6 GSRLGNPKA 14  
DB 3 GGRAPL 11

RESULT 79  
S59492  
formate dehydrogenase alpha chain - Alcaligenes eutrophus (fragment)  
C:Species: Alcaligenes eutrophus  
C:Date: 27-Apr-1996 #sequence\_revision 13-Mar-1997 #text\_change 31-Dec-2004  
C:Accession: S59492  
R:Frileddebold, J.; Meyer, F.; Bill, E.; Trautwein, A.X.; Bowlen, B.  
Biol. Chem. Hoppe-Seyler 376, 561-568, 1995  
A:Title: Structural and immunological studies on the soluble formate dehydrogenase from Alcaligenes eutrophus  
A:Reference number: S59492; PMID:9615726; PMID:8561915  
A:Accession: S59492  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-15 <FRI>  
A:Cross-references: UNIPROT:Q87815; UNIPARC:UPI000017AA0F  
C:Superfamily: NAD-dependent formate dehydrogenase, alpha subunit

Query Match 17.5%; Score 20; DB 2; Length 15;  
Best Local Similarity 50.0%; Pred. No. 7.9e+03;  
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 10 GNPAP 15  
DB 10 GTRAP 15

RESULT 80  
PA0002  
photosystem II oxygen-evolving complex protein 3 - Arabidopsis thaliana (fragment)  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 18-Nov-1994 #sequence\_revision 06-Jan-1995 #text\_change 23-Mar-1995  
C:Accession: PA0002  
R:Kamo, M.; Kawakami, T.; Miyake, N.; Tsugita, A.  
submitted to JIPID, July 1994  
A:Description: Separation and characterization of Arabidopsis proteins by two-dimensional gel electrophoresis  
A:Reference number: PA0001  
A:Accession: PA0002  
A:Molecule type: protein  
A:Residues: 1-15 <KAM>  
A:Cross-references: UNIPARC:UPI000017AFDB  
A:Experimental source: stem  
C:Keywords: photosynthesis; photosystem II

Query Match 17.5%; Score 20; DB 2; Length 15;  
Best Local Similarity 42.9%; Pred. No. 7.9e+03;  
Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 9 LGNPAP 15  
DB 7 VGGRAP 13

RESULT 81  
PL0143  
carbon-monoxide dehydrogenase (EC 1.2.99.2) medium chain - Pseudomonas carboxydohydrogen  
C:Species: Pseudomonas carboxydohydrogen  
C:Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 09-Jul-2004  
C:Accession: PL0143  
R:Kraut, M.; Hugendieck, I.; Herwig, S.; Meyer, O.  
Arch. Microbiol. 152, 335-341, 1989  
A:Title: Homology and distribution of CO dehydrogenase structural genes in carboxydohydrogen  
A:Reference number: PL0138; PMID:90055678; PMID:2818128  
A:Accession: PL0143  
A:Molecule type: protein  
A:Residues: 1-15 <KRA>  
A:Cross-references: UNIPROT:P19917; UNIPARC:UPI0000128PDB  
C:Comment: Carbon-monoxide dehydrogenase consists of three polypeptide chains: large, me  
C:Keywords: oxidoreductase

Query Match 17.5%; Score 20; DB 2; Length 15;  
Best Local Similarity 57.1%; Pred. No. 7.9e+03;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 DYEPGS 7  
DB 8 DYHRPS 14

RESULT 82  
S36896  
ribosomal protein S16 - Mycobacterium bovis (fragment)  
C:Species: Mycobacterium bovis  
C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 09-Jul-2004  
C:Accession: S36896  
R:Ohara, N.; Kimura, M.; Higashi, Y.; Yamada, T.  
FEBS Lett. 331, 9-14, 1993  
A:Title: Isolation and amino acid sequence of the 30S ribosomal protein S19 from Mycobacterium bovis  
A:Reference number: S36887; PMID:94009553; PMID:8405418  
A:Accession: S36896  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-15 <OHA>  
A:Cross-references: UNIPROT:Q9R544; UNIPARC:UPI00000B7C39

C/Keywords: protein biosynthesis; ribosome

Query Match 17.5%; Score 20; DB 2; Length 15;  
Best Local Similarity 44.4%; Pred. No. 7.9e+03;  
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 7 SRLGNP 15  
|:|:|:|:  
Db 7 TRILAKINP 15

#### RESULT 83

S04586

NADH2 dehydrogenase (ubiquinone) (BC 1.6.5.3) chain 1 - common tobacco mitochondrion (fr  
C/Species: mitochondrion Nicotiana tabacum (common tobacco)  
C/Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 09-Jul-2004

C/Accession: S04586

R/Brand, M.M.; Levings III, C.S.; Matzinger, D.F.

Mol. Gen. Genet. 204, 8-16, 1986

A/Title: The tobacco mitochondrial ATPase subunit 9 gene is closely linked to an open re  
A/Reference number: S01427; MUID:86310310; PMID:2875379

A/Accession: S04586

A/Molecule type: DNA

A/Residues: 1-15 <BLA>

A/Cross-references: UNIPROT:Q35188; UNIPARC:UPI00000986C6; EMBL:X04019; NID:G13148; PIND

C/Genetics:

A/Keywords: mitochondrion; NAD; oxidoreductase

Query Match 17.5%; Score 20; DB 2; Length 15;  
Best Local Similarity 60.0%; Pred. No. 7.9e+03;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 15 PLYKR 19  
|:|:|:|:  
Db 1 PLYSK 5

#### RESULT 84

B54877

alpha-conotoxin PN1B - cone shell (Conus pennaceus)  
C/Species: Conus pennaceus  
C/Date: 19-Mar-1997 #sequence\_revision 25-Apr-1997 #text\_change 09-Jul-2004

C/Accession: B54877

R/Painziber, M.; Hasson, A.; Oren, R.; Burlingame, A.L.; Gordon, D.; Spira, M.B.; Zlock

Biochemistry 33, 9523-9529, 1994

A/Title: New mollusc-specific alpha-conotoxins block Aplysia neuronal acetylcholine rec

A/Reference number: A54877; MUID:94347719; PMID:8068627

A/Accession: B54877

A/Molecule type: protein

A/Residues: 1-16 <FAI>

A/Cross-references: UNIPROT:P50985; UNIPARC:UPI000004C0F6

C/Comment: This alpha-conotoxin, as an acetylcholine receptor inhibitor, is a postsynap

C/Keyword: acetylcholine receptor inhibitor; amidated carboxyl end; postsynaptic neuro

F16/Modifed site: amidated carboxyl end (Cys) #status experimental

Query Match 17.5%; Score 20; DB 2; Length 16;  
Best Local Similarity 50.0%; Pred. No. 8.5e+03;  
Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 PGSRLGNP 12  
|:|:|:|:  
Db 6 PPCALSNP 13

#### RESULT 85

T37075

hypothetical protein SCJ30.08 - Streptomyces coelicolor

C/Species: Streptomyces coelicolor

C/Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 03-Dec-1999

C/Accession: T37075

R/Sanders, D.C.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.  
submitted to the EMBL Data Library, August 1999

A/Reference number: Z21621

A/Accession: T37075

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-16 <SAN>

A/Cross-references: UNIPARC:UPI000017ADCE; EMBL:AL109973; PIND:CAM53303.1; GSPDB:GN0007

A/Experimental source: strain A3 (2)

C/Genetics:

A/Keywords: SCOEDB:SCJ30.08

Query Match 17.5%; Score 20; DB 2; Length 16;  
Best Local Similarity 50.0%; Pred. No. 8.5e+03;  
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 5 PGSRLGNP 12  
|:|:|:|:  
Db 8 PRSAIGUP 15

#### RESULT 86

G24304

ribosomal protein H [validated] - Haloarcula marismortui (fragment)

C/Species: Haloarcula marismortui  
C/Date: 19-May-1989 #sequence\_revision 19-May-1989 #text\_change 21-Jul-2000

C/Accession: G24304

R/Shoham, M.; Dijk, J.; Reinhardt, R.; Wilmann-Liebold, B.

FEBS Lett. 204, 323-330, 1986

A/Title: Purification and characterization of ribosomal proteins from the 30 S subunit

A/Reference number: A24304

A/Accession: G24304

A/Molecule type: protein

A/Residues: 1-16 <SHO>

A/Cross-references: UNIPARC:UPI000017ABA2

C/Keywords: protein biosynthesis; ribosome

Query Match 17.5%; Score 20; DB 2; Length 16;  
Best Local Similarity 33.3%; Pred. No. 8.5e+03;  
Matches 4; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 5 PGSRLGNP 16  
|:|:|:|:  
Db 1 PGNKRYNDEGXL 12

#### RESULT 87

PT0237

Ig heavy chain CDR3 region (clone 2-94A) - human (fragment)

C/Species: Homo sapiens (man)  
C/Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996

C/Accession: PT0237

R/Yamada, M.; Masserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.

J. Exp. Med. 173, 395-407, 1991

A/Title: Preferential utilization of specific immunoglobulin heavy chain diversity and

A/Reference number: PT0222; MUID:91108337; PMID:1899102

A/Accession: PT0237

A/Molecule type: DNA

A/Residues: 1-16 <YAM>

A/Cross-references: UNIPARC:UPI000017CID8

A/Experimental source: B lymphocyte

C/Keywords: heterotetramer; immunoglobulin

Query Match 17.5%; Score 20; DB 2; Length 16;  
Best Local Similarity 50.0%; Pred. No. 8.5e+03;  
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYBYPG 6  
|:|:|:|:  
Db 8 DFDYWG 13

#### RESULT 88

A42291  
tail fiber protein I - phage P2 (fragment)  
C/Species: phage P2  
C/Date: 10-Jul-1992 #sequence\_revision 10-Jul-1992 #text\_change 09-Jul-2004  
C/Accession: A42291  
R/Haggard-Ljungquist, B.; Halling, C.; Calendar, R.  
J. Bacteriol. 174, 1462-1477, 1992  
A/Title: DNA sequences of the tail fiber genes of bacteriophage P2: evidence for horizon  
C/Accession: A42291, PMID:92165720, PMID:1531648  
A/Accession: A42291  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-16 <HAG>  
A/Cross-references: UNIPROT:P26701, UNIPARC:UPI000017A829, GB:M64677

Query Match 17.5%; Score 20; DB 2; Length 16;  
Best Local Similarity 100.0%; Pred. No. 8.5e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YPG 6  
|||  
Db 14 YPG 16

RESULT 89  
JT0609  
leukocyte chemoattractant peptide 6 - sheep  
C/Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)  
C/Date: 16-Sep-1992 #sequence\_revision 16-Sep-1992 #text\_change 09-Jul-2004  
C/Accession: JT0609  
R/Murdoch, W.J.; McCormick, R.J.  
Biochem. Biophys. Res. Commun. 184, 848-852, 1992  
A/Title: Sequence analysis of leukocyte chemoattractant peptides secreted by peritoneal  
A/Reference number: JT0609, PMID:92246975, PMID:1575752  
A/Accession: JT0609  
A/Molecule type: protein  
A/Residues: 1-16 <MUR>  
A/Cross-references: UNIPROT:Q7M2L0, UNIPARC:UPI000017C5AC  
C/Keywords: hydroxyproline  
F,3,6,9,12,15/modified site: hydroxyproline (Pro) #status experimental

Query Match 17.5%; Score 20; DB 2; Length 16;  
Best Local Similarity 66.7%; Pred. No. 8.5e+03;  
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 10 GNPAP 15  
|||  
Db 4 GPPAP 9

RESULT 90  
B61334  
trypsin (EC 3.4.21.4) 2 - starfish (Dermasterias imbricata) (fragment)  
C/Species: Dermasterias imbricata  
C/Date: 17-Jul-1994 #sequence\_revision 17-Jul-1994 #text\_change 09-Jul-2004  
C/Accession: B61334  
R/Estell, D.A.; Laskowski Jr., M.  
Biochemistry 19, 124-131, 1980  
A/Title: Dermasterias imbricata trypsin 1: an enzyme which rapidly hydrolyzes the reacti  
A/Reference number: A61334, PMID:80109692, PMID:7352972  
A/Accession: B61334  
A/Molecule type: protein  
A/Residues: 1-17 <EST>  
A/Cross-references: UNIPROT:Q7M432, UNIPARC:UPI0000175C3B  
C/Supfamily: trypsin, trypsin homology  
C/Keywords: hydrolase, protein digestion, serine proteinase

Query Match 17.5%; Score 20; DB 2; Length 17;  
Best Local Similarity 25.0%; Pred. No. 9e+03;  
Matches 3; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 9 LGNKPAPLYKRP 20  
:|:::|

Db 2 VQKESTASHRP 13

RESULT 91  
I49593  
cystic fibrosis transmembrane conductance regulator - mouse (fragment)  
C/Species: Mus musculus (house mouse)  
C/Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 20-Aug-1999  
C/Accession: I49593  
R/Denamur, B.; Chehab, F.P.  
Hum. Mol. Genet. 3, 1089-1094, 1994  
A/Title: Analysis of the mouse and rat CFTR promoter regions.  
A/Reference number: I49593, PMID:95072572, PMID:7526924  
A/Accession: I49593  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-17 <RES>  
A/Cross-references: UNIPARC:UPI000016CC99, GB:L04873, NID:9414726, PIDN:AAAT3562.1, PID  
C/Supfamily: cystic fibrosis transmembrane conductance regulator; ATP-binding cassette  
A/Status: CFTR

Query Match 17.5%; Score 20; DB 2; Length 17;  
Best Local Similarity 66.7%; Pred. No. 9e+03;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 13 KAPLYK 18  
|||  
Db 3 KSPLEK 8

RESULT 92  
I84733  
gene CFTR protein - rat (fragment)  
C/Species: Rattus norvegicus (Norway rat)  
C/Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 09-Jul-2004  
C/Accession: I84733  
R/Denamur, B.; Chehab, F.P.  
Hum. Mol. Genet. 3, 1089-1094, 1994  
A/Title: Analysis of the mouse and rat CFTR promoter regions.  
A/Reference number: I49593, PMID:95072572, PMID:7526924  
A/Accession: I84733  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-17 <RES>  
A/Cross-references: UNIPROT:P34158, UNIPARC:UPI000016CC99, GB:L26098, NID:9425185, PIDN  
C/Supfamily: cystic fibrosis transmembrane conductance regulator; ATP-binding cassette  
A/Status: CFTR

Query Match 17.5%; Score 20; DB 2; Length 17;  
Best Local Similarity 66.7%; Pred. No. 9e+03;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 13 KAPLYK 18  
|||  
Db 3 KSPLEK 8

RESULT 93  
B25348  
glycogen(starch) synthase (EC 2.4.1.11) P-2 peptide - rabbit (fragment)  
N/Alternate names: UDPglucose-glycogen glucosyltransferase  
C/Species: Oryctolagus cuniculus (domestic rabbit)  
C/Date: 30-Jun-1988 #sequence\_revision 30-Jun-1988 #text\_change 09-Jul-2004  
C/Accession: B25348  
J/Wang, Y.; Bell, A.W.; Hermodson, M.A.; Roach, P.J.  
J. Biol. Chem. 261, 16909-16915, 1986  
A/Title: Liver isozyme of rabbit glycogen synthase. Amino acid sequences surrounding ph  
A/Reference number: A92570, PMID:87057401, PMID:3097016  
A/Accession: B25348  
A/Molecule type: protein  
A/Residues: 1-17 <WAN>

A/Cross-references: UNIPROT:Q7M2K1, UNIPARC:UPI000017C50C  
C/Function:  
A/Description: catalyzes the alpha-1,4-glucosylation of glycogen by UDPglucose producing  
C/Keywords: glycogen/starch biosynthesis; glycosyltransferase; hexosyltransferase  
Query Match 17.5% Score 20; DB 2; Length 17;  
Best Local Similarity 60.0%; Pred. No. 9e+03;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 16 LYKRP 20  
DB 1 MYPRP 5  
RESULT 94  
S47196  
T-cell receptor J-alpha wnt.3 - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 06-Feb-1995 #sequence\_revision 06-Feb-1995 #text\_change 05-Nov-1999  
C/Accession: S47196  
R/Plaza, A.; Kono, D.H.; Theofilopoulos, A.N.  
Submitted to the EMBL Data Library, February 1993  
A/Reference number: S40133  
A/Accession: S47196  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-18 <PLA>  
A/Cross-references: UNIPARC:UPI000011611E; EMBL:X71027; NID:G506912; PIDN:CAA50344.1; PI  
C/Keywords: T-cell receptor  
Query Match 17.5% Score 20; DB 2; Length 18;  
Best Local Similarity 60.0%; Pred. No. 9.6e+03;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 5 PGSRL 9  
DB 2 PGMKL 6  
RESULT 95  
B44239  
amine oxidase (copper-containing) (EC 1.4.3.6), serum - pig (fragment)  
C/Species: Sus scrofa domestica (domestic pig)  
C/Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 09-Jul-2004  
C/Accession: B44239  
R/Janee, S.M.; Pelicic, M.M.; Scaman, C.H.; Smith, A.J.; Brown, D.E.; Dooley, D.M.; Mure,  
Biochemistry 31, 12147-12154, 1992  
A/Title: Identification of topaquinine and its consensus sequence in copper amine oxidase  
A/Reference number: A44239; MUID:93090740; PMID:11457410  
A/Accession: B44239  
A/Molecule type: protein  
A/Residues: 1-7, 'X', '9'-18 <JAN>  
A/Cross-references: UNIPROT:Q9TRK5; UNIPARC:UPI00000871BF; PIDN:ABA24427.1; PID:G261361  
A/Experimental source: serum  
A/Note: sequence extracted from NCBI backbone (NCBIF:119896)  
A/Note: we show one of the unidentified residues as tyrosine forming the topaquinine pro  
C/Keywords: oxidoreductase; quinoprotein; topaquinine  
P/8/Modified site: topaquinine (TYR) #status experimental  
Query Match 17.5% Score 20; DB 2; Length 18;  
Best Local Similarity 25.0%; Pred. No. 9.6e+03;  
Matches 3; Conservative 4; Mismatches 5; Indels 0; Gaps 0;  
QY 1 DYEPGRLGNP 12  
DB 7 NYDYVXDMIRHP 18  
RESULT 96  
B25715  
hypothetical protein - mouse (fragment)  
C/Species: Mus musculus (house mouse)  
C/Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 05-Nov-1999

C/Accession: S25715; S21390  
R/Bowtell, D.; Fu, P.; Simon, M.; Senior, P.  
Proc. Natl. Acad. Sci. U.S.A. 89, 6511-6515, 1992  
A/Title: Identification of murine homologues of the Drosophila Son of sevenless gene; p  
A/Reference number: S25714; MUID:92335328; PMID:1631150  
A/Accession: S25715  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-19 <BOW>  
A/Cross-references: UNIPARC:UPI000016D049; EMBL:Z11578; NID:G54132; PIDN:CAA77665.1; PI  
R/Bowtell, D.D.; Fu, P.; Simon, M.A.; Senior, P.V.  
Submitted to the EMBL Data Library, January 1992  
A/Description: Identification of murine homologues of the Drosophila Son of sevenless g  
A/Reference number: S21390  
A/Accession: S21390  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-19 <BO2>  
A/Cross-references: UNIPARC:UPI000016D049; EMBL:Z11578; NID:G54132; PIDN:CAA77665.1; PI  
Query Match 17.5% Score 20; DB 2; Length 19;  
Best Local Similarity 55.6%; Pred. No. 1e+04;  
Matches 5; Conservative 1; Mismatches 1; Indels 2; Gaps 1;  
QY 12 PKAPLYKRP 20  
DB 3 PPAP--RRP 9  
RESULT 97  
S43045  
translational elongation factor EF-1 alpha - rabbit  
C/Species: Oryctolagus cuniculus (domestic rabbit)  
C/Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 09-Jul-2004  
C/Accession: S43045  
R/Rosenberry, T.L.; Krall, J.A.; Dever, T.E.; Haas, R.; Louvard, D.; Merrick, W.C.  
J. Biol. Chem. 264, 7096-7099, 1989  
A/Title: Biochemical incorporation of [(3)H]ethanolamine into protein synthesis elonga  
A/Reference number: A33048; MUID:89214136; PMID:2708357  
A/Accession: S43045  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-19 <ROS>  
A/Cross-references: UNIPROT:Q7M2K4; UNIPARC:UPI000017C5E8  
Query Match 17.5% Score 20; DB 2; Length 19;  
Best Local Similarity 50.0%; Pred. No. 1e+04;  
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 5 PGSRLG 10  
DB 6 PGDNVG 11  
RESULT 98  
JP0059  
ribosomal protein L30 - Thermactinomyces intermedius (fragment)  
C/Species: Thermactinomyces intermedius  
C/Date: 10-Mar-1994 #sequence\_revision 28-Oct-1994 #text\_change 05-Oct-2004  
C/Accession: JP0059  
R/Ochi, K.  
Submitted to JIPID, February 1994  
A/Description: Phylogenetic diversity in the genus Bacillus and comparative ribosomal p  
A/Reference number: JP0042  
A/Accession: JP0059  
A/Molecule type: protein  
A/Residues: 1-20 <OCH>  
A/Cross-references: UNIPROT:Q7M167; UNIPARC:UPI0000177345  
C/Suprafamily: Ribosomal protein L30p  
C/Keywords: protein biosynthesis; ribosome  
Query Match 17.5% Score 20; DB 2; Length 20;  
Best Local Similarity 37.5%; Pred. No. 1.1e+04;

Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
 QY 7 SRLGNPKA 14  
 | : | | :  
 Db 11 SMIGRPES 18

## RESULT 99

B46174  
 RNA-binding protein TIR - human (fragment)  
 N/Alternate names: cytotoxic granule-associated RNA-binding protein; TIR-1 related prote  
 C/Species: Homo sapiens (man)  
 C/Date: 21-Sep-1993 #sequence\_revlsion 18-Nov-1994 #ext\_change 31-Dec-2004  
 C/Accession: B46174  
 R/Kawakami, A.; Tian, Q.; Duan, X.; Streuli, M.; Schlossman, S.F.; Anderson, P.  
 Proc. Natl. Acad. Sci. U.S.A. 89, 8681-8685, 1992  
 A/Title: Identification and functional characterization of a TIR-1-related nucleolysin.  
 A/Reference number: A46174; MUID:92409580; PMID:1326761  
 A/Accession: B46174  
 A/Status: preliminary  
 A/Molecule type: nucleic acid  
 A/Residues: 1-20 <KAW>  
 A/Cross-references: UNIPARC:UPI000017A36B  
 A/Note: sequence extracted from NCBI backbone (NCBIN:114067, NCBIIP:114068)

Query Match 17.5%; Score 20; DB 2; Length 20;  
 Best Local Similarity 55.6%; Pred. No. 1.1e+04;  
 Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 EYPSRLGN 11  
 | | | | |  
 Db 2 EQPDSRRVN 10

## RESULT 100

S38292  
 30K allergen - rye (fragment)  
 C/Species: Secale cereale (rye)  
 C/Date: 19-May-1994 #sequence\_revlsion 27-Feb-1997 #ext\_change 09-Jul-2004  
 C/Accession: S38292  
 R/Peterken, A.; Schramm, G.; Becker, W.M.; Schlaak, M.  
 Biol. Chem. Hoppe-Seyler 374, 855-861, 1993  
 A/Title: Comparison of four grass pollen species concerning their allergens of grass gro  
 A/Reference number: S38288; MUID:94092339; PMID:7505588  
 A/Accession: S38292  
 A/Molecule type: protein  
 A/Residues: 1-16 <PPT>  
 A/Cross-references: UNIPROT:Q7M263; UNIPARC:UPI00017B131

Query Match 17.1%; Score 19.5; DB 2; Length 16;  
 Best Local Similarity 50.0%; Pred. No. 1e+04;  
 Matches 5; Conservative 2; Mismatches 0; Indels 3; Gaps 1;

QY 5 PGSRLGNPKA 14  
 | : | | |  
 Db 10 PGRQ---PKA 16

Search completed: January 20, 2006, 19:12:10  
 Job time : 12.3462 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 20, 2006, 18:54:54 ; Search time 66.5385 Seconds

(without alignments)  
212.066 Million cell updates/sec

Title: US-09-662-293-2

Perfect score: 114  
Sequence: 1 DYEPGSRGPNPKAPLYKRP 20

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 14590

Minimum DB seq length: 0

Maximum DB seq length: 20

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : UniProt 05.80:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	33	28.9	16	2	07DLY3 SOLTU
2	33	28.9	18	2	P33889 euphorbia m
3	32	28.1	13	2	P90442_NPVSU
4	31	27.2	12	2	Q4YRT5_PLABB
5	30	26.3	12	1	GRAR_RANRU
6	30	26.3	13	2	Q6LDV4_BOVIN
7	29	25.4	14	2	O50268_GMOUJ
8	29	25.4	19	2	Q7MIM8_PHAVU
9	29	25.4	20	2	O5KR93_CRIGR
10	28	24.6	20	1	M117_BOVIN
11	28	24.6	20	2	P82163_SPIOL
12	27.5	24.1	18	2	Q79B85_9ZZZZ
13	27	23.7	15	1	K10M_LITRE
14	27	23.7	18	2	Q9UCT9_HUMAN
15	26.5	23.2	19	2	Q9S8G9_PSORP
16	26.5	23.2	20	2	Q9S8H0_PSORP
17	26	22.8	13	2	Q43174_SOLTU
18	26	22.8	19	2	Q9OV88_9MURI
19	26	22.8	20	1	P1BB_ELEMA
20	26	22.8	20	1	PYRH_PPRAP
21	26	22.8	20	2	Q4XKQ4_PLABB
22	26	22.8	20	2	Q9TR50_BOVIN
23	26	22.8	20	2	Q9R4Y6_PORGI
24	25.5	22.4	14	2	Q8JDM0_9HIV1
25	25.5	22.4	14	2	Q8JDM3_9HIV1
26	25.5	22.4	14	2	Q8JDM7_9HIV1
27	25	21.9	9	2	Q9UC36_HUMAN
28	25	21.9	13	2	Q9P116_HUMAN
29	25	21.9	13	2	Q7X9Y2_LYCPS
30	25	21.9	14	2	Q98Y97_9HIV1
31	25	21.9	15	2	Q9TWB9_GALME

32	25	21.9	15	2	Q7X9Y4_CUCSA	Q7X9Y4 cucumis sat
33	25	21.9	15	2	Q9R564_ECOLI	Q9R564 escherichia
34	25	21.9	15	2	Q9P801_MICCN	Q9P801 micropogoni
35	25	21.9	17	2	Q9EBB8_9HIV1	Q9EBB8 human immun
36	25	21.9	17	2	Q9ERK3_9HIV1	Q9ERK3 human immun
37	25	21.9	17	2	Q9BL24_9HIV1	Q9BL24 human immun
38	25	21.9	18	2	Q9TWK3_MYTBD	Q9TWK3 mytilus edu
39	25	21.9	18	2	Q38573_BPRTI	Q38573 bacterioph
40	25	21.9	19	1	CKAD_CONGE	CKAD274 cone geogr
41	25	21.9	19	2	Q9TWY2_LEIME	Q9TWY2 leishmania
42	25	21.9	20	2	Q4Z0Y4_PLABB	Q4Z0Y4 plasmodium
43	25	21.9	20	2	Q69176_CHLTR	Q69176 chlamydia t
44	25	21.9	20	2	Q85509_CHLTR	Q85509 chlamydia t
45	25	21.9	20	2	Q85510_CHLTR	Q85510 chlamydia t
46	25	21.9	20	2	Q85512_CHLTR	Q85512 chlamydia t
47	25	21.9	20	2	Q85514_CHLTR	Q85514 chlamydia t
48	25	21.9	20	2	Q85517_CHLTR	Q85517 chlamydia t
49	25	21.9	20	2	Q85519_CHLTR	Q85519 chlamydia t
50	25	21.9	20	2	Q85520_CHLTR	Q85520 chlamydia t
51	25	21.9	20	2	Q85521_CHLTR	Q85521 chlamydia t
52	25	21.9	20	2	Q85522_CHLTR	Q85522 chlamydia t
53	25	21.9	20	2	Q85523_CHLTR	Q85523 chlamydia t
54	25	21.9	20	2	Q85525_CHLTR	Q85525 chlamydia t
55	25	21.9	20	2	Q85526_CHLTR	Q85526 chlamydia t
56	25	21.9	20	2	Q85528_CHLTR	Q85528 chlamydia t
57	25	21.9	20	2	Q85530_CHLTR	Q85530 chlamydia t
58	25	21.9	20	2	Q85531_CHLTR	Q85531 chlamydia t
59	25	21.9	20	2	Q85533_CHLTR	Q85533 chlamydia t
60	25	21.9	20	2	Q53520_CHLTR	Q53520 chlamydia t
61	25	21.9	20	2	Q9R8N0_CHLTR	Q9R8N0 chlamydia t
62	25	21.9	20	2	Q9R8N4_CHLTR	Q9R8N4 chlamydia t
63	25	21.9	20	2	Q9R8P4_CHLTR	Q9R8P4 chlamydia t
64	25	21.9	20	2	Q61871_MOUSE	Q61871 mus musculu
65	25	21.9	20	2	Q9PRV5_XENLA	Q9PRV5 xenopus lae
66	25	21.9	8	2	Q6BC29_HUMAN	Q6BC29 homo sapien
67	24	21.1	9	2	Q12096_CAEV	Q12096 caprine art
68	24	21.1	9	2	Q12098_CAEV	Q12098 caprine art
69	24	21.1	9	2	Q12100_CAEV	Q12100 caprine art
70	24	21.1	9	2	Q12102_CAEV	Q12102 caprine art
71	24	21.1	9	2	Q12104_CAEV	Q12104 caprine art
72	24	21.1	10	2	Q7M500_9EUBO	Q7M500 aspergillus
73	24	21.1	11	2	Q9C057_HUMAN	Q9C057 homo sapien
74	24	21.1	12	2	Q12074_CAEV	Q12074 caprine art
75	24	21.1	12	2	Q12076_CAEV	Q12076 caprine art
76	24	21.1	12	2	Q12078_CAEV	Q12078 caprine art
77	24	21.1	12	2	Q12080_CAEV	Q12080 caprine art
78	24	21.1	12	2	Q12082_CAEV	Q12082 caprine art
79	24	21.1	12	2	Q12084_CAEV	Q12084 caprine art
80	24	21.1	12	2	Q12086_CAEV	Q12086 caprine art
81	24	21.1	12	2	Q12088_CAEV	Q12088 caprine art
82	24	21.1	12	2	Q12090_CAEV	Q12090 caprine art
83	24	21.1	12	2	Q12092_CAEV	Q12092 caprine art
84	24	21.1	12	2	Q12094_CAEV	Q12094 caprine art
85	24	21.1	12	2	Q12096_CAEV	Q12096 caprine art
86	24	21.1	12	2	Q12108_CAEV	Q12108 caprine art
87	24	21.1	12	2	Q12110_CAEV	Q12110 caprine art
88	24	21.1	12	2	Q12112_CAEV	Q12112 caprine art
89	24	21.1	12	2	Q12114_CAEV	Q12114 caprine art
90	24	21.1	12	2	Q12116_CAEV	Q12116 caprine art
91	24	21.1	12	2	Q12118_CAEV	Q12118 caprine art
92	24	21.1	13	2	Q9UDC6_HUMAN	Q9UDC6 homo sapien
93	24	21.1	15	2	Q6LAT1_DROME	Q6LAT1 drosophi
94	24	21.1	16	2	Q9NPQ7_HUMAN	Q9NPQ7 homo sapien
95	24	21.1	18	2	Q4TZV7_PAPPA	Q4TZV7 papio hamad
96	24	21.1	18	2	Q5UTB3_RAT	Q5UTB3 rattus norv
97	24	21.1	19	1	HB82_UFOHA	HB8292 uronasteyx h
98	24	21.1	19	2	Q8WTX6_HUMAN	Q8WTX6 homo sapien
99	24	21.1	20	2	Q51XB0_MAGGR	Q51XB0 magnapoth
100	24	21.1	20	2	Q9T209_SOLTU	Q9T209 solanum tub

## ALIGNMENTS

```

RESULT 1
07DLV3 SOLUTU
ID 07DLV3_SOLUTU PRELIMINARY; PRT; 16 AA.
AC 07DLV3;
DT 05-JUL-2004 (TRMBLrel. 27, Created)
DT 05-JUL-2004 (TRMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRMBLrel. 27, Last annotation update)
DE Beta-fructofuranosidase (Invertase) (EC 3.2.1.26) (Fragment).
OS Solanum tuberosum (Potato)
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC Lamiales; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4113;
RN 1;
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=96279736; PubMed=8710506; DOI=10.1093/nar/24.12.2347;
RA Bournay A.S., Hedley P.E., Maddison A., Waugh R., Machray G.C.;
RT "Exon skipping induced by cold stress in a potato invertase gene
transcript."
RL Nucleic Acids Res. 24:2347-2351(1996).
RN 12;
RP NUCLEOTIDE SEQUENCE.
RA Maddison A.L.;
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; X95820; CAA65086.1; -; Genomic DNA.
DR GO; GO:0004564; F-beta-fructofuranosidase activity; IEA.
DR GO; GO:0016798; Phosphatase activity, acting on glycosyl bonds; IEA.
DR GO; GO:0005975; Picardohydrate metabolism; IEA.
KW Glycosidase; Hydrolase.
FT NON TER 1
FT NON TER 16
SQ SEQUENCE 16 AA; 1894 MW; 003053E73810C36 CRC64;

Query Match 28.9%; Score 33; DB 2; Length 16;
Best Local Similarity 38.5%; Pred. No. 5.9e+02;
Matches 5; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 5 PGSRLGNPKAPLY 17
| : : : | : |
Db 1 PKMWINDPNMFW 13

RESULT 2
AGI_EUPMA
ID AGI_EUPMA STANDARD; PRT; 18 AA.
AC P33889;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Galactose-inhibitable lectin [Contains: Galactose-inhibitable lectin
isoform Ala-1 del] (Fragment).
OS Euphorbia marginata (Snow-on-the-mountain).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC Rosales; eurosids I; Malpighiales; Euphorbiaceae; Euphorbiaceae;
OC Euphorbiaceae; Euphorbia.
OX NCBI_TaxID=28955;
RN 1;
RP PROTEIN SEQUENCE.
RX MEDLINE=93357266; PubMed=8351129; DOI=10.1016/0304-4165(93)90093-N;
RA Stlripe F., Licastro F., Morini M.C., Parente A., Savino G.,
RA Abbondanza A., Bologna A., Falasca A.I., Rossi C.A.;
RT "Purification and partial characterization of a mitogenic lectin from
the latex of Euphorbia marginata."
RL Biochim. Biophys. Acta 1158:33-39(1993).
-1- FUNCTION: Lectin that binds galactose, galactose-containing sugars
and gentiobiose. It is strongly mitogenic for human T lymphocytes
and induces the release of interleukin-1 beta and tumor necrosis
factor alpha from cultured mononuclear cells. It has a strong
hemagglutinating activity.
-1- SUBUNIT: Homodimer.

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CC -1- DEVELOPMENTAL STAGE: The production of this lectin varies with
CC seasons being higher in late spring.
CC -1- PTM: N-glycosylated.
CC -1- PTM: An isoform with Ala-1 missing is found in 20% of the samples.
CC -1- SIMILARITY: Contains 1 ricin B-type lectin domain.
-----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC removed.
-----
CC PIR; S36120; S36120.
DR InterPro; IPR000772; Ricin_B_Lectin; PARTIAL.
DR PROSITE; PS50231; Ricin_B_Lectin; PARTIAL.
KW Direct protein sequencing; Glycoprotein; Lectin.
FT CHAIN 1 >18 Galactose-inhibitable lectin.
FT CHAIN 2 >18 Galactose-inhibitable lectin isoform Ala-
FT 1 del.
FT NON TER 18
FT NON TER 18
SQ SEQUENCE 18 AA; 1888 MW; 6F79E053BC740AA CRC64;

Query Match 28.9%; Score 33; DB 1; Length 18;
Best Local Similarity 55.6%; Pred. No. 6.7e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 YPGSLGNP 12
| | | | : |
Db 2 YPGSHISGP 10

RESULT 3
P90442_NPVSL PRELIMINARY; PRT; 13 AA.
ID P90442_NPVSL PRELIMINARY; PRT; 13 AA.
AC P90442;
DT 01-MAY-1997 (TRMBLrel. 03, Created)
DT 01-MAY-1997 (TRMBLrel. 03, Last sequence update)
DT 01-JUN-2003 (TRMBLrel. 24, Last annotation update)
DE Polyhedrin (Fragment).
OS Spodoptera littoralis nuclear polyhedrosis virus (SLNPV).
OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
OC Nucleopolyhedrovirus.
OX NCBI_TaxID=10456;
RN 1;
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=97300849; PubMed=9155869; DOI=10.1007/s007050050055;
RA Faktor O., Tolster-Achituv M., Nachum O.;
RT "Enhancer element, repetitive sequences and gene organization in an 8-
kb region containing the polyhedrin gene of the Spodoptera littoralis
RT nucleopolyhedrovirus."
RL Arch. Virol. 142:1-15(1997).
DR EMBL; X99711; CAA68046.1; -; Genomic RNA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR001746; Polyhedrin.
DR Pfam; PF00738; Polyhedrin; 1.
FT NON TER 1
FT NON TER 1
SQ SEQUENCE 13 AA; 1383 MW; 2B0CD62832655737 CRC64;

Query Match 28.1%; Score 32; DB 2; Length 13;
Best Local Similarity 66.7%; Pred. No. 6.7e+02;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 12 PKAPLYKRP 20
| | | | | |
Db 3 PDAPLYTGP 11

RESULT 4
Q4YET5_PLABE PRELIMINARY; PRT; 12 AA.
ID Q4YET5_PLABE PRELIMINARY; PRT; 12 AA.
AC Q4YET5;
DT 13-SEP-2005 (TRMBLrel. 31, Created)
DT 13-SEP-2005 (TRMBLrel. 31, Last sequence update)

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DT 13-SEP-2005 (TrEMBL:rel. 31, Last annotation update)  
 DE Hypothetical protein (Fragment).  
 GN ORFNames=PB405057.00.0;  
 OS Plasmodium berghei.  
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporidia; Plasmodium.  
 NC NCBL\_taxonomy=5821;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Hall N., Karras M., Raine J.D., Carlton J.M., Kool J.T.W.A.,  
 RA Barriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,  
 RA James K., Rutherford K., Harris B., Harris D., Churcher C.,  
 RA Quail M.A., Ormond D., Duggett J., Trueman H.B., Mendoza J.,  
 RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,  
 RA Jense C.J., Barrall B., Turner C.M.R., Waters A.P., Sinden R.S.;  
 RT "A comprehensive survey of the Plasmodium life cycle by genomic,  
 RT transcriptomic, and proteomic analyses."  
 RL Science 307:82-86(2005).  
 CC -1- CAUTION: The sequence shown here is derived from an  
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
 CC preliminary data.  
 DR EMBL; CAI01005850; CAI03484.1; -; Genomic\_DNA.  
 KM Hypothetical protein.  
 PT NON\_TER 1  
 SQ SEQUENCE 12 AA; 1468 MW; 9ATC7B45DB5B0B5A CRC64;  
 Query Match 27.2%; Score 31; DB 2; Length 12;  
 Best local Similarity 71.4%; Pred. No. 8.7e+02;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYEPGS 7  
 Db 5 DYEVAGN 11

RESULT 5  
 ID GRAR\_RANRU STANDARD; PRT; 12 AA.  
 AC PA0754;  
 DT 01-FEB-1995 (Rel. 31, Created)  
 DT 01-FEB-1995 (Rel. 31, Last sequence update)  
 DT 13-SEP-2005 (Rel. 48, Last annotation update)  
 DE Granulibertin-R.  
 OS Rana rugosa (Winkled frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eureleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranae; Rana;  
 OC Rugosa.  
 NC NCBL\_taxonomy=8410;  
 RN [1]  
 RP PROTEIN SEQUENCE.  
 RC TISSUE=Skin secretion;  
 RX MEDLINE=78062810; PubMed=589733;  
 RA Nakajima T., Yasunara T.;  
 RT "A new mast cell degranulating peptide, granulibertin-R, in the frog  
 RT (Rana rugosa) skin."  
 RL Chem. Pharm. Bull. 25:2464-2465(1977).  
 RN [2]  
 RP SYNTHESIS.  
 RX MEDLINE=78189201; PubMed=657408;  
 RA Nakajima T., Yasunara T., Hirai Y., Kikada C., Fujino M., Takeyama M.,  
 RA Koyama K., Yajima H.;  
 RT "Synthesis of the dodecapeptide amide corresponding to the entire  
 RT amino acid sequence of granulibertin-R, a new frog skin peptide from  
 RT Rana rugosa."  
 RL Chem. Pharm. Bull. 26:1222-1230(1978).  
 CC -1- FUNCTION: Mast cell degranulating peptide.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: Expressed by the skin glands.  
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CC -----  
 KM Anadartion; Amphibian defense peptide; Direct protein sequencing;  
 KW Mast cell degranulation.  
 FT MOD\_RES 12 Serine amide.  
 FT SEQUENCE 12 AA; 1424 MW; 2B974EB9CA1B5047 CRC64;  
 SQ SEQUENCE 12 AA; 1424 MW; 2B974EB9CA1B5047 CRC64;  
 Query Match 26.3%; Score 30; DB 1; Length 12;  
 Best local Similarity 66.7%; Pred. No. 1.2e+03;  
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 15 PLYKRP 20  
 Db 5 PLYRRP 10

RESULT 6  
 ID 06LIV4\_BOVIN PRELIMINARY; PRT; 13 AA.  
 AC 06LIV4;  
 DT 05-JUL-2004 (TrEMBL:rel. 27, Created)  
 DT 05-JUL-2004 (TrEMBL:rel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBL:rel. 27, Last annotation update)  
 DE Tyroglobulin (Fragment).  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eureleostomi;  
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;  
 OC Pecora; Bovidae; Bovinae; Bos.  
 NC NCBL\_taxonomy=9913;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=87204101; PubMed=3472203;  
 RA Rickerts M.H., Simons M.-U., Parma J., Mercken L., Dong Q.,  
 RA Vassart G.;  
 RT "A nonsense mutation causes hereditary goltre in the Afrikaner cattle  
 RT and ummaaks alternative splicing of tyroglobulin transcripts";  
 RL Proc. Natl. Acad. Sci. U.S.A. 84:3181-3184(1987).  
 DR EMBL; M16448; AAA30777.2; -; Genomic\_DNA.  
 FT NON\_TER 1  
 FT NON\_TER 13  
 SQ SEQUENCE 13 AA; 1354 MW; 8BB974B525A2DC5 CRC64;  
 Query Match 26.3%; Score 30; DB 2; Length 13;  
 Best local Similarity 63.6%; Pred. No. 1.4e+03;  
 Matches 7; Conservative 1; Mismatches 1; Indels 2; Gaps 1;

QY 5 PGSR--LGMPK 13  
 Db 2 PGTRSLGSRK 12

RESULT 7  
 ID 050268\_9MOLU  
 AC 050268; 9MOLU PRELIMINARY; PRT; 14 AA.  
 DT 01-NOV-1996 (TrEMBL:rel. 01, Created)  
 DT 01-DEC-2001 (TrEMBL:rel. 09, Last sequence update)  
 DT 01-DEC-2001 (TrEMBL:rel. 19, Last annotation update)  
 DE Rpl16 protein (Fragment).  
 GN Name=rpl16;  
 OS Phytolasma sp.  
 OC Bacteria; Firmicutes; Mollicutes; Achleplasmaatales;  
 OC Achleplasmaataceae; Candidatus Phytolasma.  
 NC NCBL\_taxonomy=2155;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Lim P.-O., Sears B.B.;  
 RT "DNA sequence of the ribosomal protein genes rpl2 and rpl9 from a  
 RT plant-pathogenic mycoplasma-like organism."  
 RL FEMS Microbiol. Lett. 84:71-74(1991).  
 CC -1- FUNCTION: Ribosomal protein.  
 CC -1- SUBCELLULAR LOCATION: Cytoplasm.  
 CC -1- TISSUE SPECIFICITY: Expressed by the skin glands.  
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RT "Evolutionary relationships of a plant-pathogenic mycoplasma-like  
 RT organism and Acholeplasma laidlawii deduced from two ribosomal protein  
 RT gene sequences";  
 RL J. Bacteriol. 174:2606-2611(1992).  
 DR EMBL; M74770; AAA25331.1; -; Genomic DNA.  
 FT NON\_TER 14 14  
 SQ SEQUENCE 14 AA; 1870 MW; 87C315B73386A21 CRC64;

Query Match 25.4%; Score 29; DB 2; Length 14;  
 Best Local Similarity 55.6%; Pred. No. 2.1e+03;  
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 12 PKAPLYKRP 20  
 DB 4 PKRTKTRRP 12

RESULT 8  
 Q7M1M8 PHAVU PRELIMINARY; PRT; 19 AA.

AC 07M1M8\_ 26, Created  
 DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)  
 DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)  
 DE 01-MAR-2004 (TREMBlrel. 26, Last annotation update)  
 DE Hydroxyproline-rich cell wall glycoprotein (42K and others)  
 DE (Fragment).  
 OS Phaseolus vulgaris (Kidney bean) (French bean).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC euroids; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Phaseolus.  
 OX NCBI\_TaxID=3885;  
 RN [1]  
 RP PROTEIN SEQUENCE.  
 RX MEDLINE=96011753; PubMed=7548825;  
 RA Wojtasek P., Trechowen J., Botwell G.P.;  
 RT "Specificity in the immobilisation of cell wall proteins in response  
 RT to different elicitor molecules in suspension-cultured cells of French  
 RT bean (Phaseolus vulgaris L.).";  
 RL Plant Mol. Biol. 28:1075-1087(1995).  
 DR PIR; S59485; S59485.  
 FT NON\_TER 1 19  
 SQ SEQUENCE 19 AA; 2225 MW; 53AB9D0984A87E0A CRC64;

Query Match 25.4%; Score 29; DB 2; Length 19;  
 Best Local Similarity 62.5%; Pred. No. 2.9e+03;  
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 13 KAPLYKRP 20  
 DB 9 KPPVYKRP 16

RESULT 9  
 Q5KR93 CRIGR PRELIMINARY; PRT; 20 AA.  
 AC 05KR93\_ 30, Created  
 DT 10-MAY-2005 (TREMBlrel. 30, Last sequence update)  
 DT 10-MAY-2005 (TREMBlrel. 30, Last sequence update)  
 DE 10-MAY-2005 (TREMBlrel. 30, Last annotation update)  
 DE Ovcal (Fragment).  
 GN Name=ovcal;  
 OS Cricetus griseus (Chinese hamster).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Cricetinae; Cricetulus.  
 OX NCBI\_TaxID=10029;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX PubMed=15637051; DOI=10.1074/jbc.M13017200;  
 RA Nobukuni Y., Kohno K., Miyagawa K.;  
 RT "Gene Trap Mutagenesis-based Forward Genetic Approach Reveals That the  
 RT Tumor Suppressor Ovcal is a Component of the Biosynthetic Pathway of

RT Dipthamide on Elongation Factor 2.";  
 RL J. Biol. Chem. 280:10572-10577(2005).  
 DR EMBL; AB194396; BAD86738.1; -; mRNA.  
 FT NON\_TER 1 20  
 SQ SEQUENCE 20 AA; 1984 MW; 85701624F2B38874 CRC64;

Query Match 25.4%; Score 29; DB 2; Length 20;  
 Best Local Similarity 83.3%; Pred. No. 3.1e+03;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 PGSRLG 10  
 DB 12 PGSRVG 17

RESULT 10  
 M17\_BOVIN STANDARD; PRT; 20 AA.

AC P35451; 29, Created  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DE 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE 17 kDa milk glycoprotein (Fragment).  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;  
 OC Pecora; Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP PROTEIN SEQUENCE.  
 RC TISSUE=Milk;  
 RX MEDLINE=93308294; PubMed=8320368;  
 RA Soerensen B.S., Petersen T.B.;  
 RT "Purification and characterization of three proteins isolated from the  
 RT procase peptide fraction of bovine milk.";  
 RL J. Dairy Res. 60:189-197(1993).  
 CC -1- PTM: N-glycosylated.  
 CC -1- SIMILARITY: To camel whey protein.  
 CC -----

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CC Direct protein sequencing; Glycoprotein; Milk.

KW Direct protein sequencing; Glycoprotein; Milk.  
 FT NON\_TER 1 20  
 SQ SEQUENCE 20 AA; 2234 MW; 4CCA58940462C27 CRC64;

Query Match 24.6%; Score 28; DB 1; Length 20;  
 Best Local Similarity 83.3%; Pred. No. 4.4e+03;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 NPKAPL 16  
 DB 9 NPKLPL 14

RESULT 11  
 P82163 SPIOL PRELIMINARY; PRT; 20 AA.  
 AC P82163; 14, Created  
 DT 01-JUN-2000 (TREMBlrel. 14, Last sequence update)  
 DT 01-JUN-2000 (TREMBlrel. 14, Last sequence update)  
 DE 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
 DE Chloroplast 30S ribosomal protein S13 (Fragment).  
 OS Spinacia oleracea (Spinach).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
 OC Caryophyllales; Amaranthaceae; Spinacia.  
 OX NCBI\_TaxID=3562;

```

RN [1]
RP PROTEIN SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
RC STRAIN=CV, ALMARO, TISSUE=leaf,
RX MEDLINE=20435797; PubMed=10874039; DOI=10.1074/jbc.M004350200;
RA Yamaguchi K., von Knochlauch K., Subramanian A.R.;
RT "The plant ribosomal proteins. Identification of all the proteins in
RT the 30S subunit of an organelle ribosome (chloroplast).";
RL J. Biol. Chem. 275:28455-28465(2000).
CC -1- FUNCTION. THIS PROTEIN BINDS DIRECTLY TO 16S RIBOSOMAL RNA.
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.
CC -1- MASS SPECTROMETRY: MW=14900; METHOD=MALDI.
CC -1- MISCELLANEOUS: ON THE 2D-GEL, ITS MW IS: 15.5 kDa.
CC -1- SIMILARITY: BELONGS TO THE S13P FAMILY OF RIBOSOMAL PROTEINS.
DR GO: GO:0009507; C:chloroplast; IEA.
DR GO: GO:0019843; F:rRNA binding; IEA.
DR GO: GO:0003735; F:structural constituent of ribosome; IEA.
DR InterPro: IPR001892; Ribosomal S13.
DR PROSITE: PS00646; RIBOSOMAL_S13_1; PARTIAL.
KM Chloroplast; Ribosomal protein, rRNA-binding.
FT NON_TER 20
SQ SEQUENCE 20 AA; 2401 MW; 96AEFF51BE1035106 CRC64;

Query Match 24.6%; Score 28; DB 2; Length 20;
Best Local Similarity 50.0%; Pred. No. 4.4e+03;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 8 RLGNPKAPLYKR 19
DB 2 RVGNVBEIPNNKR 13

RESULT 12
QY 079EB5_9222Z
ID 079EB5_9222Z PRELIMINARY; PRT; 18 AA.
AC 079EB5;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE NodQ1 protein (fragment).
GN Name=nodQ1;
OS Megaplasmid pSym-a.
OC Plasmid Megaplasmid pSym-a.
OC other sequences; plasmids.
OX NCBI_TaxID=28391;
RN RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=94220739; PubMed=8167368;
RA Schvedock J., Long S.R.;
RT "An open reading frame downstream of Rhizobium meliloti nodQ1 shows
RT nucleotide sequence homology to an Agrobacterium tumefaciens insertion
RT sequence.";
RL Mol. Plant Microbe Interact. 7:151-153(1994).
DR EMBL: L08667; AAA23532.1; -, Genomic_DNA.
KM Plasmid.
FT NON_TER 1
SQ SEQUENCE 18 AA; 2115 MW; 9482F267BDEABFAC CRC64;

Query Match 24.1%; Score 27.5; DB 2; Length 18;
Best Local Similarity 38.9%; Pred. No. 4.7e+03;
Matches 7; Conservative 3; Mismatches 7; Indels 1; Gaps 1;

QY 3 EYEGSRIGNPKAPLYKRP 20
DB 1 EFLDRRIGQMTPL-QRP 17

RESULT 13
KLOM_LUMTB
ID KLOM_LUMTB STANDARD; PRT; 15 AA.
AC P11918;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)

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DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Lombricine kinase (EC 2.7.3.5) (LK) (Fragment).
OS Lumbriacus terrestris (Common earthworm).
OC Eukaryota; Metazoa; Annelida; Clitellata; Oligochaeta; Haplotaxida;
OC Lumbriacina; Lumbriacidae; Lumbriacus.
OX NCBI_TaxID=6398;
RN RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=72065544; PubMed=5128744;
RA der Terrosian E., Deveses G., Pradel L.A., Kaseab R., van Rhoai N.;
RT "Comparative structural studies of the active site of ATP: guanidine
RT phosphotransferases. The essential cysteine tryptic peptide of
RT lumbriacin kinase from lumbriacus terrestris muscle.";
RL Bur. J. Biochem. 22:585-592(1971).
CC -1- CATALYTIC ACTIVITY: ATP + lombricine = ADP + N-phospholombricine.
CC -1- SUBUNIT: Homodimer.
CC -1- SIMILARITY: Belongs to the ATP:guanido phosphotransferase family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR PIR: A08416; A08416.
DR InterPro: IPR000749; ATP-gua_Ptrans.
DR PROSITE: PS00112; GUANIDO_KINASE; 1.
KM Direct protein sequencing; Kinase; Transferase.
FT ACT SITE 6
FT ACT SITE 1
FT NON_TER 1
FT NON_TER 15
SQ SEQUENCE 15 AA; 1565 MW; 2A45FE6140B90C4 CRC64;

Query Match 23.7%; Score 27; DB 1; Length 15;
Best Local Similarity 83.3%; Pred. No. 4.6e+03;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 PGSRIG 10
DB 7 PGSRIG 12

RESULT 14
QY 09UCT9_HUMAN
ID 09UCT9_HUMAN PRELIMINARY; PRT; 18 AA.
AC 09UCT9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE PG=PROLINE-rich glycoprotein (fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Barchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
OX NCBI_TaxID=9606;
RN RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=91373355; PubMed=1894623;
RA Gillette-Castro B.L., Prakobphol A., Burlingame A.L., Leffler H.,
RA Pisher S.J.;
RT "Structure and bacterial receptor activity of a human salivary
RT proline-rich glycoprotein.";
RL J. Biol. Chem. 266:17358-17368(1991).
DR GO: GO:0005576; C:extracellular region; NAS.
DR GO: GO:0008368; P:Gram-negative bacterial binding; NAS.
DR GO: GO:0009618; P:response to pathogenic bacteria; NAS.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 18 AA; 1780 MW; 9616F7B0A83D2E40 CRC64;

Query Match 23.7%; Score 27; DB 2; Length 18;
Best Local Similarity 45.5%; Pred. No. 5.7e+03;
Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

```

Qy 5 PGSRLGNPKAP 15  
 Db 4 PPPRRGKPPVKKP 14

## RESULT 15

Q9S8G9 PSOTE  
 ID Q9S8G9 PSOTE PRELIMINARY; PRT; 19 AA.

AC Q9S8G9  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)  
 DE Proline-rich protein (Fragment).  
 OS Psophocarpus tetragonolobus (Goa bean) (Asparagaceae).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC Eurosid 1; Fabales; Fabaceae; Papilionoideae; Phaseoleae;  
 OC Psophocarpus.  
 OC NCBI\_TaxId=3891;  
 RN [1]  
 RP PROTEIN SEQUENCE.  
 RX MEDLINE=95277008; PubMed=7757337;  
 RA Esaka M., Hayakawa H.;  
 RT "Specific secretion of proline-rich proteins by salt-adapted winged  
 bean cells.";  
 RL Plant Cell Physiol. 36:441-446(1995).  
 SQ SEQUENCE 19 AA; 2118 MW; 59ED45C4F0F8779A CRC64;

Query Match 23.2%; Score 26.5; DB 2; Length 19;

Best Local Similarity 42.9%; Pred. No. 7.2e+03;  
 Matches 6; Conservative 2; Mismatches 3; Indels 3; Gaps 1;

Qy 10 GNP--KAPLYKRP 20  
 Db 3 GKPPVEKPPVKKP 16

## RESULT 16

Q9S8H0 PSOTE  
 ID Q9S8H0 PSOTE PRELIMINARY; PRT; 20 AA.

AC Q9S8H0  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)  
 DE Proline-rich protein (Fragment).  
 OS Psophocarpus tetragonolobus (Goa bean) (Asparagaceae).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC Eurosid 1; Fabales; Fabaceae; Papilionoideae; Phaseoleae;  
 OC Psophocarpus.  
 OC NCBI\_TaxId=3891;  
 RN [1]  
 RP PROTEIN SEQUENCE.  
 RX MEDLINE=95277008; PubMed=7757337;  
 RA Esaka M., Hayakawa H.;  
 RT "Specific secretion of proline-rich proteins by salt-adapted winged  
 bean cells.";  
 RL Plant Cell Physiol. 36:441-446(1995).  
 SQ SEQUENCE 20 AA; 2246 MW; ABE9ED45C4F0F877 CRC64;

Query Match 23.2%; Score 26.5; DB 2; Length 20;

Best Local Similarity 42.9%; Pred. No. 7.6e+03;  
 Matches 6; Conservative 2; Mismatches 3; Indels 3; Gaps 1;

Qy 10 GNP--KAPLYKRP 20  
 Db 3 GKPPVEKPPVKKP 16

## RESULT 17

Q43174 SOLTU  
 ID Q43174 SOLTU PRELIMINARY; PRT; 13 AA.

AC Q43174;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE Beta-fructofuranosidase (Invertase) (EC 3.2.1.26) (Fragment).  
 OS Solanum tuberosum (Potato).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;  
 OC Lamiales; Solanales; Solanaceae; Solanum.  
 OC NCBI\_TaxId=4113;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=96279736; PubMed=8710506; DOI=10.1093/nar/24.12.2347;  
 RA Bounay A.S., Hedley P.E., Maddison A., Waugh R., Machray G.C.;  
 RT "Exon skipping induced by cold stress in a potato invertase gene  
 transcript.";  
 RL Nucleic Acids Res. 24:2347-2351(1996).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Maddison A.L.;

RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; X95821; CAA65087.1; -; Genomic DNA.  
 DR GO; GO:0004564; F-beta-fructofuranosidase activity; IEA.  
 DR GO; GO:0016798; F-hydrolase activity, acting on glycosyl bonds; IEA.  
 DR GO; GO:0005975; P-carbohydrate metabolism; IEA.  
 KW Glycosidase; Hydrolase.  
 FT NON\_TER 1 1  
 FT NON\_TER 13 13  
 SQ SEQUENCE 13 AA; 1541 MW; 1B3053E7384C6874 CRC64;

Query Match 22.8%; Score 26; DB 2; Length 13;

Best Local Similarity 33.3%; Pred. No. 5.6e+03;  
 Matches 3; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 9 LGNPKAPLY 17  
 Db 2 INDPNGPMY 10

## RESULT 18

Q9QVB8 9MURI  
 ID Q9QVB8 9MURI PRELIMINARY; PRT; 19 AA.

AC Q9QVB8  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE TRUE classse kallikrein (EC 3.4.21.35) (Fragment).  
 OS Mus sp. .  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Murinae; Mus.  
 OC NCBI\_TaxId=10095;  
 RN [1]  
 RP PROTEIN SEQUENCE.  
 RX MEDLINE=92348355; PubMed=1639762;  
 RA Peters J., Takahashi S., Tada M., Miyake Y.;  
 RT "MGK-6-derived true tissue kallikrein is synthesized, processed, and  
 targeted through a regulated secretory pathway in mouse pituitary ACT-  
 20 cells.";  
 RL J. Biochem. 111:643-648(1992).  
 DR GO; GO:0004293; F-tissue kallikrein activity; IEA.  
 SQ SEQUENCE 19 AA; 2296 MW; 250436479C0B6626 CRC64;

Query Match 22.8%; Score 26; DB 2; Length 19;

Best Local Similarity 100.0%; Pred. No. 8.6e+03;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 YEYP 5  
 Db 1 YEYP 4

## RESULT 19

```

FIBB_ELEMA
ID FIBB_ELEMA STANDARD; PRT; 20 AA.
AC P14536;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 01-FEB-2005 (Rel. 46, Last annotation update)
DE Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).
GN Name=FGB;
OS Elephas maximus (Indian elephant).
OC Eukaryota; Metazoa; Chordata; Cranata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Afrotheria; Proboscidea; Elephantidae; Elephas.
OX NCBI_TaxID=9783;
RN [1]
RP PROTEIN SEQUENCE.
RA O'Neill P.B., Doolittle R.P.
RT "Mammalian phylogeny based on fibrinopeptide amino acid sequences."
RL Synt. 2001. 22:590-595(1973).
CC -1- FUNCTION: Fibrinogen has a double function: yielding monomers that
CC polymerize into fibrin and acting as a cofactor in platelet
CC aggregation.
CC -1- SUBUNIT: Heterodimer; disulfide linked. Contains 2 sets of 3
CC nonidentical chains (alpha, beta and gamma). The 2 heterocliners
CC are in head to head conformation with the N-termini in a small
CC central domain (By similarity).
CC -1- DOMAIN: A long coiled coil structure formed by 3 polypeptide
CC chains connects the central module to the C-terminal domains
CC (distal modules). The long C-terminal ends of the alpha chains
CC fold back, contributing a fourth strand to the coiled coil
CC structure.
CC -1- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin,
CC which cleaves fibrinopeptides A and B from alpha and beta chains,
CC and thus exposes the N-terminal polymerization sites responsible
CC for the formation of the soft clot.
-----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use as long as its content is in no way modified and this statement is not
CC removed.
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CC
CC DR InterPro; IPR002181; Fibrinogen C.
CC PROSITE; PS00514; FIBRIN AG C DOMAIN; PARTIAL.
CC Blood coagulation; Coiled coil; Direct protein sequencing; Plasma;
CC Sulfation.
CC KW Sulfation.
CC FT PEPTIDE 1 20 Fibrinopeptide B.
CC FT MOD_RES 4 4 Sulfotyrosine.
CC FT NON_TER 20
CC SQ SEQUENCE 20 AA; 2107 MW; BAF52B95993273 CRC64;

Query Match 22.8%; Score 26; DB 1; Length 20;
Best Local Similarity 57.1%; Pred. No. 9.1e+03;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 DVEYPSG 7
Db 6 DEEPFGA 12

RESULT 20
PYRRH PYRAP STANDARD; PRT; 20 AA.
AC P3736Z; P80307;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Pyrrhocorin.
OS Pyrrhocoris apterus (8sp sucking bug).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Paraneoptera; Hemiptera; Euhemiptera; Heteroptera;
OC Panholocoptera; Pentatomomorpha; Pyrrhocoridae; Pyrrhocoridae;
OC Pyrrhocoridae.
OX NCBI_TaxID=37000;
RN [1]

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RP PROTEIN SEQUENCE.
RC TISSUE=Hemolymph;
RX MEDLINE=94271176; PubMed=8002963;
RA Cocciandich S., Dupont A., Hegy G., Lanot R., Holder F., Helru C.,
RA Hoffmann J.A., Bulet P.
RT "Novel inducible antibacterial peptides from a hemipteran insect, the
RT 8sp-sucking bug Pyrrhocoris apterus."
RL Biochem. J. 300:567-575(1994).
RN [2]
RN CARBOHYDRATE-LINKAGE SITE THR-11.
RX MEDLINE=99177428; PubMed=10076062; DOI=10.1016/S0304-4165(98)00169-X;
RA Hoffmann R., Bulet P., Uege L., Olyoos L. Jr.
RT "Range of activity and metabolic stability of synthetic antibacterial
RT glycopeptides from insects."
RL Biochim. Biophys. Acta 1426:459-467(1999).
CC -1- FUNCTION: Antibacterial peptide. Affects Gram-negative bacteria
CC E.coli 1106, P.aeruginosa, B.coli D22 and E.colocae and Gram-
CC positive bacteria M.luteus and B.subtilis.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- PTM: O-linked glycan consists of a Gal-GalNAc disaccharide, O-
CC glycosylation is essential for full biological activity.
-----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC removed.
-----
CC
CC DR PIR; S44465; S44465.
CC KW Antibiotic; Antimicrobial; Direct protein sequencing; Glycoprotein;
CC Hemolymph; Immune response; Innate immunity.
CC FT CARBOHYD 11
CC SQ SEQUENCE 20 AA; 2341 MW; F4320EC2FF29462C CRC64;

Query Match 22.8%; Score 26; DB 1; Length 20;
Best Local Similarity 50.0%; Pred. No. 9.1e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 12 PKAPLYR 19
Db 12 PPRPYNR 19

RESULT 21
Q4XKQ4_PLACH
ID Q4XKQ4 PLACH PRELIMINARY; PRT; 20 AA.
AC Q4XKQ4;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein (Fragment).
GN ORFNames=PC400091.00.0;
OS Plasmodium chabaudi.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporidia; Plasmodium.
OX NCBI_TaxID=5825;
RN [1]
RN NUCLEOTIDE SEQUENCE.
RA Hall N., Kairas M., Raine J.D., Carlton J.M., Kool J.T.W.A.,
RA Bertram M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
RA Quail M.A., Ormond D., Doggett J., Trueman H.B., Mendoza J.,
RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
RA Janse C.J., Bartell B., Turner C.M.R., Waters A.P., Sinden R.S.,
RT "A comprehensive survey of the Plasmodium life cycle by genomic,
RT transcriptomic, and proteomic analyses."
RL Science 307:82-86(2005).
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC DR EMBL; CAJ01005069; CAH82508.1; -, Genomic_DNA.
CC KW Hypothetical protein.
CC FT NON_TER 1
CC SQ SEQUENCE 20 AA; 2345 MW; 0C1C6A76C57D4C85 CRC64;

```

Query Match 22.8%; Score 26; DB 2; Length 20;  
Best Local Similarity 71.4%; Pred. No. 9.1e+03;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 PGSRGN 11  
| | | | |  
DB 3 PTOURLN 9

## RESULT 22

Q9TR50\_BOVIN PRELIMINARY; PRT; 20 AA.  
ID Q9TR50;  
AC Q9TR50;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)  
DE Amphoterin homolog (Fragment).  
OS Bos taurus (Bovine).  
OC Bkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;  
OC Pecora; Bovidae; Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]  
RP PROTEIN SEQUENCE.  
RX MEDLINE=96029671; PubMed=7592757; DOI=10.1074/jbc.270.43.25752;  
RA Horl O., Brett J., Slatery T., Gao R., Zhang J., Chen J.X.,  
RA Nagashima M., Lundh E.R., Vijay S., Nitecki D.,  
RT "The receptor for advanced glycation end products (RAGE) is a cellular  
binding site for amphoterin. Mediation of neurite outgrowth and co-  
RT expression of rage and amphoterin in the developing nervous system.",  
RL J. Biol. Chem. 270:25752-25761(1995).  
DR HSP; P07155; IAA.  
SQ SEQUENCE 20 AA; 2229 MW; 9B615F547CD3B518 CRC64;

Query Match 22.8%; Score 26; DB 2; Length 20;  
Best Local Similarity 55.6%; Pred. No. 9.1e+03;  
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 10 GNPKAPLYK 18  
| | | | |  
DB 3 GNPKAPLYK 11

## RESULT 23

Q9R4Y6\_PORCI PRELIMINARY; PRT; 20 AA.  
ID Q9R4Y6;  
AC Q9R4Y6;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Major outer membrane protein (Fragment).  
OS Porphyromonas gingivalis (Bacteroides gingivalis).  
OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;  
OC Porphyromonadaceae; Porphyromonas.  
OX NCBI\_TaxID=837;  
RN [1]  
RP PROTEIN SEQUENCE.  
RX MEDLINE=94268318; PubMed=8208139;  
RA Kokeguchi S., Miyamoto M., Ohyama H., Hongyo H., Takigawa M.,  
RA Kurihara H., Murayama Y., Kato K.,  
RT "Biochemical properties of the major outer membrane proteins of  
RT Porphyromonas gingivalis.",  
RL Microbios 77:247-252(1994).  
SQ SEQUENCE 20 AA; 2150 MW; FD89405CE953DA41 CRC64;

Query Match 22.8%; Score 26; DB 2; Length 20;  
Best Local Similarity 50.0%; Pred. No. 9.1e+03;  
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 DYHPPSRIG 10  
| | | | |  
DB 11 DYHPPSRIG 20

RESULT 24  
Q8UDM0\_9HIV1 PRELIMINARY; PRT; 14 AA.  
ID Q8UDM0;  
AC Q8UDM0;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Truncated tat protein (Fragment).  
GN Name=tat;  
OS Human immunodeficiency virus 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus;  
OC Primate lentivirus group.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=22032414; PubMed=12036486; DOI=10.1089/08922020753747914;  
RA Long E.M., Rainwater S.M., Laveys L., Mandalia K., Overbaugh J.,  
RT "HIV type 1 variants transmitted to women in Kenya require the CCR5  
RT coreceptor for entry, regardless of the genetic complexity of the  
RT infecting virus.",  
RL AIDS Res. Hum. Retroviruses 18:567-576(2002).  
DR EMBL; AF407150; AAM66205.1; -; Genomic\_DNA.  
FT NON TER 1  
SQ SEQUENCE 14 AA; 1442 MW; 37C58F7BF82D7AA8 CRC64;

Query Match 22.4%; Score 25.5; DB 2; Length 14;  
Best Local Similarity 50.0%; Pred. No. 7.3e+03;  
Matches 6; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

QY 5 PGSRG-GNPKAP 15  
| | | | |  
DB 1 PGSRG-GNPKAP 12

RESULT 25  
Q8UDM3\_9HIV1 PRELIMINARY; PRT; 14 AA.  
ID Q8UDM3;  
AC Q8UDM3;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Truncated tat protein (Fragment).  
GN Name=tat;  
OS Human immunodeficiency virus 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus;  
OC Primate lentivirus group.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=22032414; PubMed=12036486; DOI=10.1089/08922020753747914;  
RA Long E.M., Rainwater S.M., Laveys L., Mandalia K., Overbaugh J.,  
RT "HIV type 1 variants transmitted to women in Kenya require the CCR5  
RT coreceptor for entry, regardless of the genetic complexity of the  
RT infecting virus.",  
RL AIDS Res. Hum. Retroviruses 18:567-576(2002).  
DR EMBL; AF407149; AAM66202.1; -; Genomic\_DNA.  
FT NON TER 1  
SQ SEQUENCE 14 AA; 1442 MW; 37C58F7BF82D7AA8 CRC64;

Query Match 22.4%; Score 25.5; DB 2; Length 14;  
Best Local Similarity 50.0%; Pred. No. 7.3e+03;  
Matches 6; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

QY 5 PGSRG-GNPKAP 15  
| | | | |  
DB 1 PGSRG-GNPKAP 12

RESULT 26  
Q8UDM7\_9HIV1 PRELIMINARY; PRT; 14 AA.  
ID Q8UDM7;  
AC Q8UDM7;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Truncated tat protein (Fragment).  
GN Name=tat;  
OS Human immunodeficiency virus 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus;  
OC Primate lentivirus group.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=22032414; PubMed=12036486; DOI=10.1089/08922020753747914;  
RA Long E.M., Rainwater S.M., Laveys L., Mandalia K., Overbaugh J.,  
RT "HIV type 1 variants transmitted to women in Kenya require the CCR5  
RT coreceptor for entry, regardless of the genetic complexity of the  
RT infecting virus.",  
RL AIDS Res. Hum. Retroviruses 18:567-576(2002).  
DR EMBL; AF407149; AAM66202.1; -; Genomic\_DNA.  
FT NON TER 1  
SQ SEQUENCE 14 AA; 1442 MW; 37C58F7BF82D7AA8 CRC64;

AC Q8JDM7;  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Truncated tat protein (Fragment).  
 GN Name=tat;  
 OS Human immunodeficiency virus 1.  
 OC Viruses; Retrovirdae; Lentivirus;  
 OC Primate lentivirus group.  
 OC NCBI\_TaxID=11676;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=22032414; PubMed=12036486; DOI=10.1089/08922202753747914;  
 RA Long B.M., Rainwater S.M., Lavrey L., Mandalia K., Overbaugh J.;  
 RT "HIV type 1 variants transmitted to women in Kenya require the CCR5  
 RT coreceptor for entry, regardless of the genetic complexity of the  
 RT infecting virus."  
 RL AIDS Res. Hum. Retroviruses 18:567-576(2002).  
 DR EMBL; AF407148; AAM66198.1; -; Genomic\_DNA.  
 FT NON\_TER 1  
 SQ SEQUENCE 14 AA; 1442 MW; 37C58F7BF82D7AA8 CRC64;

Query Match 22.4%; Score 25.5; DB 2; Length 14;  
 Best Local Similarity 50.0%; Pred. No. 7.3e+03;  
 Matches 6; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

OY 5 PGSRL-GNPKAP 15  
 DB 1 PSSQLRGDPTGP 12

RESULT 27  
 Q9UC36 HUMAN PRELIMINARY; PRT; 9 AA.  
 ID Q9UC36\_HUMAN PRELIMINARY; PRT; 9 AA.  
 AC Q9UC36;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE 28 kDa heat shock protein homolog fragment 1 (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 RP PROTEIN SEQUENCE.  
 RX MEDLINE=92218434; PubMed=156006;  
 RA Kato K., Shinohara H., Goto S., Inaguma Y., Morishita R., Asano T.;  
 RT "Copurification of small heat shock protein with alpha B crystallin  
 RT from human skeletal muscle."  
 RL J. Biol. Chem. 267:7718-7725(1992).  
 DR GO; GO:0006986; P:response to unfolded protein; NAS.  
 FT NON\_TER 1  
 FT NON\_TER 1  
 SQ SEQUENCE 9 AA; 1220 MW; 26933415B1F77B43 CRC64;

Query Match 21.9%; Score 25; DB 2; Length 9;  
 Best Local Similarity 83.3%; Pred. No. 2.2e+06;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 4 YPGSRL 9  
 DB 3 YPGSRL 8

RESULT 28  
 Q9P116 HUMAN PRELIMINARY; PRT; 12 AA.  
 ID Q9P116\_HUMAN PRELIMINARY; PRT; 12 AA.  
 AC Q9P116;  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Apolipoprotein B receptor 2 (Fragment).

OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;  
 OC Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Korschinek I., Charehbaghi-Schnell E., Lang I., Binder R.B.;  
 RL Submitted (FE8-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF129170; AAF66440.1; -; Genomic\_DNA.  
 DR GO; GO:0004872; P:receptor activity; IEA.  
 KW Lipoprotein; Receptor.  
 FT NON\_TER 1  
 FT NON\_TER 1  
 SQ SEQUENCE 12 AA; 1467 MW; 4B8935410404877 CRC64;

Query Match 21.9%; Score 25; DB 2; Length 12;  
 Best Local Similarity 45.5%; Pred. No. 7.4e+03;  
 Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 5 PGSRLGNPKAP 15  
 DB 1 PPTPLGNRRRP 11

RESULT 29  
 Q7X9Y2 LYCES  
 ID Q7X9Y2\_LYCES PRELIMINARY; PRT; 13 AA.  
 AC Q7X9Y2;  
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE TAG1 (Fragment).  
 GN Name=TAG1;  
 OS Lycopersicon esculentum (Tomato).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;  
 OC Lamiales; Solanales; Solanaceae; Solanum; Lycopersicon.  
 OC NCBI\_TaxID=4081;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=22667639; PubMed=12782724; DOI=10.1105/tpc.009548;  
 RA Hong R.L., Hamaguchi L., Busch M.A., Weigel D.;  
 RT "Regulatory elements of the floral homeotic gene AGAMOUS identified by  
 RT phylogenetic footprinting and shadowing."  
 RL Plant Cell 15:1296-1309(2003).  
 DR EMBL; AY254705; AAP35239.1; -; Genomic\_DNA.  
 FT NON\_TER 1  
 FT NON\_TER 1  
 SQ SEQUENCE 13 AA; 1598 MW; CA858C01BF9E444D CRC64;

Query Match 21.9%; Score 25; DB 2; Length 13;  
 Best Local Similarity 50.0%; Pred. No. 8e+03;  
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 2 YEPGSRL 9  
 DB 3 YEVANNRV 10

RESULT 30  
 Q98Y97 SHIV1  
 ID Q98Y97\_SHIV1 PRELIMINARY; PRT; 14 AA.  
 AC Q98Y97;  
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE Truncated pol protein (Fragment).  
 GN Name=pol;  
 OS Human immunodeficiency virus 1.  
 OC Viruses; Retrovirdae; Retroviridae; Lentivirus;  
 OC Primate lentivirus group.  
 OC NCBI\_TaxID=11676;

```

RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22056123; PubMed=12060770; DOI=10.1073/pnas.112177799;
RA Beerenwinkler N., Schmidt B., Walter H., Kaiser R., Lengauer T.,
RT Hoffmann D., Korn K., Seibig U.;
RT "Diversity and complexity of HIV-1 drug resistance: a bioinformatics
RT approach to predicting phenotype from genotype."
RT Proc. Natl. Acad. Sci. U.S.A. 99:8271-8276(2002).
DR EMBL; AF347572; AK32648.1; -; Genomic_RNA.
FT NON_TER
SQ SEQUENCE 14 AA; 1748 MW; C2921F7CAB276416 CRC64;

Query Match
Best Local Similarity 44.4%; Score 25; DB 2; Length 14;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 12 PRAPLYKRP 20
DB 1 POTTLMQRP 9

RESULT 31
Q9TWE9_GALME PRELIMINARY; PRT; 15 AA.
ID Q9TWE9;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TRENBLrel. 14, Last annotation update)
DE PROPHENOLOXIDASE (fragment).
OS Galleria mellonella (Wax moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Dityrista; Pyraloidea;
OC Pyralidae; Galleriinae; Galleria.
OX NCBI_Taxid=7137;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=96137142; PubMed=8580908; DOI=10.1016/0955-1748(95)00040-2;
RA Kopecek P., Weise C., Giez P.;
RT "The prophenoloxidase from the wax moth Galleria mellonella:
RT purification and characterization of the proenzyme."
RT Insect Biochem. Mol. Biol. 25:1081-1091(1995).
SQ SEQUENCE 15 AA; 1695 MW; C78B5B2430AFD4A CRC64;

Query Match
Best Local Similarity 21.9%; Score 25; DB 2; Length 15;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 EYPSGR 8
DB 10 DYFGIR 15

RESULT 32
Q7X9Y4_CUCSA PRELIMINARY; PRT; 15 AA.
ID Q7X9Y4;
DT 01-OCT-2003 (TRENBLrel. 25, Created)
DT 01-OCT-2003 (TRENBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE CAG2 (Fragment).
GN Name=CAG2;
OS Cucumis sativus (Cucumber).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC euroside 1; Cucurbitales; Cucurbitaceae; Cucumis.
OX NCBI_Taxid=3659;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22667639; PubMed=12782724; DOI=10.1105/epc.009548;
RA Hong R.L., Hamaguchi U., Buech M.A., Weigel D.;
RT "Regulatory elements of the floral homeotic gene AGAMOUS identified by
RT phylogenetic footprinting and shadowing."
RT Plant Cell 15:1296-1309(2003).

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DR EMBL; AY254703; AAP35237.1; -; Genomic_DNA.
FT NON_TER
SQ SEQUENCE 15 AA; 1825 MW; 159B31EFC989114 CRC64;

Query Match
Best Local Similarity 50.0%; Score 25; DB 2; Length 15;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 YEYPSRL 9
DB 6 YEXANNRV 13

RESULT 33
Q9R564_ECOLI PRELIMINARY; PRT; 15 AA.
ID Q9R564;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE 36 kDa porin homolog (Outer membrane protein) (fragment).
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_Taxid=562;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=93328296; PubMed=8392972;
RA Dytoc M., Soni R., Cockcroft F.II., De Azavedo J., Louie M.,
RT Bruntton J., Sherman P.;
RT "Multiple determinants of verotoxin-producing Escherichia coli O157:H7
RT attachment-effacement."
RT Infect. Immun. 61:3382-3391(1993).
DR HSP; P02934; 10UP.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0008279; C:outer membrane (sensu Gram-negative Bacteria); IEA.
DR InterPro; IPR000498; OmpA tmem.
DR Pfam; PF01389; OmpA membrane; 1.
SQ SEQUENCE 15 AA; 1708 MW; 1DF32F81313A21BE CRC64;

Query Match
Best Local Similarity 57.1%; Score 25; DB 2; Length 15;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 YPSRLG 10
DB 8 YTGARDG 14

RESULT 34
Q9PS01_MTCUN PRELIMINARY; PRT; 15 AA.
ID Q9PS01;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TRENBLrel. 13, Last annotation update)
DE Gonadotropin alpha subunit (fragment).
OS Micropogonias undulatus (Atlantic croaker).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidae;
OC Sciænidæ; Micropogonias.
OX NCBI_Taxid=29154;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=94010173; PubMed=8405898; DOI=10.1006/gen.1993.1112;
RA Copeland P.A., Thomas P.;
RT "Isolation of gonadotropin subunits and evidence for two distinct
RT gonadotropins in Atlantic croaker (Micropogonias undulatus)."
RT Gen. Comp. Endocrinol. 91:115-125(1993).
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0005179; F:hormone activity; IEA.

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DR InterPro: IPR000476; Glyco hormone.  
SQ PRODOM: PD002047; Glyco hormone; 1.  
SQ SEQUENCE 15 AA; 1691 MW; 012P924A460B28E9 CRC64;  
Query Match 21.9%; Score 25; DB 2; Length 15;  
Best Local Similarity 50.0%; Pred. No. 9.4e+03;  
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
QY 4 YPGSRIGN 11  
DB 1 YPNTLSN 8  
RESULT 35  
Q9EBE8\_9HIV1  
ID Q9EBE8\_9HIV1 PRELIMINARY; PRT; 17 AA.  
AC Q9EBE8;  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
DE Truncated pol protein (Fragment).  
GN Name=pol;  
OS Human immunodeficiency virus 1.  
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;  
OC Lentiviruses; Primate lentivirus group.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=039D12;  
RX MEDLINE=20408577; PubMed=10952598;  
RA DOI=10.1128/AAC.44.9.2475-2484.2000;  
RA Bacheler L.T., Anton E., Kudish P., Baker D., Bunville J.,  
RA Krakowski K., Bolling L., Aujaay M., Wang X.V., Ellis D., Becker M.F.,  
RA Laet A.L., George H.V., Spalding D.R., Hollis G., Abremski K.;  
RT "Human immunodeficiency virus type 1 mutations selected in patients  
RT failing efavirenz combination therapy.";  
RT Antimicrob. Agents Chemother. 44:2475-2484(2000).  
[2]  
RN NUCLEOTIDE SEQUENCE.  
RP STRAIN=039D12;  
RC Abremski K.E., Bacheler L.T., Li J.;  
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY003625; AAC03309.1; -; Genomic\_RNA.  
FT CHAIN <1 17  
FT NON\_TER 1 17  
FT SEQUENCE 17 AA; 1906 MW; 1B34A845B7DEBCA9 CRC64;  
Query Match 21.9%; Score 25; DB 2; Length 17;  
Best Local Similarity 44.4%; Pred. No. 1.1e+04;  
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
QY 12 PKAPLYKRP 20  
DB 1 PQTLMQRP 9  
RESULT 36  
Q9EKP3\_9HIV1  
ID Q9EKP3\_9HIV1 PRELIMINARY; PRT; 17 AA.  
AC Q9EKP3;  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Truncated pol protein (Fragment).  
GN Name=pol;  
OS Human immunodeficiency virus 1.  
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;  
OC Lentiviruses; Primate lentivirus group.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=037G06;  
RX MEDLINE=20408577; PubMed=10952598;  
RA DOI=10.1128/AAC.44.9.2475-2484.2000;  
RA Bacheler L.T., Anton E., Kudish P., Baker D., Bunville J.,  
RA Krakowski K., Bolling L., Aujaay M., Wang X.V., Ellis D., Becker M.F.,  
RA Laet A.L., George H.V., Spalding D.R., Hollis G., Abremski K.;  
RT "Human immunodeficiency virus type 1 mutations selected in patients  
RT failing efavirenz combination therapy.";  
RT Antimicrob. Agents Chemother. 44:2475-2484(2000).  
[2]  
RN NUCLEOTIDE SEQUENCE.  
RP STRAIN=037G06;  
RC Abremski K.E., Bacheler L.T., Li J.;  
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY000247; AAF88276.1; -; Genomic\_RNA.  
FT CHAIN <1 17  
FT NON\_TER 1 17  
FT SEQUENCE 17 AA; 1978 MW; 5A37CE45B7DEBCA9 CRC64;  
Query Match 21.9%; Score 25; DB 2; Length 17;  
Best Local Similarity 44.4%; Pred. No. 1.1e+04;  
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
QY 12 PKAPLYKRP 20  
DB 1 PQTLMQRP 9  
RESULT 38  
Q9TWK3\_MYTEB  
ID Q9TWK3\_MYTEB PRELIMINARY; PRT; 18 AA.  
AC Q9TWK3;  
RX MEDLINE=20408577; PubMed=10952598;

RX DOI=10.1128/AAC.44.9.2475-2484.2000;  
RA Bacheler L.T., Anton E., Kudish P., Baker D., Bunville J.,  
RA Krakowski K., Bolling L., Aujaay M., Wang X.V., Ellis D., Becker M.F.,  
RA Laet A.L., George H.V., Spalding D.R., Hollis G., Abremski K.;  
RT "Human immunodeficiency virus type 1 mutations selected in patients  
RT failing efavirenz combination therapy.";  
RT Antimicrob. Agents Chemother. 44:2475-2484(2000).  
[2]  
RN NUCLEOTIDE SEQUENCE.  
RP STRAIN=037G06;  
RC Abremski K.E., Bacheler L.T., Li J.;  
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY000379; AAF88407.1; -; Genomic\_RNA.  
FT CHAIN <1 17  
FT NON\_TER 1 17  
FT SEQUENCE 17 AA; 1963 MW; 6C34AE45A57DEBCD CRC64;  
Query Match 21.9%; Score 25; DB 2; Length 17;  
Best Local Similarity 44.4%; Pred. No. 1.1e+04;  
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
QY 12 PKAPLYKRP 20  
DB 1 PQTLMQRP 9  
RESULT 37  
Q9EL24\_9HIV1  
ID Q9EL24\_9HIV1 PRELIMINARY; PRT; 17 AA.  
AC Q9EL24;  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
DE Truncated pol protein (Fragment).  
GN Name=pol;  
OS Human immunodeficiency virus 1.  
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;  
OC Lentiviruses; Primate lentivirus group.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=095C04;  
RX MEDLINE=20408577; PubMed=10952598;  
RA DOI=10.1128/AAC.44.9.2475-2484.2000;  
RA Bacheler L.T., Anton E., Kudish P., Baker D., Bunville J.,  
RA Krakowski K., Bolling L., Aujaay M., Wang X.V., Ellis D., Becker M.F.,  
RA Laet A.L., George H.V., Spalding D.R., Hollis G., Abremski K.;  
RT "Human immunodeficiency virus type 1 mutations selected in patients  
RT failing efavirenz combination therapy.";  
RT Antimicrob. Agents Chemother. 44:2475-2484(2000).  
[2]  
RN NUCLEOTIDE SEQUENCE.  
RP STRAIN=095C04;  
RC Abremski K.E., Bacheler L.T., Li J.;  
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY000247; AAF88276.1; -; Genomic\_RNA.  
FT CHAIN <1 17  
FT NON\_TER 1 17  
FT SEQUENCE 17 AA; 1978 MW; 5A37CE45B7DEBCA9 CRC64;  
Query Match 21.9%; Score 25; DB 2; Length 17;  
Best Local Similarity 44.4%; Pred. No. 1.1e+04;  
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
QY 12 PKAPLYKRP 20  
DB 1 PQTLMQRP 9  
RESULT 38  
Q9TWK3\_MYTEB  
ID Q9TWK3\_MYTEB PRELIMINARY; PRT; 18 AA.  
AC Q9TWK3;

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DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 13, Last annotation update)
DE Proximal collagen (Fragment).
OS Mytilus edulis (Blue mussel).
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Mytiloida;
OC Mytilioidae; Mytilidae; Mytilinae; Mytilus.
OC NCBI_TaxID=6550;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=95230211; PubMed=7714453;
RA Qin X., Waite J.H.;
RT "Exotic collagen gradients in the byssus of the mussel Mytilus
RT edulis."
RL J. Exp. Biol. 198;633-644(1995).
SQ SEQUENCE 18 AA; 1643 MW; D27B5AF84C6BA04 CRC64;

Query Match 21.9%; Score 25; DB 2; Length 18;
Best Local Similarity 46.2%; Pred. No. 1.2e+04;
Matches 6; Conservative 2; Mismatches 3; Indels 2; Gaps 1;

QY 5 PGS--RLGNPKAP 15
DB 4 PGNGQPGNGPGR 16

RESULT 39
ID Q38573_BPKUI PRELIMINARY; PRT; 18 AA.
AC Q38573;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Coat protein (Fragment).
OS Bacteriophage KUI.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
OC Levivirus; Levivirus subgroup II.
OC NCBI_TaxID=12021;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=96207403; PubMed=8615017; DOI=10.1006/viro.1996.0174;
RA Groenewald H., Oudot F., van Duin J.V.;
RT "RNA phage KUI has an insertion of 18 nucleotides in the start codon
RT of its lysis gene."
RL Virology 218:141-147(1996).
DR EMBL; S81763; AAD14371.1; -; Genomic_RNA.
DR HSSP; P07234; IUNA.
KW Capsid protein.
FT NON TER 1
SQ SEQUENCE 18 AA; 1825 MW; 2D4092DC226D8904 CRC64;

Query Match 21.9%; Score 25; DB 2; Length 18;
Best Local Similarity 57.1%; Pred. No. 1.2e+04;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 8 RLGNPKA 14
DB 1 KIGNPVA 7

RESULT 40
ID CXAD_CONGE STANDARD; PRT; 19 AA.
AC P60274;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Alpha-conotoxin GID.
OS Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbecomha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OC NCBI_TaxID=6491;

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RN [1]
RP PROTEIN SEQUENCE, STRUCTURE BY NMR, SYNTHESIS, MASS SPECTROMETRY, AND
RP MUTAGENESIS OF ARG-12.
RC TISSUE=Venom;
RX PubMed=12419800; DOI=10.1074/jbc.M210280200;
RA Nicke A., Loughman M.L., Millard E.L., Alewood P.F., Adams D.J.,
RA Daly N.L., Craik D.J., Lewis R.J.;
RT "Isolation, structure, and activity of GID, a novel alpha 4/7-
RT conotoxin with an extended N-terminal sequence."
RL J. Biol. Chem. 278:3137-3144(2003).
CC -1- FUNCTION: Alpha-conotoxins act on postsynaptic membranes, they
CC bind to the nicotinic acetylcholine receptors (nAChR) and thus
CC inhibit them. This peptide reversibly inhibits alpha-7, alpha-
CC 3/beta-2, and alpha-4/beta-2 subunits.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -1- MASS SPECTROMETRY: MW=2184.9; METHOD=UNKNOWN; RANGE=1-19;
CC NOTE=Ref.1.
CC -1- SIMILARITY: Belongs to the conotoxin A superfamily. Alpha-type
CC family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR PDB; 1MTQ; NMR; -
DR InterPro; IPR013007; Alpha_conotoxin.
DR PROSITE; PS60014; ALPHA_CONOTOXIN; 1.
KW 3D-structure; Acetylcholine receptor inhibitor;
KW Direct protein sequencing; Gamma-carboxyglutamic acid; Hydroxylation;
KW Neurotoxin; Postsynaptic neurotoxin; Toxin.
FT MOD_RES 4 4
FT MOD_RES 16 16
FT DISULFID 5 11
FT DISULFID 6 19
FT MUTAGEN 1 4
SQ SEQUENCE 12 12
MUTAGEN 19 AA; 2130 MW; 0D14B58724C98F0E CRC64;

Query Match 21.9%; Score 25; DB 1; Length 19;
Best Local Similarity 50.0%; Pred. No. 1.2e+04;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 5 PGSRLGNP 12
DB 9 PACRVNRP 16

RESULT 41
ID Q9TWY2_LEIME PRELIMINARY; PRT; 19 AA.
AC Q9TWY2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Membrane-bound acid phosphatase (Fragment).
OS Leishmania mexicana.
OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OC NCBI_TaxID=5665;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=9131238; PubMed=1857378; DOI=10.1016/0166-6851(91)90152-V;
RA Menz B., Winter G., Ilg T., Lottspeich F., Overath P.;
RT "Purification and characterization of a membrane-bound acid
RT phosphatase of Leishmania mexicana."
RL Mol. Biochem. Parasitol. 47:101-108(1991).
DR InterPro; IPR000560; H18AC_phsphtase.
DR Pfam; PF00328; Acid_phosphat_A; 1.

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FT NON\_TER 1 1  
 FT NON\_TER 19 19  
 SQ SEQUENCE 19 AA; 2178 MW; EC44360F28A7D71B CRC64;

Query Match  
 Best Local Similarity 21.9%; Score 25; DB 2; Length 19;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 14 APLVK 18  
 DB 1 APMYK 5

## RESULT 42

0420Y4\_PLABE PRELIMINARY; PRT; 20 AA.

AC 0420Y4;  
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
 DE Hypothetical protein (Fragment).  
 GN ORFNames=PB103079.00.0;  
 OS Plasmodium berghei.

OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
 OX NCBI\_Taxid=5821;  
 RN [1]

## NUCLEOTIDE SEQUENCE.

RA Hall N., Karras M., Ratne J.D., Carlton J.M., Kool J.T.W.A.,  
 RA Brittan M., Florens L., Jensen C.S., Pain A., Christophides G.K.,  
 RA James K., Rutherford K., Harris B., Harris D., Churcher C.,  
 RA Quail M.A., Ormond D., Doggett J., Trueman H.B., Mendoza J.,  
 RA Bidwell S.L., Rejmanek M.A., Carnocci D.J., Yates J.R., Kafatos F.C.,  
 RA Jansz C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.,  
 RT A comprehensive survey of the Plasmodium life cycle by genomic,  
 RT transcriptomic, and proteomic analyses.";  
 RL Science 307:82-86(2005).

-1- CAUTION: The sequence shown here is derived from an  
 EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
 preliminary data.

DR EMBL; CA01010123; CAH96056.1; -; Genomic\_DNA.  
 KW Hypothetical protein.

FT NON\_TER 1  
 SQ SEQUENCE 20 AA; 2219 MW; B9231579795PEF7 CRC64;

Query Match  
 Best Local Similarity 21.9%; Score 25; DB 2; Length 20;  
 Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 12 PKAPLYR 19  
 DB 3 PKGPNMKR 10

## RESULT 43

069176\_CHLTR PRELIMINARY; PRT; 20 AA.

AC 069176;  
 DT 01-AUG-1998 (TrEMBLrel. 07, Created)  
 DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Major outer membrane protein (Fragment).  
 GN Name=omp-1;  
 OS Chlamydia trachomatis.

OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.  
 OX NCBI\_Taxid=813;  
 RN [1]

## NUCLEOTIDE SEQUENCE.

RA Hejeh Y.-H., Bobo L.D.,  
 RA Submitted (May-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF065436; AAC17176.1; -; Genomic\_DNA.

FT NON\_TER 1  
 SQ SEQUENCE 20 AA; 1929 MW; 504C8985119AF1F3 CRC64;

Query Match  
 Best Local Similarity 21.9%; Score 25; DB 2; Length 20;  
 Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 5 PGSRLGNPKAP 15  
 DB 3 PTATGNAAP 13

## RESULT 44

085509\_CHLTR PRELIMINARY; PRT; 20 AA.

AC 085509;  
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)  
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)  
 DE Major outer membrane protein (Fragment).  
 GN Name=omp-1;  
 OS Chlamydia trachomatis.

OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.  
 OX NCBI\_Taxid=813;  
 RN [1]

## NUCLEOTIDE SEQUENCE.

RA Hejeh Y.-H., Bobo L.D.,  
 RA Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF070235; AAC25205.1; -; Genomic\_DNA.

FT NON\_TER 1  
 SQ SEQUENCE 20 AA; 1929 MW; 504C8985119AF1F3 CRC64;

Query Match  
 Best Local Similarity 21.9%; Score 25; DB 2; Length 20;  
 Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 5 PGSRLGNPKAP 15  
 DB 3 PTATGNAAP 13

## RESULT 45

085510\_CHLTR PRELIMINARY; PRT; 20 AA.

AC 085510;  
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)  
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)  
 DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)  
 DE Major outer membrane protein (Fragment).  
 GN Name=omp-1;  
 OS Chlamydia trachomatis.

OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.  
 OX NCBI\_Taxid=813;  
 RN [1]

## NUCLEOTIDE SEQUENCE.

RA Hejeh Y.-H., Bobo L.D.,  
 RA Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF070239; AAC25209.1; -; Genomic\_DNA.

FT NON\_TER 1  
 SQ SEQUENCE 20 AA; 1957 MW; 504C9B32B19AF1F3 CRC64;

Query Match  
 Best Local Similarity 21.9%; Score 25; DB 2; Length 20;  
 Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 5 PGSRLGNPKAP 15  
 DB 3 PTATGNAAP 13

## RESULT 46

```
085512 CHLTR
ID 085512 CHLTR PRELIMINARY; PRT; 20 AA.
AC 085512;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DE Major outer membrane protein (Fragment).
GN Name=omp-1;
OS Chlamydia trachomatis.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_Taxid=813;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=B2a;
RA Heish Y.-H., Bobo L.D.;
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL, AF070251, AAC25221.1; -, Genomic_DNA.
FT NON_TER 1
SQ SEQUENCE 20 AA; 1929 MW; 504C8985119AF1F3 CRC64;

Query Match
Best Local Similarity 21.9%; Score 25; DB 2; Length 20;
Pred. No. 1.3e+04;
Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 5 PGSRLGNPKAP 15
Db 3 PTATTGNMAAP 13

RESULT 47
085514 CHLTR
ID 085514 CHLTR PRELIMINARY; PRT; 20 AA.
AC 085514;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DE Major outer membrane protein (Fragment).
GN Name=omp-1;
OS Chlamydia trachomatis.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_Taxid=813;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=B24a;
RA Heish Y.-H., Bobo L.D.;
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL, AF070255; AAC25225.1; -, Genomic_DNA.
FT NON_TER 1
SQ SEQUENCE 20 AA; 1929 MW; 504C8985119AF1F3 CRC64;

Query Match
Best Local Similarity 21.9%; Score 25; DB 2; Length 20;
Pred. No. 1.3e+04;
Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 5 PGSRLGNPKAP 15
Db 3 PTATTGNMAAP 13

RESULT 48
085517 CHLTR
ID 085517 CHLTR PRELIMINARY; PRT; 20 AA.
AC 085517;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DE Major outer membrane protein (Fragment).
GN Name=omp-1;
OS Chlamydia trachomatis.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_Taxid=813;
```

```
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=B2b;
RA Heish Y.-H., Bobo L.D.;
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL, AF070259; AAC25229.1; -, Genomic_DNA.
FT NON_TER 1
SQ SEQUENCE 20 AA; 1929 MW; 504C8985119AF1F3 CRC64;

Query Match
Best Local Similarity 21.9%; Score 25; DB 2; Length 20;
Pred. No. 1.3e+04;
Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 5 PGSRLGNPKAP 15
Db 3 PTATTGNMAAP 13

RESULT 49
085519 CHLTR
ID 085519 CHLTR PRELIMINARY; PRT; 20 AA.
AC 085519;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DE Major outer membrane protein (Fragment).
GN Name=omp-1;
OS Chlamydia trachomatis.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_Taxid=813;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=B2c;
RA Heish Y.-H., Bobo L.D.;
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL, AF070263; AAC25233.1; -, Genomic_DNA.
FT NON_TER 1
SQ SEQUENCE 20 AA; 1929 MW; 504C8985119AF1F3 CRC64;

Query Match
Best Local Similarity 21.9%; Score 25; DB 2; Length 20;
Pred. No. 1.3e+04;
Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 5 PGSRLGNPKAP 15
Db 3 PTATTGNMAAP 13

RESULT 50
085520 CHLTR
ID 085520 CHLTR PRELIMINARY; PRT; 20 AA.
AC 085520;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DE Major outer membrane protein (Fragment).
GN Name=omp-1;
OS Chlamydia trachomatis.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_Taxid=813;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=B2d;
RA Heish Y.-H., Bobo L.D.;
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL, AF070267; AAC25237.1; -, Genomic_DNA.
FT NON_TER 1
SQ SEQUENCE 20 AA; 1929 MW; 504C8985119AF1F3 CRC64;

Query Match
Best Local Similarity 21.9%; Score 25; DB 2; Length 20;
Pred. No. 1.3e+04;
Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
```

Best Local Similarity 45.5%; Pred. No. 1.3e+04;  
Matches 5, Conservative 1, Mismatches 5, Indels 0, Gaps 0;

QY 5 PGSRLGNPKAP 15  
| : || ||  
Db 3 PRTATGNAAP 13

## RESULT 51

085521\_CHLTR PRELIMINARY; PRT; 20 AA.

AC 085521;  
DT 01-NOV-1998 (TREMBLrel. 08, Created)  
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)  
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)  
DE Major outer membrane protein (Fragment).  
GN Name-comp-1;  
OS Chlamydia trachomatis.  
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.  
OX NCBI\_Taxid=813;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=B24b;  
RA HeiJeh Y.-H.; Bobo L.D.;  
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF070271; AAC25241.1; -; Genomic\_DNA.  
FT NON\_TER 1 20  
SQ SEQUENCE 20 AA; 1929 MW; 504C8985119AF1F3 CRC64;

Query Match 21.9%; Score 25; DB 2; Length 20;  
Best Local Similarity 45.5%; Pred. No. 1.3e+04;  
Matches 5, Conservative 1, Mismatches 5, Indels 0, Gaps 0;

QY 5 PGSRLGNPKAP 15  
| : || ||  
Db 3 PRTATGNAAP 13

## RESULT 52

085522\_CHLTR PRELIMINARY; PRT; 20 AA.

AC 085522;  
DT 01-NOV-1998 (TREMBLrel. 08, Created)  
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)  
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)  
DE Major outer membrane protein (Fragment).  
GN Name-comp-1;  
OS Chlamydia trachomatis.  
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.  
OX NCBI\_Taxid=813;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=B23a;  
RA HeiJeh Y.-H.; Bobo L.D.;  
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF070275; AAC25245.1; -; Genomic\_DNA.  
FT NON\_TER 1 20  
SQ SEQUENCE 20 AA; 1929 MW; 504C8985119AF1F3 CRC64;

Query Match 21.9%; Score 25; DB 2; Length 20;  
Best Local Similarity 45.5%; Pred. No. 1.3e+04;  
Matches 5, Conservative 1, Mismatches 5, Indels 0, Gaps 0;

QY 5 PGSRLGNPKAP 15  
| : || ||  
Db 3 PRTATGNAAP 13

RESULT 53  
085523\_CHLTR  
ID 085523\_CHLTR PRELIMINARY; PRT; 20 AA.

AC 085523;  
DT 01-NOV-1998 (TREMBLrel. 08, Created)  
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)  
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)  
DE Major outer membrane protein (Fragment).  
GN Name-comp-1;  
OS Chlamydia trachomatis.  
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.  
OX NCBI\_Taxid=813;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.

QY 5 PGSRLGNPKAP 15  
| : || ||  
Db 3 PRTATGNAAP 13

Query Match 21.9%; Score 25; DB 2; Length 20;  
Best Local Similarity 45.5%; Pred. No. 1.3e+04;  
Matches 5, Conservative 1, Mismatches 5, Indels 0, Gaps 0;

QY 5 PGSRLGNPKAP 15  
| : || ||  
Db 3 PRTATGNAAP 13

## RESULT 54

085525\_CHLTR PRELIMINARY; PRT; 20 AA.

AC 085525;  
DT 01-NOV-1998 (TREMBLrel. 08, Created)  
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)  
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)  
DE Major outer membrane protein (Fragment).  
GN Name-comp-1;  
OS Chlamydia trachomatis.  
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.  
OX NCBI\_Taxid=813;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=B2f;  
RA HeiJeh Y.-H.; Bobo L.D.;  
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF070283; AAC25253.1; -; Genomic\_DNA.  
FT NON\_TER 1 20  
SQ SEQUENCE 20 AA; 1929 MW; 504C8985119AF1F3 CRC64;

Query Match 21.9%; Score 25; DB 2; Length 20;  
Best Local Similarity 45.5%; Pred. No. 1.3e+04;  
Matches 5, Conservative 1, Mismatches 5, Indels 0, Gaps 0;

QY 5 PGSRLGNPKAP 15  
| : || ||  
Db 3 PRTATGNAAP 13

## RESULT 55

085526\_CHLTR PRELIMINARY; PRT; 20 AA.

AC 085526;  
DT 01-NOV-1998 (TREMBLrel. 08, Created)  
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)  
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)  
DE Major outer membrane protein (Fragment).  
GN Name-comp-1;  
OS Chlamydia trachomatis.  
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.  
OX NCBI\_Taxid=813;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.

RC STRAIN=B3a;  
RA Heleh Y.-H., Bobo L.D.;  
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF070287; AAC25257.1; -, Genomic\_DNA.  
FT NON\_TER 1  
FT NON\_TER 20  
SQ SEQUENCE 20 AA; 1929 MW; 504C8985119AF1F3 CRC64;

Query Match 21.9%; Score 25; DB 2; Length 20;  
Best Local Similarity 45.5%; Pred. No. 1.3e+04;  
Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 5 PGSRLGNPKAP 15  
| : || ||  
Db 3 PTTATGNNAAP 13

RESULT 56  
ID 085528 CHLTR PRELIMINARY; PRT; 20 AA.  
AC 085528;  
DT 01-NOV-1998 (TREMBlrel. 08, Created)  
DR 01-NOV-1998 (TREMBlrel. 08, Last sequence update)  
DE Major outer membrane protein (Fragment).  
GN Name=omp-1;  
OS Chlamydia trachomatis.  
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.  
OX NCBI\_TaxID=813;  
RN (1)  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=B4a;  
RA Heleh Y.-H., Bobo L.D.;  
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF070291; AAC25261.1; -, Genomic\_DNA.  
FT NON\_TER 1  
FT NON\_TER 20  
SQ SEQUENCE 20 AA; 1929 MW; 504C8985119AF1F3 CRC64;

Query Match 21.9%; Score 25; DB 2; Length 20;  
Best Local Similarity 45.5%; Pred. No. 1.3e+04;  
Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 5 PGSRLGNPKAP 15  
| : || ||  
Db 3 PTTATGNNAAP 13

RESULT 57  
ID 085530 CHLTR PRELIMINARY; PRT; 20 AA.  
AC 085530;  
DT 01-NOV-1998 (TREMBlrel. 08, Created)  
DR 01-NOV-1998 (TREMBlrel. 08, Last sequence update)  
DE Major outer membrane protein (Fragment).  
GN Name=omp-1;  
OS Chlamydia trachomatis.  
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.  
OX NCBI\_TaxID=813;  
RN (1)  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=B4b;  
RA Heleh Y.-H., Bobo L.D.;  
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF070295; AAC25265.1; -, Genomic\_DNA.  
FT NON\_TER 1  
FT NON\_TER 20  
SQ SEQUENCE 20 AA; 1929 MW; 504C8985119AF1F3 CRC64;

Query Match 21.9%; Score 25; DB 2; Length 20;  
Best Local Similarity 45.5%; Pred. No. 1.3e+04;  
Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 5 PGSRLGNPKAP 15  
| : || ||  
Db 3 PTTATGNNAAP 13

RESULT 58  
ID 085531 CHLTR PRELIMINARY; PRT; 20 AA.  
AC 085531;  
DT 01-NOV-1998 (TREMBlrel. 08, Created)  
DR 01-NOV-1998 (TREMBlrel. 08, Last sequence update)  
DE Major outer membrane protein (Fragment).  
GN Name=omp-1;  
OS Chlamydia trachomatis.  
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.  
OX NCBI\_TaxID=813;  
RN (1)  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=B4c;  
RA Heleh Y.-H., Bobo L.D.;  
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF070299; AAC25269.1; -, Genomic\_DNA.  
FT NON\_TER 1  
FT NON\_TER 20  
SQ SEQUENCE 20 AA; 1929 MW; 504C8985119AF1F3 CRC64;

Query Match 21.9%; Score 25; DB 2; Length 20;  
Best Local Similarity 45.5%; Pred. No. 1.3e+04;  
Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 5 PGSRLGNPKAP 15  
| : || ||  
Db 3 PTTATGNNAAP 13

RESULT 59  
ID 085533 CHLTR PRELIMINARY; PRT; 20 AA.  
AC 085533;  
DT 01-NOV-1998 (TREMBlrel. 08, Created)  
DR 01-NOV-1998 (TREMBlrel. 08, Last sequence update)  
DE Major outer membrane protein (Fragment).  
GN Name=omp-1;  
OS Chlamydia trachomatis.  
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.  
OX NCBI\_TaxID=813;  
RN (1)  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=B4d;  
RA Heleh Y.-H., Bobo L.D.;  
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF070303; AAC25273.1; -, Genomic\_DNA.  
FT NON\_TER 1  
FT NON\_TER 20  
SQ SEQUENCE 20 AA; 1929 MW; 504C8985119AF1F3 CRC64;

Query Match 21.9%; Score 25; DB 2; Length 20;  
Best Local Similarity 45.5%; Pred. No. 1.3e+04;  
Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 5 PGSRLGNPKAP 15  
| : || ||  
Db 3 PTTATGNNAAP 13

RESULT 60  
ID 053520 CHLTR PRELIMINARY; PRT; 20 AA.  
AC 053520;  
DT 01-NOV-1996 (TREMBlrel. 01, Created)

DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)  
 DE Major outer membrane protein (Fragment).  
 GN Name=omp1;  
 OS Chlamydia trachomatis.  
 OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.  
 ON NCBI\_TaxId=813;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=95318541; PubMed=7797929;  
 RA Hayes L.J., Pecharatana S., Bailey R.L., Hampton T.J., Pickett M.A.,  
 RA Mabey D.C., Watt P.J., Ward M.E.;  
 RT "Extent and kinetics of genetic change in the omp1 gene of Chlamydia  
 trachomatis in two villages with endemic trachoma."  
 RT J. Infect. Dis. 172:268-272(1995).  
 DR EMBL; 877980; AAB34695.1; -; Genomic\_DNA.  
 FT NON\_TER 20  
 SQ SEQUENCE 20 AA; 1959 MW; 51FC8985119AF1F3 CRC64;  
 Query Match 21.9%; Score 25; DB 2; Length 20;  
 Best Local Similarity 45.5%; Pred. No. 1.3e+04;  
 Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;  
 QY 5 PGSRGNPKAP 15  
 DB 3 PTTTGNAAP 13

RESULT 61  
 Q9R8N0 CHLTR  
 ID Q9R8N0 CHLTR PRELIMINARY; PRT; 20 AA.  
 AC Q9R8N0  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
 DE Major outer membrane protein (Fragment).  
 GN Name=omp-1;  
 OS Chlamydia trachomatis.  
 OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.  
 ON NCBI\_TaxId=813;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=B124a;  
 RA Heileh Y.-H., Bobo L.D.;  
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF070247; AAC25217.1; -; Genomic\_DNA.  
 FT NON\_TER 1  
 FT NON\_TER 20  
 SQ SEQUENCE 20 AA; 1959 MW; 505C8885119AF1F3 CRC64;  
 Query Match 21.9%; Score 25; DB 2; Length 20;  
 Best Local Similarity 45.5%; Pred. No. 1.3e+04;  
 Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;  
 QY 5 PGSRGNPKAP 15  
 DB 3 PTTTGNAAP 13

RESULT 62  
 Q9R8N4 CHLTR  
 ID Q9R8N4 CHLTR PRELIMINARY; PRT; 20 AA.  
 AC Q9R8N4  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
 DE Major outer membrane protein (Fragment).  
 GN Name=omp-1;  
 OS Chlamydia trachomatis.  
 OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.  
 ON NCBI\_TaxId=813;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.

RC STRAIN=B12a;  
 RA Heileh Y.-H., Bobo L.D.;  
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF070243; AAC25213.1; -; Genomic\_DNA.  
 FT NON\_TER 1  
 FT NON\_TER 20  
 SQ SEQUENCE 20 AA; 1959 MW; 505C8885119AF1F3 CRC64;  
 Query Match 21.9%; Score 25; DB 2; Length 20;  
 Best Local Similarity 45.5%; Pred. No. 1.3e+04;  
 Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;  
 QY 5 PGSRGNPKAP 15  
 DB 3 PTTTGNAAP 13

RESULT 63  
 Q9R8P4 CHLTR  
 ID Q9R8P4 CHLTR PRELIMINARY; PRT; 20 AA.  
 AC Q9R8P4  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
 DE Major outer membrane protein (Fragment).  
 GN Name=omp-1;  
 OS Chlamydia trachomatis.  
 OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.  
 ON NCBI\_TaxId=813;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=Ref Ba;  
 RA Heileh Y.-H., Bobo L.D.;  
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF070231; AAC25201.1; -; Genomic\_DNA.  
 FT NON\_TER 1  
 FT NON\_TER 20  
 SQ SEQUENCE 20 AA; 1959 MW; 505C8885119AF1F3 CRC64;  
 Query Match 21.9%; Score 25; DB 2; Length 20;  
 Best Local Similarity 45.5%; Pred. No. 1.3e+04;  
 Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;  
 QY 5 PGSRGNPKAP 15  
 DB 3 PTTTGNAAP 13

RESULT 64  
 Q61871 MOUSE  
 ID Q61871 MOUSE PRELIMINARY; PRT; 20 AA.  
 AC Q61871  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Envelope protein (Fragment).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Murinae; Mus.  
 ON NCBI\_TaxId=10090;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=AKR; TISSUE=Thymus;  
 RX MEDLINE=88091045; PubMed=2826802;  
 RA Laigret F., Repaske R., Boulukos K., Rabson A.B., Khan A.S.;  
 RT "Potential progenitor sequences of mink cell focus-forming (MCF)  
 murine leukemia viruses: ecotropic, xenotropic, and MCF-related viral  
 RNAs are detected concurrently in thymus tissues of AKR mice."  
 RL J. Virol. 62:376-386(1988).  
 DR EMBL; M19049; AAA18408.1; -; mRNA.  
 DR GO; GO:0019028; C:viral capsid; IEA.  
 DR GO; GO:0019031; C:viral envelope; IEA.

DR GO; GO:0005198; P:structural molecule activity; IEA.  
DR InterPro; IPR002050; Env polypeptide.  
DR Pfam; PF00429; TUV\_coat; 1.  
KW Envelope protein.

FT NON\_TER 20  
SQ SEQUENCE 20 AA; 2240 MW; 285338B2EB5C9DD CRC64;

Query Match 21.9%; Score 25; DB 2; Length 20;  
Best Local Similarity 83.3%; Pred. No. 1.3e+04;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 NPXAPL 16  
DB 15 NPWAPL 20

RESULT 65  
Q9PRV5\_XENLA PRELIMINARY; PRT; 20 AA.

AC Q9PRV5;  
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)  
DE NI(2+)-binding protein, PNIX (Fragment).  
OS Xenopus laevis (African clawed frog).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;  
OC Xenopodinae; Xenopus; Xenopus.  
NCBI\_TaxID=8335;

RA MEDLINE=95000642; PubMed=7917276;  
RA Grbac-Ivanovic S., Antonijczuk K., Varghese A.H., Plozman M.C.,  
RA Antonijczuk A., Korza G., Ozols J., Sunderman P.W.Tr.;  
RT "Lipoviteilin 2 beta is the 31 kD NI(2+)-binding protein (pnixb) in  
RT Xenopus oocytes and embryos.";  
RT Mol. Reprod. Dev. 38:256-263(1994).  
SQ SEQUENCE 20 AA; 2318 MW; 9681AB6C0E5BAE44 CRC64;

Query Match 21.9%; Score 25; DB 2; Length 20;  
Best Local Similarity 55.6%; Pred. No. 1.3e+04;  
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 EYPSRLGN 11  
DB 12 EHRGRLSS 20

RESULT 66  
O6BC29\_HUMAN PRELIMINARY; PRT; 8 AA.

AC O6BC29;  
DT 25-OCT-2004 (TREMBlrel. 28, Created)  
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)  
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)  
DE Protein S (Fragment).  
GN Name=PROS1;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;  
OC Homo.

OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Hamasaki N.;  
RT "Protein S variant in Exon3."  
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB162156; BAD36740.1; -; Genomic\_DNA.  
FT NON\_TER 1  
FT NON\_TER 1  
SQ SEQUENCE 8 AA; 1108 MW; D33B5377B59DB5A CRC64;

Query Match 21.1%; Score 24; DB 2; Length 8;

Best Local Similarity 80.0%; Pred. No. 2.2e+06;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYERP 5  
DB 1 DYERP 5

RESULT 67  
O12096\_CAEV PRELIMINARY; PRT; 9 AA.

AC O12096;  
DT 01-JUL-1997 (TREMBlrel. 04, Created)  
DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)  
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
DE Tat protein (Fragment).  
GN Name=tat;  
OS Caprine arthritis encephalitis virus (CAEV).  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus;  
OC Ovine/caprine lentivirus.  
OX NCBI\_TaxID=11660;

RA NUCLEOTIDE SEQUENCE.  
RA Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;  
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.  
DR EMBL; U81439; AAB60832.1; -; Genomic\_RNA.  
FT NON\_TER 1  
SQ SEQUENCE 9 AA; 922 MW; 21B644EB7340BB CRC64;

Query Match 21.1%; Score 24; DB 2; Length 9;  
Best Local Similarity 71.4%; Pred. No. 2.2e+06;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 GSRLGNP 12  
DB 2 GSRLGNP 8

RESULT 68  
O12098\_CAEV PRELIMINARY; PRT; 9 AA.

AC O12098;  
DT 01-JUL-1997 (TREMBlrel. 04, Created)  
DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)  
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
DE Tat protein (Fragment).  
GN Name=tat;  
OS Caprine arthritis encephalitis virus (CAEV).  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus;  
OC Ovine/caprine lentivirus.  
OX NCBI\_TaxID=11660;

RA NUCLEOTIDE SEQUENCE.  
RA Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;  
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.  
DR EMBL; U81440; AAB60835.1; -; Genomic\_RNA.  
FT NON\_TER 1  
SQ SEQUENCE 9 AA; 922 MW; 21B644EB7340BB CRC64;

Query Match 21.1%; Score 24; DB 2; Length 9;  
Best Local Similarity 71.4%; Pred. No. 2.2e+06;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 GSRLGNP 12  
DB 2 GSRLGNP 8

RESULT 69  
O12100\_CAEV PRELIMINARY; PRT; 9 AA.

AC O12100;  
DT 01-JUL-1997 (TREMBlrel. 04, Created)



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DT 01-JUL-1997 (TEMBLrel. 04, Last sequence update)
DE 01-DEC-2001 (TEMBLrel. 19, Last annotation update)
GN Tat protein (Fragment).
OS Caprine arthritis encephalitis virus (CAEV).
OC Viruses; Retroviridae; Lentivirus;
OC Ovine/caprine lentivirus.
OX NCBI_TaxId=11660;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Turelli P., Guisguen F., Mornex J.-F., Vigne R., Querat G.;
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U01441; AAB60836.1; -; Genomic_RNA.
FT NON TER 1
SQ SEQUENCE 9 AA; 922 MW; 21B8644BB7340EB8 CRC64;

Query Match 21.1%; Score 24; DB 2; Length 9;
Best Local Similarity 71.4%; Pred. No. 2.2e+06;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 GSRLGNP 12
DB 2 GCRLCNP 8

RESULT 70
012102 CAEV PRELIMINARY; PRT; 9 AA.
AC 012102;
DT 01-JUL-1997 (TEMBLrel. 04, Created)
DT 01-JUL-1997 (TEMBLrel. 04, Last sequence update)
DT 01-DEC-2001 (TEMBLrel. 19, Last annotation update)
DE Tat protein (Fragment).
GN Name=atc;
OS Caprine arthritis encephalitis virus (CAEV).
OC Viruses; Retroviridae; Lentivirus;
OC Ovine/caprine lentivirus.
OX NCBI_TaxId=11660;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Turelli P., Guisguen F., Mornex J.-F., Vigne R., Querat G.;
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U01442; AAB60838.1; -; Genomic_RNA.
FT NON TER 1
SQ SEQUENCE 9 AA; 922 MW; 21B8644BB7340EB8 CRC64;

Query Match 21.1%; Score 24; DB 2; Length 9;
Best Local Similarity 71.4%; Pred. No. 2.2e+06;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 GSRLGNP 12
DB 2 GCRLCNP 8

RESULT 71
012104 CAEV PRELIMINARY; PRT; 9 AA.
AC 012104;
DT 01-JUL-1997 (TEMBLrel. 04, Created)
DT 01-JUL-1997 (TEMBLrel. 04, Last sequence update)
DT 01-DEC-2001 (TEMBLrel. 19, Last annotation update)
DE Tat protein (Fragment).
GN Name=atc;
OS Caprine arthritis encephalitis virus (CAEV).
OC Viruses; Retroviridae; Lentivirus;
OC Ovine/caprine lentivirus.
OX NCBI_TaxId=11660;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Turelli P., Guisguen F., Mornex J.-F., Vigne R., Querat G.;
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U01443; AAB60840.1; -; Genomic_RNA.

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FT NON TER 1
SQ SEQUENCE 9 AA; 922 MW; 21B8644BB7340EB8 CRC64;

Query Match 21.1%; Score 24; DB 2; Length 9;
Best Local Similarity 71.4%; Pred. No. 2.2e+06;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 GSRLGNP 12
DB 2 GCRLCNP 8

RESULT 72
07M500 SEURO PRELIMINARY; PRT; 10 AA.
ID 07M500;
AC 07M500;
DT 01-MAR-2004 (TEMBLrel. 26, Created)
DT 01-MAR-2004 (TEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TEMBLrel. 26, Last annotation update)
DE Polysialacturonase (EC 3.2.1.15) IV (Fragment).
OS Aspergillus sp.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxId=5065;
RN [1]
RP PROTEIN SEQUENCE.
RA Strailova B., Dzurava M., Markovic O., Joernvall H.;
RT "An essential tyrosine residue of Aspergillus polysialacturonase."
RL FEBS Lett. 382:164-166 (1996).
RN [2]
RP PROTEIN SEQUENCE.
RX PubMed=6612742;
RA Strailova B., Dzurava M., Markovic O., Joernvall H.;
RT "An essential tyrosine residue of Aspergillus polysialacturonase."
RL FEBS Lett. 382:164-166 (1996).
DR PIR; S62880; S62880.
DR GO; GO:0004650; P:polysialacturonase activity; IEA.
FT NON TER 1
SQ SEQUENCE 10 AA; 1146 MW; D58E3F133861BB5D CRC64;

Query Match 21.1%; Score 24; DB 2; Length 10;
Best Local Similarity 66.7%; Pred. No. 8.6e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 DYEYPG 6
DB 1 DYAYTG 6

RESULT 73
09C057 HUMAN PRELIMINARY; PRT; 11 AA.
ID 09C057;
AC 09C057;
DT 01-JUN-2001 (TEMBLrel. 17, Created)
DT 01-JUN-2001 (TEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TEMBLrel. 17, Last annotation update)
DE HEX (Fragment).
GN Name=HEX;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCBI_TaxId=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Oyama Y., Kurabayashi M., Nagai R., Shimomura Y., Sekiguchi K.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF182950; AAK12833.1; -; Genomic_DNA.
FT NON TER 11
SQ SEQUENCE 11 AA; 1125 MW; 2644D7FBE686761F7 CRC64;

Query Match 21.1%; Score 24; DB 2; Length 11;

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Best Local Similarity 44.4%; Pred. No. 9.6e+03;  
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 YEYPSRLG 10  
DB 3 YPHPEPAG 11

## RESULT 74

012074 CAEV  
ID 012074\_CAEV PRELIMINARY; PRT; 12 AA.

AC 012074;  
DT 01-JUL-1997 (TRENBLREL. 04, Created)  
DT 01-JUL-1997 (TRENBLREL. 04, Last sequence update)  
DT 01-JUN-2003 (TRENBLREL. 24, Last annotation update)  
DE Tat protein (Fragment).  
GN Name-tat;  
OS Caprine arthritis encephalitis virus (CAEV).  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus;  
OC Ovine/caprine lentivirus.  
OX NCBI\_Taxid=11660;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;  
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.  
DR EMBL; U81428; AAB60810.1; -; Genomic RNA.  
DR GO; GO:0016563; F:transcriptional activator activity; IEA.  
DR GO; GO:0045941; P:positive regulation of transcription; IEA.  
DR InterPro; IPR004247; LentiViral\_Tat.  
DR Pfam; PF02998; LentiViral\_Tat; I.  
FT NON\_TER 1  
SQ SEQUENCE 12 AA; 1266 MW; 5A60BBB1B8644EB7 CRC64;

Query Match 21.1%; Score 24; DB 2; Length 12;  
Best Local Similarity 71.4%; Pred. No. 1.1e+04;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 GSRLGNP 12  
DB 2 GCRLCNP 8

RESULT 75  
012076 CAEV  
ID 012076\_CAEV PRELIMINARY; PRT; 12 AA.

AC 012076;  
DT 01-JUL-1997 (TRENBLREL. 04, Created)  
DT 01-JUL-1997 (TRENBLREL. 04, Last sequence update)  
DT 01-JUN-2003 (TRENBLREL. 24, Last annotation update)  
DE Tat protein (Fragment).  
GN Name-tat;  
OS Caprine arthritis encephalitis virus (CAEV).  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus;  
OC Ovine/caprine lentivirus.  
OX NCBI\_Taxid=11660;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;  
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.  
DR EMBL; U81429; AAB60812.1; -; Genomic RNA.  
DR GO; GO:0016563; F:transcriptional activator activity; IEA.  
DR GO; GO:0045941; P:positive regulation of transcription; IEA.  
DR InterPro; IPR004247; LentiViral\_Tat.  
DR Pfam; PF02998; LentiViral\_Tat; I.  
FT NON\_TER 1  
SQ SEQUENCE 12 AA; 1266 MW; 5A60BBB1B8644EB7 CRC64;

Query Match 21.1%; Score 24; DB 2; Length 12;  
Best Local Similarity 71.4%; Pred. No. 1.1e+04;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 GSRLGNP 12  
DB 2 GCRLCNP 8

DB 2 GCRLCNP 8

## RESULT 76

012078 CAEV PRELIMINARY; PRT; 12 AA.

AC 012078;  
DT 01-JUL-1997 (TRENBLREL. 04, Created)  
DT 01-JUL-1997 (TRENBLREL. 04, Last sequence update)  
DT 01-JUN-2003 (TRENBLREL. 24, Last annotation update)  
DE Tat protein (Fragment).  
GN Name-tat;  
OS Caprine arthritis encephalitis virus (CAEV).  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus;  
OC Ovine/caprine lentivirus.  
OX NCBI\_Taxid=11660;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;  
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.  
DR EMBL; U81430; AAB60814.1; -; Genomic RNA.  
DR GO; GO:0016563; F:transcriptional activator activity; IEA.  
DR GO; GO:0045941; P:positive regulation of transcription; IEA.  
DR InterPro; IPR004247; LentiViral\_Tat.  
DR Pfam; PF02998; LentiViral\_Tat; I.  
FT NON\_TER 1  
SQ SEQUENCE 12 AA; 1266 MW; 5A60BBB1B8644EB7 CRC64;

Query Match 21.1%; Score 24; DB 2; Length 12;  
Best Local Similarity 71.4%; Pred. No. 1.1e+04;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 GSRLGNP 12  
DB 2 GCRLCNP 8

RESULT 77  
012080 CAEV  
ID 012080\_CAEV PRELIMINARY; PRT; 12 AA.

AC 012080;  
DT 01-JUL-1997 (TRENBLREL. 04, Created)  
DT 01-JUL-1997 (TRENBLREL. 04, Last sequence update)  
DT 01-JUN-2003 (TRENBLREL. 24, Last annotation update)  
DE Tat protein (Fragment).  
GN Name-tat;  
OS Caprine arthritis encephalitis virus (CAEV).  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus;  
OC Ovine/caprine lentivirus.  
OX NCBI\_Taxid=11660;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;  
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.  
DR EMBL; U81431; AAB60816.1; -; Genomic RNA.  
DR GO; GO:0016563; F:transcriptional activator activity; IEA.  
DR GO; GO:0045941; P:positive regulation of transcription; IEA.  
DR InterPro; IPR004247; LentiViral\_Tat.  
DR Pfam; PF02998; LentiViral\_Tat; I.  
FT NON\_TER 1  
SQ SEQUENCE 12 AA; 1266 MW; 5A60BBB1B8644EB7 CRC64;

Query Match 21.1%; Score 24; DB 2; Length 12;  
Best Local Similarity 71.4%; Pred. No. 1.1e+04;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 GSRLGNP 12  
DB 2 GCRLCNP 8

RESULT 78  
012082 CAEV

ID 012082\_CAEV PRELIMINARY; PRT; 12 AA.  
AC 012082;  
DT 01-JUL-1997 (TrEMBLrel. 04, Created)  
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)  
DE 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Tat protein (Fragment).  
GN Name=tac;  
OS Caprine arthritis encephalitis virus (CAEV).  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus;  
OC Ovine/caprine lentivirus.  
OX NCBI\_TaxID=11660;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Turelli P., Guiguen P., Mornex J.-F., Vigne R., Querat G.;  
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.  
DR EMBL; U81432; AAB60818.1; -, Genomic RNA.  
DR GO; GO:0016563; P:transcriptional activator activity; IEA.  
DR GO; GO:0045941; P:positive regulation of transcription; IEA.  
DR InterPro; IPR004247; Lenticviral Tat.  
DR Pfam; PF02998; Lenticviral\_Tat; I.  
FT NON TER 1  
SQ SEQUENCE 12 AA; 1266 MW; 5A60BB1B8644EB7 CRC64;  
  
Query Match 21.1%; Score 24; DB 2; Length 12;  
Best Local Similarity 71.4%; Pred. No. 1.1e+04;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 6 GSRLGNP 12  
DB 2 GCRLCNP 8  
  
RESULT 79  
ID 012084\_CAEV PRELIMINARY; PRT; 12 AA.  
AC 012084;  
DT 01-JUL-1997 (TrEMBLrel. 04, Created)  
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)  
DE 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Tat protein (Fragment).  
GN Name=tac;  
OS Caprine arthritis encephalitis virus (CAEV).  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus;  
OC Ovine/caprine lentivirus.  
OX NCBI\_TaxID=11660;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Turelli P., Guiguen P., Mornex J.-F., Vigne R., Querat G.;  
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.  
DR EMBL; U81433; AAB60820.1; -, Genomic RNA.  
DR GO; GO:0016563; P:transcriptional activator activity; IEA.  
DR GO; GO:0045941; P:positive regulation of transcription; IEA.  
DR InterPro; IPR004247; Lenticviral Tat.  
DR Pfam; PF02998; Lenticviral\_Tat; I.  
FT NON TER 1  
SQ SEQUENCE 12 AA; 1266 MW; 5A60BB1B8644EB7 CRC64;  
  
Query Match 21.1%; Score 24; DB 2; Length 12;  
Best Local Similarity 71.4%; Pred. No. 1.1e+04;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 6 GSRLGNP 12  
DB 2 GCRLCNP 8  
  
RESULT 80  
ID 012086\_CAEV PRELIMINARY; PRT; 12 AA.  
AC 012086;  
DT 01-JUL-1997 (TrEMBLrel. 04, Created)  
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)  
DE 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE Tat protein (Fragment).  
GN Name=tac;  
OS Caprine arthritis encephalitis virus (CAEV).  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus;  
OC Ovine/caprine lentivirus.  
OX NCBI\_TaxID=11660;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Turelli P., Guiguen P., Mornex J.-F., Vigne R., Querat G.;  
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.  
DR EMBL; U81434; AAB60822.1; -, Genomic RNA.  
DR GO; GO:0016563; P:transcriptional activator activity; IEA.  
DR GO; GO:0045941; P:positive regulation of transcription; IEA.  
DR InterPro; IPR004247; Lenticviral Tat.  
DR Pfam; PF02998; Lenticviral\_Tat; I.  
FT NON TER 1  
SQ SEQUENCE 12 AA; 1266 MW; 5A60BB1B8644EB7 CRC64;  
  
Query Match 21.1%; Score 24; DB 2; Length 12;  
Best Local Similarity 71.4%; Pred. No. 1.1e+04;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 6 GSRLGNP 12  
DB 2 GCRLCNP 8  
  
RESULT 81  
ID 012088\_CAEV PRELIMINARY; PRT; 12 AA.  
AC 012088;  
DT 01-JUL-1997 (TrEMBLrel. 04, Created)  
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Tat protein (Fragment).  
GN Name=tac;  
OS Caprine arthritis encephalitis virus (CAEV).  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus;  
OC Ovine/caprine lentivirus.  
OX NCBI\_TaxID=11660;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Turelli P., Guiguen P., Mornex J.-F., Vigne R., Querat G.;  
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.  
DR EMBL; U81435; AAB60824.1; -, Genomic RNA.  
FT NON TER 1  
SQ SEQUENCE 12 AA; 1279 MW; 4B90BB1B8644EB7 CRC64;  
  
Query Match 21.1%; Score 24; DB 2; Length 12;  
Best Local Similarity 71.4%; Pred. No. 1.1e+04;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 6 GSRLGNP 12  
DB 2 GCRLCNP 8  
  
RESULT 82  
ID 012090\_CAEV PRELIMINARY; PRT; 12 AA.  
AC 012090;  
DT 01-JUL-1997 (TrEMBLrel. 04, Created)  
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Tat protein (Fragment).  
GN Name=tac;  
OS Caprine arthritis encephalitis virus (CAEV).  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus;  
OC Ovine/caprine lentivirus.  
OX NCBI\_TaxID=11660;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Turelli P., Guiguen P., Mornex J.-F., Vigne R., Querat G.;

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RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U81436; AAB60826.1; -; Genomic RNA.
DR GO; GO:0016563; F:transcriptional activator activity; IEA.
DR GO; GO:0045941; P:positive regulation of transcription; IEA.
DR InterPro; IPR004247; Lentiviral_Tat.
DR Pfam; PF02998; Lentiviral_Tat; 1.
FT NON_TER 1
SQ SEQUENCE 12 AA; 1266 MW; 5A60BB1B8644EB7 CRC64;

Query Match 21.1%; Score 24; DB 2; Length 12;
Best Local Similarity 71.4%; Pred. No. 1.1e+04;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 GSRLGNP 12
DB 2 GCRLCNP 8

RESULT 83
ID 012092_CAEV PRELIMINARY; PRT; 12 AA.
AC 012092;
DT 01-JUL-1997 (TREMBLrel. 04, Created)
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Tat protein (Fragment).
GN Name=tat;
OS Caprine arthritis encephalitis virus (CAEV).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus;
OC Ovine/caprine lentivirus.
OX NCB1_TaxId=11660;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U81437; AAB60828.1; -; Genomic RNA.
DR GO; GO:0016563; F:transcriptional activator activity; IEA.
DR GO; GO:0045941; P:positive regulation of transcription; IEA.
DR InterPro; IPR004247; Lentiviral_Tat.
DR Pfam; PF02998; Lentiviral_Tat; 1.
FT NON_TER 1
SQ SEQUENCE 12 AA; 1266 MW; 5A60BB1B8644EB7 CRC64;

Query Match 21.1%; Score 24; DB 2; Length 12;
Best Local Similarity 71.4%; Pred. No. 1.1e+04;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 GSRLGNP 12
DB 2 GCRLCNP 8

RESULT 84
ID 012094_CAEV PRELIMINARY; PRT; 12 AA.
AC 012094;
DT 01-JUL-1997 (TREMBLrel. 04, Created)
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Tat protein (Fragment).
GN Name=tat;
OS Caprine arthritis encephalitis virus (CAEV).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus;
OC Ovine/caprine lentivirus.
OX NCB1_TaxId=11660;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U81438; AAB60830.1; -; Genomic RNA.
DR GO; GO:0016563; F:transcriptional activator activity; IEA.
DR GO; GO:0045941; P:positive regulation of transcription; IEA.
DR InterPro; IPR004247; Lentiviral_Tat.

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DR Pfam; PF02998; Lentiviral_Tat; 1.
FT NON_TER 1
SQ SEQUENCE 12 AA; 1266 MW; 5A60BB1B8644EB7 CRC64;

Query Match 21.1%; Score 24; DB 2; Length 12;
Best Local Similarity 71.4%; Pred. No. 1.1e+04;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 GSRLGNP 12
DB 2 GCRLCNP 8

RESULT 85
ID 012106_CAEV PRELIMINARY; PRT; 12 AA.
AC 012106;
DT 01-JUL-1997 (TREMBLrel. 04, Created)
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Tat protein (Fragment).
GN Name=tat;
OS Caprine arthritis encephalitis virus (CAEV).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus;
OC Ovine/caprine lentivirus.
OX NCB1_TaxId=11660;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U81444; AAB60842.1; -; Genomic RNA.
DR GO; GO:0016563; F:transcriptional activator activity; IEA.
DR GO; GO:0045941; P:positive regulation of transcription; IEA.
DR InterPro; IPR004247; Lentiviral_Tat.
DR Pfam; PF02998; Lentiviral_Tat; 1.
FT NON_TER 1
SQ SEQUENCE 12 AA; 1266 MW; 5A60BB1B8644EB7 CRC64;

Query Match 21.1%; Score 24; DB 2; Length 12;
Best Local Similarity 71.4%; Pred. No. 1.1e+04;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 GSRLGNP 12
DB 2 GCRLCNP 8

RESULT 86
ID 012108_CAEV PRELIMINARY; PRT; 12 AA.
AC 012108;
DT 01-JUL-1997 (TREMBLrel. 04, Created)
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Tat protein (Fragment).
GN Name=tat;
OS Caprine arthritis encephalitis virus (CAEV).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus;
OC Ovine/caprine lentivirus.
OX NCB1_TaxId=11660;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U81445; AAB60844.1; -; Genomic RNA.
DR GO; GO:0016563; F:transcriptional activator activity; IEA.
DR GO; GO:0045941; P:positive regulation of transcription; IEA.
DR InterPro; IPR004247; Lentiviral_Tat.
DR Pfam; PF02998; Lentiviral_Tat; 1.
FT NON_TER 1
SQ SEQUENCE 12 AA; 1266 MW; 5A60BB1B8644EB7 CRC64;

Query Match 21.1%; Score 24; DB 2; Length 12;

```

Best Local Similarity 71.4%; Pred. No. 1.1e+04;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 GSRLGNP 12  
DB 2 GCRLCNP 8

RESULT 87  
012110\_CAEV  
ID 012110\_CAEV PRELIMINARY; PRT; 12 AA.  
AC 012110;  
DT 01-JUL-1997 (T-EMBLrel. 04, Created)  
DT 01-JUL-1997 (T-EMBLrel. 04, Last sequence update)  
DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)  
DE Tat protein (Fragment).  
GN Name=tac;  
OS Caprine arthritis encephalitis virus (CAEV).  
OC Viruses; Retroviridae; Lentivirus;  
OC Ovine/caprine lentivirus.  
OX NCBI\_TaxID=11660;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;  
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.  
DR EMBL; U81446; AAB60846.1; -; Genomic RNA.  
DR GO; GO:0016563; P:transcriptional activator activity; IEA.  
DR GO; GO:0045941; P:positive regulation of transcription; IEA.  
DR InterPro; IPR004247; Lentiviral\_Tat.  
DR Pfam; PF02998; Lentiviral\_Tat; I.  
PT NON\_TER  
SQ SEQUENCE 12 AA; 1266 MW; 5A60BBB1B8644EB7 CRC64;

Query Match 21.1%; Score 24; DB 2; Length 12;  
Best Local Similarity 71.4%; Pred. No. 1.1e+04;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 GSRLGNP 12  
DB 2 GCRLCNP 8

RESULT 88  
012112\_CAEV  
ID 012112\_CAEV PRELIMINARY; PRT; 12 AA.  
AC 012112;  
DT 01-JUL-1997 (T-EMBLrel. 04, Created)  
DT 01-JUL-1997 (T-EMBLrel. 04, Last sequence update)  
DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)  
DE Tat protein (Fragment).  
GN Name=tac;  
OS Caprine arthritis encephalitis virus (CAEV).  
OC Viruses; Retroviridae; Lentivirus;  
OC Ovine/caprine lentivirus.  
OX NCBI\_TaxID=11660;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;  
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.  
DR EMBL; U81447; AAB60848.1; -; Genomic RNA.  
DR GO; GO:0016563; P:transcriptional activator activity; IEA.  
DR GO; GO:0045941; P:positive regulation of transcription; IEA.  
DR InterPro; IPR004247; Lentiviral\_Tat.  
DR Pfam; PF02998; Lentiviral\_Tat; I.  
PT NON\_TER  
SQ SEQUENCE 12 AA; 1266 MW; 5A60BBB1B8644EB7 CRC64;

Query Match 21.1%; Score 24; DB 2; Length 12;  
Best Local Similarity 71.4%; Pred. No. 1.1e+04;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 GSRLGNP 12  
DB 2 GCRLCNP 8

DB 2 GCRLCNP 8

RESULT 89  
012114\_CAEV  
ID 012114\_CAEV PRELIMINARY; PRT; 12 AA.  
AC 012114;  
DT 01-JUL-1997 (T-EMBLrel. 04, Created)  
DT 01-JUL-1997 (T-EMBLrel. 04, Last sequence update)  
DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)  
DE Tat protein (Fragment).  
GN Name=tac;  
OS Caprine arthritis encephalitis virus (CAEV).  
OC Viruses; Retroviridae; Lentivirus;  
OC Ovine/caprine lentivirus.  
OX NCBI\_TaxID=11660;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;  
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.  
DR EMBL; U81448; AAB60850.1; -; Genomic RNA.  
DR GO; GO:0016563; P:transcriptional activator activity; IEA.  
DR GO; GO:0045941; P:positive regulation of transcription; IEA.  
DR InterPro; IPR004247; Lentiviral\_Tat.  
DR Pfam; PF02998; Lentiviral\_Tat; I.  
PT NON\_TER  
SQ SEQUENCE 12 AA; 1266 MW; 5A60BBB1B8644EB7 CRC64;

Query Match 21.1%; Score 24; DB 2; Length 12;  
Best Local Similarity 71.4%; Pred. No. 1.1e+04;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 GSRLGNP 12  
DB 2 GCRLCNP 8

RESULT 90  
012116\_CAEV  
ID 012116\_CAEV PRELIMINARY; PRT; 12 AA.  
AC 012116;  
DT 01-JUL-1997 (T-EMBLrel. 04, Created)  
DT 01-JUL-1997 (T-EMBLrel. 04, Last sequence update)  
DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)  
DE Tat protein (Fragment).  
GN Name=tac;  
OS Caprine arthritis encephalitis virus (CAEV).  
OC Viruses; Retroviridae; Lentivirus;  
OC Ovine/caprine lentivirus.  
OX NCBI\_TaxID=11660;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;  
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.  
DR EMBL; U81449; AAB60852.1; -; Genomic RNA.  
DR GO; GO:0016563; P:transcriptional activator activity; IEA.  
DR GO; GO:0045941; P:positive regulation of transcription; IEA.  
DR InterPro; IPR004247; Lentiviral\_Tat.  
DR Pfam; PF02998; Lentiviral\_Tat; I.  
PT NON\_TER  
SQ SEQUENCE 12 AA; 1266 MW; 5A60BBB1B8644EB7 CRC64;

Query Match 21.1%; Score 24; DB 2; Length 12;  
Best Local Similarity 71.4%; Pred. No. 1.1e+04;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 GSRLGNP 12  
DB 2 GCRLCNP 8

RESULT 91  
012118\_CAEV

ID 012118 CAEV PRELIMINARY; PRT; 12 AA.  
 AC 012118;  
 DT 01-JUL-1997 (T-EMBLrel. 04, Created)  
 DT 01-JUL-1997 (T-EMBLrel. 04, Last sequence update)  
 DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)  
 DE Tat protein (Fragment).  
 GN NameTat;  
 OS Caprine arthritis encephalitis virus (CAEV).  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus;  
 OC Ovine/caprine lentivirus.  
 OC NCBI\_TaxID=11660;  
 RX [1]  
 RN NUCLEOTIDE SEQUENCE.  
 RA Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;  
 RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.  
 DR EMBL, U01450; AAB60854.1; -, Genomic RNA.  
 DR GO; GO:0016563; F:transcriptional activator activity; IEA.  
 DR GO; GO:0045941; P:positive regulation of transcription; IEA.  
 DR InterPro; IPR004247; Lentiviral Tat.  
 DR Pfam; PF02998; Lentiviral\_Tat; 1.  
 FT NON TER 1 1  
 SQ SEQUENCE 12 AA; 1266 MW; 5A60BBB1E8644EB7 CRC64;  
 Query Match 21.1%; Score 24; DB 2; Length 12;  
 Best Local Similarity 71.4%; Pred. No. 1.1e+04;  
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 GSRLGNP 12  
 Db 2 GCRLGNP 8  
 RESULT 92  
 Q9UDC6 HUMAN PRELIMINARY; PRT; 13 AA.  
 AC Q9UDC6;  
 DT 01-MAY-2000 (T-EMBLrel. 13, Created)  
 DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)  
 DT 01-JUN-2002 (T-EMBLrel. 21, Last annotation update)  
 DE ENDOTHELIN-derived RELATING factor, nitric oxide synthase  
 (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;  
 OC Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=93054573; PubMed=1385404;  
 RA Janssens S.P., Simouchi A., Quettermous T., Bloch D.B., Bloch K.D.;  
 RT "Cloning and expression of a cDNA encoding human endothelium-derived  
 RT relating factor/nitric oxide synthase.";  
 RL J. Biol. Chem. 267:22694-22694(1992).  
 FT NON TER 1 1  
 SQ SEQUENCE 13 AA; 1390 MW; 3231B6DFEC7EB867 CRC64;  
 Query Match 21.1%; Score 24; DB 2; Length 13;  
 Best Local Similarity 36.4%; Pred. No. 1.1e+04;  
 Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 YEYFGSLGNP 12  
 Db 3 FDEPGSDTNSP 13  
 RESULT 93  
 O6LAI1 DROME PRELIMINARY; PRT; 15 AA.  
 AC O6LAI1;  
 DT 05-JUL-2004 (T-EMBLrel. 27, Created)  
 DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)  
 DT 10-MAY-2005 (T-EMBLrel. 30, Last annotation update)

DE Andropin (Fragment).  
 GN Name=And;  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OC NCBI\_TaxID=7227;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=Montemayor.  
 RX MEDLINE=98393576; PubMed=9725836;  
 RA Ramos-Onsins S., Aguade M.;  
 RT "Molecular evolution of the Ceeropin multigene family in Drosophila:  
 RT functional genes vs pseudogenes.";  
 RL Genetics 150:157-171(1998).  
 DR EMBL, Y16853; CAA76430.1; -, Genomic DNA.  
 DR EMBL, Y16854; CAA76436.1; -, Genomic DNA.  
 DR EMBL, Y16855; CAA76442.1; -, Genomic DNA.  
 DR EMBL, Y16856; CAA76448.1; -, Genomic DNA.  
 DR EMBL, Y16857; CAA76454.1; -, Genomic DNA.  
 DR EMBL, Y16858; CAA76460.1; -, Genomic DNA.  
 DR EMBL, Y16859; CAA76466.1; -, Genomic DNA.  
 DR EMBL, Y16861; CAA76476.1; -, Genomic DNA.  
 DR EMBL, Y16852; CAA76424.1; -, Genomic DNA.  
 FT NON TER 1 1  
 SQ SEQUENCE 15 AA; 1659 MW; C86F9313DEE24182 CRC64;  
 Query Match 21.1%; Score 24; DB 2; Length 15;  
 Best Local Similarity 55.6%; Pred. No. 1.3e+04;  
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 5 PGSRLGNPK 13  
 Db 7 PPKRLINPK 15  
 RESULT 94  
 O9NP07 HUMAN PRELIMINARY; PRT; 16 AA.  
 AC O9NP07;  
 DT 01-OCT-2000 (T-EMBLrel. 15, Created)  
 DT 01-OCT-2000 (T-EMBLrel. 15, Last sequence update)  
 DT 01-DEC-2001 (T-EMBLrel. 19, Last annotation update)  
 DE Hypothetical protein (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;  
 OC Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Aulfray C., Amborge W., Ballabio A., Estivill X., Gibson K.,  
 RA Lehnach H., Pousetka A., Lundeberg U.;  
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Pivtinec R., Estivill X., Escarceller M., Sumoy L.;  
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL, AL389982; CAB97537.1; -, mRNA.  
 KW Hypothetical protein.  
 FT NON TER 1 1  
 SQ SEQUENCE 16 AA; 1484 MW; 97C92837C881A371 CRC64;  
 Query Match 21.1%; Score 24; DB 2; Length 16;  
 Best Local Similarity 66.7%; Pred. No. 1.4e+04;  
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 10 GNPXAP 15  
 Db 2 GQPSAP 7  
 RESULT 95

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Q4TZV7_PAPHA
ID Q4TZV7_PAPHA PRELIMINARY; PRT; 18 AA.
AC Q4TZV7;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Ubiquitous TPR-motif protein Y isoform (Fragment).
GN Name=UTY;
OS Papio hamadryas (Hamadryas baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Cercopithecoidea; Cercopithecinae; Papio.
OX NCBI_TaxID=9557;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Lawson Handley L.J., Hammond R.L., Emarest G., Reber A., Perrin N.;
RT "Low Y chromosome polymorphism in Saudi-Arabian hamadryas baboons
(Papio hamadryas hamadryas)".
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; DQ023315; AAY58227.1; -; Genomic_DNA.
FT NON_TER 1
FT NON_TER 18
SQ SEQUENCE 18 AA; 1861 MW; BAE4844395B69B86 CRC64;

Query Match 21.1%; Score 24; DB 2; Length 18;
Best Local Similarity 66.7%; Pred. No. 1.6e+04;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 11 NPXAPL 16
Db 1 NPKNPV 6

RESULT 96
Q507E3_RAT
ID Q507E3_RAT PRELIMINARY; PRT; 18 AA.
AC Q507E3;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Proto-oncogene c-fos (Fragment).
GN Name=c-Fos;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA STRAIN=Mistar; TISSUE=Liver;
RA Weller E.;
RT "c-fos expression in visual cortex".
RL Submitted (OCT-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY786174; AAY41063.1; -; Genomic_DNA.
FT NON_TER 18
FT NON_TER 18
SQ SEQUENCE 18 AA; 1990 MW; A378217C052C6052 CRC64;

Query Match 21.1%; Score 24; DB 2; Length 18;
Best Local Similarity 62.5%; Pred. No. 1.6e+04;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 DVEYPSR 8
Db 9 DVEASSR 16

RESULT 97
HBH2_UROHA
ID HBH2_UROHA STANDARD; PRT; 19 AA.
AC P18952;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)

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DE Hemoglobin beta-2 chain (Fragment).
OS Uromastix hardwickii (Indian spiny-tailed lizard).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodactylidae; Squamata; Iguania; Acrodonta; Agamidae; Uromastixinae;
OC Uromastix.
OX NCBI_TaxID=40250;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=84029159; Pubmed=6628672; DOI=10.1016/0014-5793(83)80774-1;
RA Naqvi S., Zaidi Z.H., von Bahr-Lindstrom H., Carlquist M.,
RA Joernvall H.;
RT "Characterization of hemoglobin from the lizard Uromastix
hardwickii".
RL FEBS Lett. 162:290-295(1983).
CC -1- FUNCTION: Involved in oxygen transport from the lung to the
CC various peripheral tissues.
CC -1- SUBUNIT: Heterotetramer of two alpha chains and two beta chains.
CC -1- TISSUE SPECIFICITY: Red blood cells.
CC -1- SIMILARITY: Belongs to the globin family.
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CC This Swiss-Prot entry is copyright. It is produced through a collaboration
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CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
-----
CC PIR; A05305; A05305.
DR InterPro; IPR000971; Globin.
DR PROSITE; PS01033; GLOBIN; PARTIAL.
KW Direct protein sequencing; Erythrocyte; Heme; Iron; Metal-binding;
KW Oxygen transport; Transport.
FT NON_TER 1
FT NON_TER 19
SQ SEQUENCE 19 AA; 1914 MW; C40AD8EA30019057 CRC64;

Query Match 21.1%; Score 24; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.7e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GNPX 13
Db 16 GNPX 19

RESULT 98
Q8WTX6_HUMAN
ID Q8WTX6_HUMAN PRELIMINARY; PRT; 19 AA.
AC Q8WTX6;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hypothetical protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA TISSUE=Eye.
RX MEDLINE=22386257; Pubmed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marnusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.U., Ueda T.B., Yoshizuki S., Carninci P., Frange C.,
RA Raha S.S., Loquellano N.A., Petersen R.D., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Villalon D.K., Murray D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketterman M., Madan A., Rodrigues S., Sanchez A.,

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RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield V.S.N., Krzywicki M.I., Skalska U., Smalins D.E.,  
 RA Scherch A., Schen J.E., Jones S.J.M., Maira M.A.,  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAUSBERG R.;  
 RA Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC021928; AA021928.1; -; mRNA.  
 KW Hypothetical protein.  
 FT NON TER 1  
 SQ SEQUENCE 19 AA; 2251 MW; AE463E57E7A8702 CRC64;  
 Query Match 21.1%; Score 24; DB 2; Length 19;  
 Best Local Similarity 60.0%; Pred. No. 1.7e+04;  
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYKFP 5  
 DB 7 DYKFP 11  
 RESULT 99  
 Q51K80 MAGGR PRELIMINARY; PRT; 20 AA.  
 ID Q51K80 MAGGR PRELIMINARY;  
 AC Q51K80;  
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
 DE Predicted protein.  
 OS ORFNames=MG09625.4;  
 GN Magnaporthe grisea 70-15.  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 OC Sordariomycetes; Incertae sedis; Magnaporthaceae; Magnaporthe.  
 OX NCBI\_TaxID=242507;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=70-15;  
 RA Birren B., Nussbaum C., Abebe A., Aboueleil A., Adekoya E.,  
 RA Altshuler M., Allen N., Allen T., An P., Anderson M., Anderson S.,  
 RA Arachchi H., Ambrose J., Bachantang P., Baldwin J., Barry A.,  
 RA Bayl T., Bitcharsen B., Bloom T., Bye J., Boguslavsky L.,  
 RA Borowsky M., Boukhalter B., Brunache A., Butler J., Calixte N.,  
 RA Calvo S., Camarata J., Campo K., Chang J., Chesnatsang Y., Clifton M.,  
 RA Collymore A., Considine T., Cook A., Cooke P., Corum B., Cuomo C.,  
 RA David R., Dawoe T., Degray S., Dodge S., Dooley K., Dorje P.,  
 RA Dorjee K., Dorris L., Duffey N., Dupes A., Elkins T., Engels R.,  
 RA Erickson J., Farina K., Fato S., Ferreira P., Fischer H.,  
 RA Fitzgerald M., Foley K., Gage D., Galegan J., Garin G., Gnerre S.,  
 RA Ghitke A., Goyette A., Graham J., Grandbois E., Gyaltsen K., Hafez N.,  
 RA Hagopian D., Hages B., Hall J., Hatcher B., Heller A., Higgins H.,  
 RA Honan T., Horn A., Houde N., Hughes L., Hulme W., Husby E., Iliev I.,  
 RA Jaffe D., Jones C., Kamal M., Kamat A., Kamysseles M., Karlsson B.,  
 RA Kelle C., Kieu A., Kiser P., Kodira C., Kulbokas E., Labucci K.,  
 RA Lama D., Landers T., Leger J., Levine S., Lewis D., Lewis T.,  
 RA Lindblad-toh K., Liu X., Lokytang T., Lokytang Y., Lucien O.,  
 RA Lui A., Ma L.J., Mabbitt R., MacDonald J., Maclean C., Major J.,  
 RA Manning J., Maraballa R., Maru K., Matthews C., Mancelli B.,  
 RA McCarthy M., McDonough S., Mcghee T., Meldrum J., Menes L.,  
 RA Mesirov J., Mihalov A., Mihova T., Mikkelson T., Mienga V., Moru K.,  
 RA Mozer J., Mulrain L., Munson G., Mykiet J., News C., Nguyen C.,  
 RA Nguyen N., Nguyen T., Nicol R., Nielsen C., Nizzari M., Norbu C.,  
 RA Norbu N., O'donnell P., Okoawo O., O'leary S., Omotosho B.,  
 RA O'Neill K., Omen S., Parker S., Perrin D., Phunkhang P., Pigan B.,  
 RA Purcell S., Rachupka T., Ramasamy U., Rameau R., Ray V., Raymond C.,  
 RA Recta R., Richardson S., Rice C., Rodriguez J., Rogers J., Rogov P.,  
 RA Rutman M., Schupbach R., Seaman C., Settipalli S., Sharpe T.,  
 RA Sheridan J., Sherpa N., Shi J., Smirnov S., Smith C., Sounguez C.,

RA Spencer B., Stalker J., Stange-thomann N., Stavropoulos S.,  
 RA Stenson K., Stone S., Stone S., Scrubs M., Talmas J., Tchuinga P.,  
 RA Tensing P., Tsefaye S., Theodore J., Thoulisang Y., Topham K.,  
 RA Towey S., Tsamla T., Tsomo N., Vallee D., Vassiliev H.,  
 RA Venkataraman V., Vinson J., Vo A., Wade C., Wang S., Wangchuk T.,  
 RA Wangdi T., Whitaker C., Wilkinson J., Wu Y., Wyman D., Yadav S.,  
 RA Yang S., Yang X., Yeager S., Yee E., Young G., Zainoun J., Zembeck L.,  
 RA Zimmer A., Zody M., Zander E.;  
 RT "The genome sequence of Magnaporthe grisea.";  
 RT Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=70-15;  
 RA Dean R., Mitchell T., Brown D., Pan H., Thon M.;  
 RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=70-15;  
 RA Zhu H., Blackmon B.;  
 RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.  
 CC -1- CAUTION: The sequence shown here is derived from an  
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
 CC preliminary data.  
 DR EMBL; AACU0101666; EAA48088.1; -; Genomic DNA.  
 SQ SEQUENCE 20 AA; 2251 MW; CFS8A2FEF8B2226C4 CRC64;

QY 13 KAPLYKRP 20  
 DB 8 QAGIKRP 15  
 Query Match 21.1%; Score 24; DB 2; Length 20;  
 Best Local Similarity 50.0%; Pred. No. 1.8e+04;  
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

RESULT 100  
 Q9T2Q9 SOLTU PRELIMINARY; PRT; 20 AA.  
 ID Q9T2Q9 SOLTU PRELIMINARY;  
 AC Q9T2Q9;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Cytochrome-C reductase 14 kDa subunit (EC 1.10.2.2) (Fragment).  
 OS Solanum tuberosum (potato).  
 OC Mitochondrion.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
 OC asterids; lamiales; Solanales; Solanaceae; Solanum.  
 OX NCBI\_TaxID=4113;  
 RN [1]  
 RP PROTEIN SEQUENCE.  
 RX MEDLINE=94198758; PubMed=7764624; DOI=10.1007/BF00191612;  
 RA Braun H.-P., Kruit V., Schmitz U.K.;  
 RT "Molecular identification of the ten subunits of cytochrome-c  
 RT reductase from potato mitochondria.";  
 RL Planta 193:99-106(1994).  
 DR GO; GO:0008121; F:ubiquinol-cytochrome-c reductase activity; IEA.  
 SQ SEQUENCE 20 AA; 2302 MW; 3565E32D111F826 CRC64;

QY 15 PLYKR 19  
 DB 14 PLYKR 18  
 Query Match 21.1%; Score 24; DB 2; Length 20;  
 Best Local Similarity 80.0%; Pred. No. 1.8e+04;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Search completed: January 20, 2006, 19:11:04  
 JDB time : 69.5385 secs



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OM protein - protein search, using sw model

Run on: January 20, 2006, 18:54:14 ; Search time 75.5769 Seconds  
(without alignments)  
116.273 Million cell updates/sec

Title: US-09-662-293-3

Perfect score: 115  
Sequence: 1 DIPHTNIMKYLVCESVNGG 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 244163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 680474

Minimum DB seq length: 0  
Maximum DB seq length: 20

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

A\_Geneseq\_21: \*  
1: geneseq219808: \*  
2: geneseq219908: \*  
3: geneseq220008: \*  
4: geneseq220018: \*  
5: geneseq220028: \*  
6: geneseq220038: \*  
7: geneseq220048: \*  
8: geneseq220058: \*  
9: geneseq220068: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	115	100.0	20	3	AAV52512 House dus
2	115	100.0	20	5	AAU96316 Der HMW-m
3	109	94.8	19	3	AAV52520 House dus
4	109	94.8	19	5	AAU96324 Der HMW-m
5	37.5	32.6	20	4	AAAM18898 Peptide #
6	37.5	32.6	20	4	ABR38020 Peptide #
7	37.5	32.6	20	4	AAAM1434 Peptide #
8	37.5	32.6	20	4	ABR32254 Protein #
9	37.5	32.6	20	4	AAAM1153 Human bra
10	37.5	32.6	20	4	AAAM58647 Human bra
11	37.5	32.6	20	4	ABG52865 Human liv
12	37.5	32.6	20	5	ABG40950 Human pep
13	35	30.4	7	9	ADC27861 Synthetic
14	35	30.4	7	9	ADY56230 Carotenol
15	35	30.4	10	9	ABG6055 H3 or D3-
16	35	30.4	10	9	ABG6029 Tumour-ase
17	35	30.4	15	2	AAW30771 Prostate
18	35	30.4	15	2	AAW58054 Human pro
19	35	30.4	15	2	AAW58055 Human pro
20	35	30.4	15	7	ADM37502 HLA bindi
21	35	30.4	15	7	ADM35209 HLA bindi
22	35	30.4	15	7	ADM33268 HLA bindi
23	35	30.4	15	7	ADM33976 HLA bindi
24	35	30.4	15	8	ADN65435 HLA bindi

25	35	30.4	19	2	AAW30783 Prostate
26	35	30.4	20	2	AAV31158 Human PSA
27	35	30.4	20	4	AAV71939 Ubiquitin
28	34.5	30.0	15	7	ADP70892 Human 161
29	34.5	30.0	15	7	ADP70440 Human 161
30	34	29.6	12	8	ADN08675 Corton wi
31	33	28.7	10	6	ABR47248 Scaphyloc
32	33	28.7	10	9	ADY92058 Human tum
33	33	28.7	20	9	ADX70566 Vaccinia
34	32	27.8	10	2	AAV38258 HIV-deriv
35	32	27.8	10	2	AAV45830 Immunogen
36	32	27.8	10	4	ABP14809 HIV AD3 s
37	32	27.8	10	5	ABJ15141 Immunogen
38	32	27.8	10	5	ABJ15176 Immunogen
39	32	27.8	10	6	ABU70353 Human imm
40	32	27.8	10	6	ABU69777 Human imm
41	32	27.8	10	6	ABU69799 Human imm
42	32	27.8	10	6	ABU69801 Human imm
43	32	27.8	10	6	ABU69729 Human imm
44	32	27.8	10	7	ADD96334 HIV-1 cro
45	32	27.8	10	7	ADD96886 HIV-1 cro
46	32	27.8	10	7	ADD96262 HIV-1 cro
47	32	27.8	10	7	ADD96332 HIV-1 cro
48	32	27.8	10	7	ADD96310 HIV-1 cro
49	32	27.8	14	6	ABG75542 Human spe
50	32	27.8	14	7	ADP53446 KPCPC 603
51	32	27.8	14	8	ADT1277 hSARS vir
52	32	27.8	14	8	ADP80692 SARS viru
53	32	27.8	14	8	ADT38807 hSARS vir
54	32	27.8	15	2	AAW5207 Helper T-
55	32	27.8	15	4	ABP24655 HIV DR su
56	32	27.8	15	7	ADN14050 HIV helpe
57	32	27.8	15	7	ADM36336 HLA bindi
58	32	27.8	15	9	ADV22436 HIV-1 Pol
59	32	27.8	15	9	ADV22435 HIV-1 Pol
60	32	27.8	17	8	ADT24615 HIV-1 HLA
61	32	27.8	20	7	ADC69725 Cotton fl
62	31	27.0	8	2	AAW79123 Peptide o
63	31	27.0	12	1	AAV50408 Human leu
64	31	27.0	12	8	ADQ15533 Targeting
65	31	27.0	13	1	AAV40114 Sequence
66	31	27.0	15	5	ABG61667 Human HGP
67	31	27.0	15	9	ADV21780 SIV pol p
68	31	27.0	15	9	ADV21781 SIV pol p
69	31	27.0	16	3	AAV90148 Ligand ep
70	31	27.0	17	2	AAV65652 uPAR-bind
71	31	27.0	17	2	AAV6550 Antagonis
72	31	27.0	17	2	AAV76568 Clone 20
73	31	27.0	17	2	AAV76564 Clone 20
74	31	27.0	17	3	AAV79011 Droxinase
75	31	27.0	17	3	AAV7140 UXR antag
76	31	27.0	17	3	AAV90149 Ligand ep
77	31	27.0	17	4	AAV74578 Context-d
78	31	27.0	17	5	ABR73284 UXR antag
79	31	27.0	17	7	ADG25913 INPIONCHO
80	31	27.0	17	7	ADJ73438 Somatosta
81	31	27.0	17	8	ADJ52033 CHI delet
82	31	27.0	17	8	ADJ52032 CHI delet
83	31	27.0	18	4	ABR39967 Peptide #
84	31	27.0	18	4	AAW33587 Peptide #
85	31	27.0	18	4	AAW73385 Human bon
86	31	27.0	18	4	AAW60712 Human bon
87	31	27.0	18	4	ABG55102 Human liv
88	31	27.0	18	5	ABG43339 Human pep
89	31	27.0	19	9	ADV53056 Hedgehog
90	31	27.0	19	9	ADV52657 Hedgehog
91	31	27.0	20	2	AAW85293 Helper T-
92	31	27.0	20	3	AAV90154 UPAR targ
93	30.5	26.5	14	2	AAW88603 Secreted
94	30.5	26.5	15	7	ADP70889 Human 161
95	30.5	26.5	15	7	ADP70286 Human 161
96	30.5	26.5	15	7	ADP70871 Human 161
97	30	26.1	8	8	ADP92805 Consensus

98	30	26.1	9	4	AAM22945	Aam22945 HIV pep1
99	30	26.1	9	4	AAM22902	Aam22902 HIV pep1
100	30	26.1	9	9	ADY92047	Ady92047 Human tum

## ALIGNMENTS

## RESULT 1

ID AAY52512 standard; peptide, 20 AA.

AC	AAY52512;	
DT	22-FEB-2000	(first entry)
DE	House dust mite allergen protein (map) A/B fragment map(2).	
XX		
XX	Mite allergen protein; map; high molecular weight; HMW-map; allergy;	
KW	house dust mite; IGE; immunoglobulin E; allergen; mapA; mapB;	
KM	hypersensitivity reaction; therapy; treatment; diagnosis; human; feline;	
KW	canine; veterinary; antibody; vaccine; immunisation.	
XX		
OS	Dermatophagoides farinae.	
XX		
PN	WO954349-A2.	
XX		
PD	28-OCT-1999.	
XX		
PF	16-APR-1999;	99WO-US008524.
XX		
PR	17-APR-1998;	98US-00062013.
XX		
PR	13-MAY-1998;	98US-0085295P.
XX		
PR	02-SEP-1998;	98US-0098909P.
XX		
PA	(HESK-) HESKA CORP.	
XX		
PI	Mccall CA, Hunter SW, Weber ER;	
XX		
DR	WPI; 2000-052700/04.	
XX		
PT	Novel high molecular weight Dermatophagoides nucleic acid polypeptides	
XX	used to modify an animals' hypersensitivity to mite allergens.	
PS	Claim 3; Page 69; 154pp; English.	

Sequences AAY52510-Y52522 represent proteolytic fragments of Dermatophagoides farinae high molecular weight mite allergen protein (HMW-map) composition. The HMW-map composition was isolated from a D. farinae homogenate by gel filtration, with each fraction being analysed for the presence of proteins that bound to IGE present in mite-allergic dog antiserum. The HMW-map composition comprises mapA (a 109 kD protein) and mapB (98 kD). Mite allergenic proteins and peptides, and nucleic acids encoding them, may be used in therapeutic compositions to modify an animal's hypersensitivity reaction to mite allergens. Animals that may be treated include mammals and birds, especially felines, canines, equines, humans, other pets, and work or domestic animals. The proteins or fragments may also be used to diagnose allergies via a skin test. The proteins and peptides can also be used to raise antibodies, which have a variety of potential uses. For example, they can be used as vaccines to passively immunise animals against dust mite hypersensitivity, as positive controls in test kits and as tools to recover desired dust mite allergens from a mixture of proteins

SQ Sequence 20 AA;

Query Match 100.0%; Score 115; DB 3; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1,1e-11;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	DIPHPNTNHHKYLVCESVNGG	20
DB	1	DIPHPNTNHHKYLVCESVNGG	20

## RESULT 2

ID AAU96316 standard; peptide, 20 AA.

AC	AAU96316;	
DT	15-JUL-2002	(first entry)
DE	Der HMW-map polypeptide #3.	
XX		
KW	Der HMW-map; American house dust mite; anti-allergic; mite; IGE;	
KM	mite allergenic protein; immunoglobulin E; hypersensitivity;	
KW	immunocomplex formation.	
XX		
OS	Dermatophagoides farinae.	
XX		
PN	WO200222807-A2.	
XX		
PD	21-MAR-2002.	
XX		
PF	14-SEP-2001;	2001WO-US028730.
XX		
PR	14-SEP-2000;	2000US-00662293.
XX		
PA	(HESK-) HESKA CORP.	
XX		
PI	Mccall CA, Hunter SW, Weber ER;	
XX		
DR	WPI; 2002-351888/38.	
XX		
PT	New mite allergenic protein isolated from Dermatophagoides, designated	
XX	Der HMW-map protein, useful as a vaccine for treating mite allergy.	
PS	Claim 12; Page 70; 161pp; English.	

The invention relates to an isolated mite allergenic protein of Dermatophagoides, designated Der HMW-map protein, and its related nucleic acid. The Der HMW-map protein is useful for eliciting an immune response against Der HMW-map protein. The protein or a reagent comprising a non-proteinaceous epitope is useful for identifying an animal (e.g., dog, cat) susceptible to or having an allergic response to a mite. A therapeutic composition is useful for desensitising a host animal to an allergic response to a mite. The DNA and protein can be used in the detection of anti-Der HMW-map antibodies in animal fluids, and inhibition of immunoglobulin (Ig)E or Der HMW-map protein activity associated with a disease. Antibodies that bind to Der HMW-map are useful for inhibiting binding of proteins to IGE, to prevent immunocomplex formation, thus reducing hypersensitivity responses to mite allergens, and as vaccines against mite allergen hypersensitivity. Sequences AAU96314-AAU96342 represent Der HMW-map polypeptides of the invention

SQ Sequence 20 AA;

Query Match 100.0%; Score 115; DB 5; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1,1e-11;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	DIPHPNTNHHKYLVCESVNGG	20
DB	1	DIPHPNTNHHKYLVCESVNGG	20

## RESULT 3

ID AAY52520 standard; peptide, 19 AA.

AC	AAY52520;	
DT	22-FEB-2000	(first entry)
DE	House dust mite allergen protein (map) A/B fragment map(10).	

```

XX KM Mite allergen protein; map; high molecular weight; HMW-map; allergy;
XX KM house dust mite; IgE; immunoglobulin E; allergen; mapA; mapB;
XX KM hypersensitivity reaction; therapy; treatment; diagnosis; human; feline;
XX KM canine; veterinary; antibody; vaccine; immunisation.
XX OS Dermatophagoides farinae.
XX PN MO9954349-A2.
XX PD 28-OCT-1999.
XX PF 16-APR-1999; 99WO-US0808524.
XX PR 17-APR-1998; 98US-00062013.
XX PR 13-MAY-1998; 98US-0085295P.
XX PR 02-SEP-1998; 98US-0098909P.
XX PA (HESK-) HESKA CORP.
XX PI McCall CA, Hunter SW, Weber ER;
XX DR WPI; 2000-052700/04.
XX PT Novel high molecular weight Dermatophagoides nucleic acid polypeptides
XX PT used to modify an animals' hypersensitivity to mite allergens.
XX PS Claim 3; Page 70; 154pp; English.
XX SC Sequences AA52510-Y52522 represent proteolytic fragments of
XX CC Dermatophagoides farinae high molecular weight mite allergen protein (HMW
XX CC -map) composition. The HMW-map composition was isolated from a D. farinae
XX CC homogenate by gel filtration, with each fraction being analysed for the
XX CC presence of proteins that bound to IgE present in mite-allergic dog
XX CC antiserum. The HMW-map composition comprises mapA (a 109 kD protein) and
XX CC mapB (98 kD). Mite allergenic proteins and peptides, and nucleic acids
XX CC encoding them, may be used in therapeutic compositions to modify an
XX CC animal's hypersensitivity reaction to mite allergens. Animals that may be
XX CC created include mammals and birds, especially felines, canines, equines,
XX CC humans, other pets, and work or domestic animals. The proteins or
XX CC fragments may also be used to diagnose allergies via a skin test. The
XX CC proteins and peptides can also be used to raise antibodies, which have a
XX CC variety of potential uses. For example, they can be used as vaccines to
XX CC passively immunise animals against dust mite hypersensitivity, as
XX CC positive controls in test kits and as tools to recover desired dust mite
XX CC allergens from a mixture of proteins
XX SC Sequence 19 AA;
XX
XX Query Match          94.8%; Score 109; DB 3; Length 19;
XX Best Local Similarity 100.0%; Pred. No. 1e-10;
XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY      1 DIPHPTNIHKYLVCSVNG 19
XX      |||||
XX DB      1 DIPHPTNIHKYLVCSVNG 19
XX
XX RESULT 4
XX AAU96324
XX ID AAU96324 standard; peptide; 19 AA.
XX AC AAU96324;
XX XX
XX DT 15-JUL-2002 (first entry)
XX XX
XX DB Der HMW-map polypeptide #11.
XX XX
XX KM Der HMW-map; American house dust mite; antiallergic; mite; IgE;
XX KM mite allergenic protein; immunoglobulin E; hypersensitivity;
XX KM immunocomplex formation.
XX OS Dermatophagoides farinae.

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XX XX WO200222807-A2.
XX PN 21-MAR-2002.
XX PD
XX PF 14-SEP-2001; 2001WO-US028730.
XX PR 14-SEP-2000; 2000US-00662293.
XX PA (HESK-) HESKA CORP.
XX PI McCall CA, Hunter SW, Weber ER;
XX DR WPI; 2002-351888/38.
XX PT New mite allergenic protein isolated from Dermatophagoides, designated
XX PT Der HMW-map protein, useful as a vaccine for treating mite allergy.
XX PS Claim 12; Page 71; 161pp; English.
XX SC The invention relates to an isolated mite allergenic protein of
XX CC Dermatophagoides, designated Der HMW-map protein, and its related nucleic
XX CC acid. The Der HMW-map protein is useful for eliciting an immune response
XX CC against Der HMW-map protein. The protein or a reagent comprising a non-
XX CC proteinaceous epitope is useful for identifying an animal (e.g., dog,
XX CC cat) susceptible to or having an allergic response to a mite. A
XX CC therapeutic composition is useful for desensitising a host animal to an
XX CC allergic response to a mite. The DNA and protein can be used in the
XX CC detection of anti-Der HMW-map antibodies in animal fluids, and inhibition
XX CC of immunoglobulin (Ig)E or Der HMW-map protein activity associated with a
XX CC disease. Antibodies that bind to Der HMW-map are useful for inhibiting
XX CC binding of proteins to IgE, to prevent immunocomplex formation, thus
XX CC reducing hypersensitivity responses to mite allergens, and as vaccines
XX CC against mite allergen hypersensitivity. Sequences AAU96314-AAU96342
XX SC represent Der HMW-map polypeptides of the invention
XX SC Sequence 19 AA;
XX
XX Query Match          94.8%; Score 109; DB 5; Length 19;
XX Best Local Similarity 100.0%; Pred. No. 1e-10;
XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY      1 DIPHPTNIHKYLVCSVNG 19
XX      |||||
XX DB      1 DIPHPTNIHKYLVCSVNG 19
XX
XX RESULT 5
XX AAM18898
XX ID AAM18898 standard; protein; 20 AA.
XX AC AAM18898;
XX XX
XX DT 12-OCT-2001 (first entry)
XX XX
XX DB Peptide #5332 encoded by probe for measuring cervical gene expression.
XX KM Probe; human; microarray; gene expression; cervical epithelial cell;
XX KM cervical cancer.
XX OS Homo sapiens.
XX PN WO200157278-A2.
XX PD 09-AUG-2001.
XX PF 30-JAN-2001; 2001WO-US000670.
XX PR 04-FEB-2000; 2000US-0180312P.
XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 30-JUN-2000; 2000US-00608408.
XX PR 03-AUG-2000; 2000US-00632365.
XX PR 21-SEP-2000; 2000US-0234687P.

```

PR 27-SEP-2000; 2000US-0236359P.  
PR 04-OCT-2000; 2000GB-00024263.  
XX  
XX (MOLE-) MOLECULAR DYNAMICS INC.  
XX PA Penn SG, Hanzel DK, Chen W, Rank DR;  
XX PI WPI; 2001-488901/53.  
XX DR  
XX Human genome-derived single exon nucleic acid probes useful for analyzing  
XX PT gene expression in human cervical epithelial cells.  
XX  
XX Claim 27; SEQ ID NO 23724; 487pp; English.  
XX  
XX The present invention relates to human single exon nucleic acid probes  
XX (SENP: see AAI10068-AA128459). The present sequence is a peptide encoded  
XX by one such probe. The SENPs are derived from human HeLa cells. The SENPs  
XX can be used to produce a single exon microarray, which can be used for  
XX measuring human gene expression in a sample derived from human cervical  
XX epithelial cells. By measuring gene expression, the probes are therefore  
XX useful in grading and/or staging of diseases of the cervix, notably  
XX cervical cancer. Note: The sequence data for this patent did not form  
XX part of the printed specification, but was obtained in electronic format  
XX directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
SQ Sequence 20 AA;

Query Match 32.6%; Score 37.5; DB 4; Length 20;  
Best Local Similarity 42.9%; Pred. No. 80;  
Matches 6; Conservative 5; Mismatches 2; Indels 1; Gaps 1;  
Qy 2 IPHPTIRKYLVE 15  
:|||:|:|:|:  
Db 8 LPHP-HSHTHLQ 20

RESULT 6  
ABB38020  
ID ABB38020 standard; peptide; 20 AA.  
XX  
XX ABB38020;  
AC  
XX  
XX 04-FEB-2002 (first entry)  
DT  
XX  
XX Peptide #5526 encoded by human foetal liver single exon probe.  
DE  
XX  
XX Human; foetal liver; gene expression; single exon nucleic acid probe.  
KM  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO200157277-A2.  
PN  
XX  
XX 09-AUG-2001.  
PD  
XX  
XX 30-JAN-2001; 2001WO-US000669.  
PF  
XX  
XX 04-FEB-2000; 2000US-0180312P.  
PR  
XX  
XX 26-MAY-2000; 2000US-0207456P.  
PR  
XX  
XX 30-JUN-2000; 2000US-00608408.  
PR  
XX  
XX 03-AUG-2000; 2000US-00632366.  
PR  
XX  
XX 21-SEP-2000; 2000US-0234687P.  
PR  
XX  
XX 27-SEP-2000; 2000US-0236359P.  
PR  
XX  
XX 04-OCT-2000; 2000GB-00024263.  
PA  
XX  
XX (MOLE-) MOLECULAR DYNAMICS INC.  
PI  
XX  
XX Penn SG, Hanzel DK, Chen W, Rank DR;  
XX  
XX WPI; 2001-483447/52.  
DR  
XX  
XX Human genome-derived single exon nucleic acid probes useful for analyzing  
XX PT gene expression in human fetal liver.  
XX

PS Claim 27; SEQ ID NO 30655; 639pp + Sequence Listing; English.  
XX  
XX The invention relates to a single exon nucleic acid probe for measuring  
XX human gene expression in a sample derived from human foetal liver. The  
XX single exon nucleic acid probes may be used for predicting, measuring and  
XX displaying gene expression in samples derived from human fetal liver. The  
XX present sequence is a peptide encoded by a single exon nucleic acid probe  
XX of the invention. Note: The sequence data for this patent did not form  
XX part of the printed specification, but was obtained in electronic format  
XX directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
SQ Sequence 20 AA;

Query Match 32.6%; Score 37.5; DB 4; Length 20;  
Best Local Similarity 42.9%; Pred. No. 80;  
Matches 6; Conservative 5; Mismatches 2; Indels 1; Gaps 1;  
Qy 2 IPHPTIRKYLVE 15  
:|||:|:|:|:  
Db 8 LPHP-HSHTHLQ 20

RESULT 7  
AAM31434  
ID AAM31434 standard; protein; 20 AA.  
XX  
XX AAM31434;  
AC  
XX  
XX 17-OCT-2001 (first entry)  
DT  
XX  
XX Peptide #5471 encoded by probe for measuring placental gene expression.  
DE  
XX  
XX Probe; microarray; human; placenta; antenatal diagnosis;  
KM  
XX  
XX genetic disorder.  
KW  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO200157272-A2.  
PN  
XX  
XX 09-AUG-2001.  
PD  
XX  
XX 30-JAN-2001; 2001WO-US000663.  
PF  
XX  
XX 04-FEB-2000; 2000US-0180312P.  
PR  
XX  
XX 26-MAY-2000; 2000US-0207456P.  
PR  
XX  
XX 30-JUN-2000; 2000US-00608408.  
PR  
XX  
XX 03-AUG-2000; 2000US-00632366.  
PR  
XX  
XX 21-SEP-2000; 2000US-0234687P.  
PR  
XX  
XX 27-SEP-2000; 2000US-0236359P.  
PR  
XX  
XX 04-OCT-2000; 2000GB-00024263.  
PA  
XX  
XX (MOLE-) MOLECULAR DYNAMICS INC.  
PI  
XX  
XX Penn SG, Hanzel DK, Chen W, Rank DR;  
XX  
XX WPI; 2001-488897/53.  
DR  
XX  
XX Human genome-derived single exon nucleic acid probes useful for analyzing  
XX PT gene expression in human placenta.  
XX  
XX Claim 27; SEQ ID NO 31703; 654pp; English.  
PS  
XX  
XX The present invention relates to single exon nucleic acid probes (SENP:  
XX see AAI31315-AA157546). The present sequence is a peptide encoded by one  
XX such probe. The probes are useful for producing a microarray for  
XX predicting, measuring and displaying gene expression in samples derived  
XX from human placenta. The probes are useful for antenatal diagnosis of  
XX human genetic disorders  
XX

SQ Sequence 20 AA;  
Query Match 32.6%; Score 37.5; DB 4; Length 20;  
Best Local Similarity 42.9%; Pred. No. 80;

Matches 6; Conservative 5; Mismatches 2; Indels 1; Gaps 1;  
 QY 2 IHPPTNHHKXVCE 15  
 :|||:|:|:|:  
 Db 8 LPHP-HSHTHLCCQ 20

RESULT 8  
 ABB23254  
 ID ABB23254 standard; protein; 20 AA.  
 AC ABB23254;  
 XX  
 XX

DT 23-JAN-2002 (first entry)  
 XX

DE Protein #5253 encoded by probe for measuring heart cell gene expression.

KW Human; gene expression; heart; microarray; vascular system;  
 KW cardiovascular disease; hypertension; cardiac arrhythmia;  
 KW congenital heart disease.  
 XX

OS Homo sapiens.  
 XX

PN WO200157274-A2.  
 XX

PD 09-AUG-2001.  
 XX

PF 30-JAN-2001; 2001WO-US000666.  
 XX

PR 04-FEB-2000; 2000US-0180312P.  
 XX

PR 26-MAY-2000; 2000US-0207456P.  
 XX

PR 30-JUN-2000; 2000US-00608408.  
 XX

PR 03-AUG-2000; 2000US-00632366.  
 XX

PR 21-SEP-2000; 2000US-0234687P.  
 XX

PR 27-SEP-2000; 2000US-0236359P.  
 XX

PR 04-OCT-2000; 2000GB-00024263.  
 XX

PA (MOLE-) MOLECULAR DYNAMICS INC.  
 XX

PI Penn SG, Hanzel DK, Chen W, Rank DR;  
 XX

DR WPI; 2001-488990/53.  
 XX

PT Single exon nucleic acid probes for analyzing gene expression in human  
 XX hearts.  
 XX

PS Claim 15; SEQ ID NO 25024; 530bp; English.  
 XX

CC The present invention relates to single exon nucleic acid probes for  
 XX measuring human gene expression in a sample derived from human heart (see  
 CC ABA21535-ADA41105). The present sequence is a protein encoded by one such  
 CC probe. The probes may be used for predicting, measuring and displaying  
 CC gene expression in samples derived from the human heart via microarrays.  
 CC By measuring gene expression, the probes are useful for predicting,  
 CC diagnosing, grading, staging, monitoring and prognosing diseases of the  
 CC human heart and vascular system e.g. cardiovascular disease,  
 CC hypertension, cardiac arrhythmias and congenital heart disease. Note: The  
 CC sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences  
 XX

CC Sequence 20 AA;  
 XX

Query Match 32.6%; Score 37.5; DB 4; Length 20;  
 Best Local Similarity 42.9%; Pred. No. 80;  
 Matches 6; Conservative 5; Mismatches 2; Indels 1; Gaps 1;

QY 2 IHPPTNHHKXVCE 15  
 :|||:|:|:|:  
 Db 8 LPHP-HSHTHLCCQ 20

RESULT 9

AAM71153  
 ID AAM71153 standard; protein; 20 AA.  
 AC AAM71153;  
 XX

DT 06-NOV-2001 (first entry)  
 XX

DE Human bone marrow expressed probe encoded protein SEQ ID NO: 31459.

KW Human; bone marrow expressed exon; gene expression analysis; probe;  
 KW microarray; cancer; leukaemia; lymphoma; myeloma.  
 XX

OS Homo sapiens.  
 XX

PN WO200157276-A2.  
 XX

PD 09-AUG-2001.  
 XX

PF 30-JAN-2001; 2001WO-US000666.  
 XX

PR 04-FEB-2000; 2000US-0180312P.  
 XX

PR 26-MAY-2000; 2000US-0207456P.  
 XX

PR 30-JUN-2000; 2000US-00608408.  
 XX

PR 03-AUG-2000; 2000US-00632366.  
 XX

PR 21-SEP-2000; 2000US-0234687P.  
 XX

PR 27-SEP-2000; 2000US-0236359P.  
 XX

PR 04-OCT-2000; 2000GB-00024263.  
 XX

PA (MOLE-) MOLECULAR DYNAMICS INC.  
 XX

PI Penn SG, Hanzel DK, Chen W, Rank DR;  
 XX

DR WPI; 2001-488990/53.  
 XX

PT Human genome-derived single exon nucleic acid probes useful for analyzing  
 XX gene expression in human bone marrow.  
 XX

PS Example 4; SEQ ID NO 31459; 658bp + Sequence Listing; English.  
 XX

CC The present invention provides a number of single exon nucleic acid  
 CC probes which are derived from genomic sequences expressed in the human  
 CC bone marrow. They can be used to measure gene expression in bone marrow  
 CC samples, which may enable the improved diagnosis and treatment of cancers  
 CC such as lymphoma, leukaemia and myeloma. The present sequence is a  
 CC protein encoded by one of the probes of the invention  
 XX

CC Sequence 20 AA;  
 XX

Query Match 32.6%; Score 37.5; DB 4; Length 20;  
 Best Local Similarity 42.9%; Pred. No. 80;  
 Matches 6; Conservative 5; Mismatches 2; Indels 1; Gaps 1;

QY 2 IHPPTNHHKXVCE 15  
 :|||:|:~|:|:|:  
 Db 8 LPHP-HSHTHLCCQ 20

RESULT 10

AAM58647  
 ID AAM58647 standard; protein; 20 AA.  
 AC AAM58647;  
 XX

DT 05-NOV-2001 (first entry)  
 XX

DE Human brain expressed single exon probe encoded protein SEQ ID NO: 30752.

KW Human; brain expressed exon; gene expression analysis; probe; microarray;  
 KW Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer.  
 XX

OS Homo sapiens.  
 XX

PN WO200157275-A2.  
 XX

XX 09-AUG-2001.  
 PD Penn SG, Hanzel DK, Chen W, Rank DR;  
 XX WPI; 2001-483446/52.  
 PF 30-JAN-2001; 2001WO-US000667.  
 XX 04-FEB-2000; 2000US-0180312P.  
 PR 26-MAY-2000; 2000US-0207456P.  
 PR 30-JUN-2000; 2000US-00608408.  
 PR 03-AUG-2000; 2000US-00632366.  
 PR 21-SEP-2000; 2000US-0234687P.  
 PR 27-SEP-2000; 2000US-0236359P.  
 PR 04-OCT-2000; 2000GB-00024263.  
 XX (MOLE-) MOLECULAR DYNAMICS INC.  
 PA Penn SG, Hanzel DK, Chen W, Rank DR;  
 XX WPI; 2001-483446/52.  
 DR Single exon nucleic acid probes for analyzing gene expression in human  
 XX brains.  
 PT Example 4; SEQ ID NO 30752; 650bp + Sequence Listing; English.  
 PS The present invention provides a number of single exon nucleic acid  
 CC probes which are derived from genomic sequences expressed in the human  
 CC brain. They can be used to measure gene expression in brain cell samples,  
 CC which may enable the diagnosis and improved treatment of nervous system  
 CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,  
 CC epilepsy and cancers. The present sequence is a protein encoded by one of  
 CC the probes of the invention  
 XX  
 SQ Sequence 20 AA;

Query Match 32.6%; Score 37.5; DB 4; Length 20;  
 Best Local Similarity 42.9%; Pred. No. 80;  
 Matches 6; Conservative 5; Mismatches 2; Indels 1; Gaps 1;  
 QY 2 IPHPTNHHKYLVC 15  
 DB 8 LPHP-HSHTHLQC 20

RESULT 11  
 ABG52865  
 ID ABG52865 standard; peptide; 20 AA.  
 XX  
 AC ABG52865;  
 XX  
 DT 25-FEB-2003 (first entry)  
 XX  
 DB Human liver peptide, SEQ ID No 31513.  
 XX  
 KW Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia;  
 KW hypercholesterolaemia; coronary heart disease.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200157273-A2.  
 XX  
 PD 09-AUG-2001.  
 XX  
 PF 30-JAN-2001; 2001WO-US000664.  
 XX  
 PR 04-FEB-2000; 2000US-0180312P.  
 PR 26-MAY-2000; 2000US-0207456P.  
 PR 30-JUN-2000; 2000US-00608408.  
 PR 03-AUG-2000; 2000US-00632366.  
 PR 21-SEP-2000; 2000US-0234687P.  
 PR 27-SEP-2000; 2000US-0236359P.  
 PR 04-OCT-2000; 2000GB-00024263.  
 XX  
 PA (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;  
 PI WPI; 2001-488898/53.  
 XX  
 DR Human genome-derived single exon nucleic acid probes useful for analyzing  
 XX gene expression in human adult liver.  
 PT Claim 27; SEQ ID NO 31513; 650bp; English.  
 XX  
 PS The invention relates to a single exon nucleic acid probe (SENP) (i) for  
 CC measuring human gene expression in a sample derived from human adult  
 CC liver, comprising one of 13109 defined nucleotide sequences given in the  
 CC specification (or complements/ fragments). The probe hybridizes at high  
 CC stringency to a nucleic acid molecule expressed in the human adult liver.  
 CC (i) may be used for predicting, measuring and displaying gene expression  
 CC in samples derived from human adult liver. The genes identified may be  
 CC involved in genetic liver diseases such as cirrhosis,  
 CC hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is  
 CC associated with coronary heart disease. ABG47348-ABG59930 represent human  
 CC liver single exon encoded peptides of the invention. Note: The sequence  
 CC information for this patent does not appear in the printed specification  
 CC but was obtained in electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 20 AA;

Query Match 32.6%; Score 37.5; DB 4; Length 20;  
 Best Local Similarity 42.9%; Pred. No. 80;  
 Matches 6; Conservative 5; Mismatches 2; Indels 1; Gaps 1;  
 QY 2 IPHPTNHHKYLVC 15  
 DB 8 LPHP-HSHTHLQC 20

RESULT 12  
 ABG40950  
 ID ABG40950 standard; peptide; 20 AA.  
 XX  
 AC ABG40950;  
 XX  
 DT 19-AUG-2002 (first entry)  
 XX  
 DB Human peptide encoded by genome-derived single exon probe SEQ ID 30615.  
 XX  
 KW Human; single exon probe; asthma; lung cancer; COPD; ILD;  
 KW chronic obstructive pulmonary disease; interstitial lung disease;  
 KW familial idiopathic pulmonary fibrosis; neurofibromatosis;  
 KW tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;  
 KW Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemorrhoidosis;  
 KW pulmonary histiocytosis; lymphangioleiomyomatosis; Karagener syndrome;  
 KW pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;  
 KW primary ciliary dyskinesia; pulmonary hypertension;  
 KW hyaline membrane disease.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200166003-A2.  
 XX  
 PD 15-NOV-2001.  
 XX  
 PF 30-JAN-2001; 2001WO-US000665.  
 XX  
 PR 04-FEB-2000; 2000US-0180312P.  
 PR 26-MAY-2000; 2000US-0207456P.  
 PR 30-JUN-2000; 2000US-00608408.  
 PR 03-AUG-2000; 2000US-00632366.  
 PR 21-SEP-2000; 2000US-0234687P.  
 PR 27-SEP-2000; 2000US-0236359P.  
 PR 04-OCT-2000; 2000GB-00024263.  
 XX  
 PA (MOLE-) MOLECULAR DYNAMICS INC.



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PA (MURR/) MURRAY C J.  
PA (WANG/) WANG H.  
PA (WINE/) WINETZKY D S.  
XX  
PI Wolfgang A. Baldwin TM, Van Gastel FJC, Janssen GG, Murray CJ;  
PI Wang H, Winetzky DS;  
XX  
DR WPI; 2005-222220/23.  
XX  
PT New peptides that bind to carotenoid compounds, useful as detergents for  
PT targeting or removing stains on textiles or fabrics, in personal care or  
PT food industry applications, or in various diagnostic applications.  
XX  
PS claim 1; SEQ ID NO 54; 107pp; English.  
XX  
CC The invention relates to 432 cyclic or linear carotenoid-binding phage  
CC display peptides (ADY56178-ADY56609); to carotenoid-binding peptides  
CC which comprise a repeatable motif selected from PPP, SSP, SSK, SPT, PLP,  
CC SLH, SPV, TTT, NTS, ABS, TPV or a motif shown in ADY56623-ADY56651; and  
CC to a complex comprising a phenol-oxidizing enzyme (especially a  
CC stachybotry's laccase such as ADY56177 or variants thereof) covalently  
CC attached to one of the 432 carotenoid-binding peptides. The invention  
CC also relates to polynucleotides encoding a carotenoid-binding peptide,  
CC and expression vectors and host cells comprising a polynucleotide  
CC encoding a phenol-oxidizing enzyme/carotenoid-binding peptide complex.  
CC The carotenoid-binding peptides are useful in complexes with a phenol-  
CC oxidizing enzyme for enhancing the selectivity of the enzyme to a target  
CC carotenoid stain on a textile or other surface, where the enzyme can then  
CC act to bleach the stain. Such enzyme/peptide complexes can be used in  
CC detergent or cleaning compositions for targeting or removing food stains  
CC (e.g., tomato or paprika) on fabrics, and can also be used in the textile  
CC industry in the treatment, processing, finishing, polishing or production  
CC of fibers. The enzyme/peptide complexes are additionally useful in  
CC personal care applications (e.g., in skin cosmetics as skin tanners), in  
CC food industry applications (e.g., as fruit ripening agents) or in  
CC diagnostic uses, such as in pharmaceutical applications e.g., to localize  
CC the presence of carotenoids in tissues. The present sequence represents a  
CC specifically claimed carotenoid-binding cyclic peptide isolated from a  
CC phage display library.  
XX  
SQ Sequence 7 AA;  
XX  
Query Match 30.4%; Score 35; DB 9; Length 7;  
Best Local Similarity 83.3%; Pred. No. 2e+06;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 3 PHPTNI 8  
Db 1 PHPTNL 6  
XX  
RESULT 15  
ABCO6055  
ID ABCO6055 standard; peptide; 10 AA.  
XX  
AC ABCO6055;  
XX  
DT 20-OCT-2005 (first entry)  
XX  
DE H3 or D3-acetylated tumor-associated peptide.  
XX  
KW cytostatic; vaccine; gene therapy; pharmaceutical; immunotherapy; tumor;  
KW cancer; neoplasm.  
XX  
OS Unidentified.  
XX  
PN WO2005076009-A2.  
XX  
PD 18-AUG-2005.  
XX

XX  
PF 28-JAN-2005; 2005WO-EP000873.  
XX  
PR 28-JAN-2004; 2004DE-10005273.  
PR 06-MAR-2004; 2004DE-10011503.  
XX  
PA (IMMA-) IMMATICS BIOTECHNOLOGIES GMBH.  
XX  
PI Lemmel C, Rammensee H;  
XX  
DR WPI; 2005-618379/63.  
XX  
PT Identifying and quantifying tumor-associated peptides by chemically  
PT identifying modifying peptides to generate different physical  
PT characteristics, useful for treating tumorous and/or adenomatous  
PT diseases.  
XX  
PS Disclosure; Page 12; 43pp; English.  
XX  
CC The invention describes a method of identifying and quantifying tumor-  
CC associated peptides comprising chemically identifying modifying peptides  
CC from samples in order to generate different physical characteristics in  
CC the peptides from the different samples. The peptides are useful for  
CC producing a medicament for the treatment of tumorous diseases and/or  
CC adenomatous diseases, such as renal, lung, colon, stomach, pancreatic,  
CC breast, prostate, ovarian and/or skin cancer. The peptide is used  
CC together with an adjuvant. A peptide bound to an antigen-presenting cell  
CC is used. The peptides are also useful for the labeling of leukocytes, in  
CC particular of T-lymphocytes, for evaluating the progress of therapy in a  
CC tumorous disease, and for producing an antibody. The nucleic acid and/or  
CC vector and/or cell are useful in producing a medicament for the treatment  
CC of tumorous and/or adenomatous diseases. This is the amino acid sequence  
CC of a tumor-associated peptide that binds human MHC class I.  
XX  
SQ Sequence 10 AA;  
XX  
Query Match 30.4%; Score 35; DB 9; Length 10;  
Best Local Similarity 50.0%; Pred. No. 92;  
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
QY 1 DIPHTNIHK 10  
Db 1 DAHPHTNVR 10  
XX  
RESULT 16  
ABCO6029  
ID ABCO6029 standard; peptide; 10 AA.  
XX  
AC ABCO6029;  
XX  
DT 20-OCT-2005 (first entry)  
XX  
DE Tumor-associated peptide SEQ ID NO 12.  
XX  
KW cytostatic; vaccine; gene therapy; pharmaceutical; immunotherapy; tumor;  
KW cancer; neoplasm.  
XX  
OS Homo sapiens.  
XX  
PN WO2005076009-A2.  
XX  
PD 18-AUG-2005.  
XX  
PF 28-JAN-2005; 2005WO-EP000873.  
XX  
PR 28-JAN-2004; 2004DE-10005273.  
PR 06-MAR-2004; 2004DE-10011503.  
XX  
PA (IMMA-) IMMATICS BIOTECHNOLOGIES GMBH.  
XX  
PI Lemmel C, Rammensee H;  
XX



DR WPI, 2005-618379/63.  
 XX Identifying and quantifying tumor-associated peptides by chemically  
 PT identically modifying peptides to generate different physical  
 PT characteristics, useful for treating tumorous and/or adenomatous  
 PT diseases.  
 XX Claim 19; SEQ ID NO 12; 43pp; English.  
 XX  
 CC The invention describes a method of identifying and quantifying tumor-  
 CC associated peptides comprising chemically identically modifying peptides  
 CC from samples in order to generate different physical characteristics in  
 CC the peptides from the different samples. The peptides are useful for  
 CC producing a medicament for the treatment of tumorous diseases and/or  
 CC adenomatous diseases, such as renal, lung, colon, stomach, pancreatic,  
 CC breast, prostate, ovarian and/or skin cancer. The peptide is used  
 CC together with an adjuvant. A peptide bound to an antigen-presenting cell  
 CC is used. The peptides are also useful for the labeling of leukocytes, in  
 CC particular of T-lymphocytes, for evaluating the progress of therapy in a  
 CC tumorous disease, and for producing an antibody. The nucleic acid and/or  
 CC vector and/or cell are useful in producing a medicament for the treatment  
 CC of tumorous and/or adenomatous diseases. This is the amino acid sequence  
 CC of a tumor-associated peptide that binds human MHC class I.  
 CC  
 SQ Sequence 10 AA;  
 XX  
 Query Match 30.4%; Score 35; DB 9; Length 10;  
 Best Local Similarity 50.0%; Pred. No. 92;  
 Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 DIPHTNTHK 10  
 | | | | | : |  
 1 DAHPNTNVR 10  
 DB  
 RESULT 17  
 AAW30771  
 ID AAW30771 standard; peptide; 15 AA.  
 XX  
 AC AAW30771;  
 XX  
 DT 27-FEB-1998 (first entry)  
 XX  
 DE Prostate Specific Antigen (PSA) derived peptide ABT3.  
 XX  
 DE Prostate specific antigen; PSA; immunogenic; human glandular kallikrein;  
 XX hK2; antigen; antibody; detection; diagnosis; prostate cancer.  
 KM  
 KM Synthetic.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9729199-A2.  
 XX  
 PD 14-AUG-1997.  
 XX  
 PF 06-FEB-1997, 97WO-US001911.  
 XX  
 PR 06-FEB-1996; 96US-00595945.  
 XX  
 PA (ABBO ) ABBOTT LAB.  
 XX  
 PI Dowell BL, Bridon DP, Qiu X, Lillja H, Piltanen T, Vihinen M,  
 XX Petersson IK;  
 DR WPI, 1997-415352/38.  
 XX  
 PT Prostate Specific Antigen peptide(a) - useful for diagnosis of prostate  
 PT cancer.  
 XX  
 PS Claim 2; Page 10; 42pp; English.  
 XX  
 CC AAW30769-84 are synthetic peptides derived from the prostate specific  
 CC antigen (PSA) sequence. These peptides are identical to a highly

CC immunogenic region of PSA, and also comprise one or more amino acids  
 CC identical or non-identical to the amino acid sequence of human glandular  
 CC kallikrein (hK2). The peptides are used as antigens for the production of  
 CC antibodies which are used to detect PSA in a test sample (claimed). This  
 CC is useful for diagnosis of prostate cancer. The peptides enable the  
 CC production of antisera necessary to determine the amount of total PSA,  
 CC free PSA and PSA-ACT complex present in a sample and thus improve the  
 CC ability of the clinician to distinguish, e.g., between BPH (benign  
 CC prostatic hyperplasia) and prostatic cancer in a patient  
 CC  
 SQ Sequence 15 AA;  
 XX  
 Query Match 30.4%; Score 35; DB 2; Length 15;  
 Best Local Similarity 36.4%; Pred. No. 1.5e+02;  
 Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;  
 QY 4 HPTNHYLYVC 14  
 | | | | | : | | | |  
 5 HPQKVTKFMVC 15  
 DB  
 RESULT 18  
 AAW58054  
 ID AAW58054 standard; peptide; 15 AA.  
 XX  
 AC AAW58054;  
 XX  
 DT 11-AUG-1998 (first entry)  
 XX  
 DE Human prostate specific antigen SEQ ID NO:72.  
 XX  
 DE Human; prostate specific antigen; PSA; epitope; monoclonal antibody;  
 XX detection; cancer; serine protease.  
 KM  
 KM Synthetic.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9810292-A1.  
 XX  
 PD 12-MAR-1998.  
 XX  
 PF 25-AUG-1997; 97WO-US014909.  
 XX  
 PR 06-SEP-1996; 96US-0025404P.  
 XX  
 PA (CENZ ) CENTOCOR INC.  
 XX  
 PI Heavner GA;  
 XX  
 DR WPI, 1998-193789/17.  
 XX  
 PT Monoclonal antibodies specific for prostate specific antigen - useful,  
 PT e.g. in screening for prostate or breast cancer and especially to  
 PT distinguish between benign prostatic hyperplasia and prostate cancer.  
 XX  
 PS Example; Page 59; 84pp; English.  
 XX  
 CC The present sequence represents a prostate specific antigen (PSA)  
 CC peptide. Monoclonal antibodies specific for PSA and hybridomas producing  
 CC them have been developed. The antibodies: (a) bind to free PSA; (b) are  
 CC monoclonal antibody 365 binding to amino acids 82-87 of free PSA (LQRRFL)  
 CC or fragment, and (c) are monoclonal antibodies 10, 11, 16 or 22.2 and  
 CC 15.2, 156 or 225 binding to amino acids 139-144 (BSLFLTP) and 55-60  
 CC (SLRFPB) respectively of free and bound PSA, or fragments. The antibodies  
 CC are useful to detect PSA. For detecting free PSA only, an immunoassay  
 CC comprising a solid support with attached labelled monoclonal antibody  
 CC specific for free PSA (especially (b)) and a PSA standard can be used. To  
 CC detect both free and bound PSA, a second solid support with attached  
 CC (differently labelled) monoclonal antibody binding free and bound PSA  
 CC (especially selected from (c)) can be used either with, or in place of,  
 CC the first solid support. The antibodies are useful in cancer screening,  
 CC especially prostate and breast cancer. By obtaining total and free PSA  
 CC values, their ratio can be used to separate prostatic cancer (PCA) from

CC benign prostatic hyperplasia (BHP) patients. Measurement of PSA is also  
 CC useful after radical prostatectomy, to predict disease persistence. The  
 CC antibodies allow evaluation of PSA free/total ratio, enabling separation  
 CC of BPH and PCA patients with PSA values 4-10 ng/ml not previously  
 CC possible by total PSA testing, avoiding biopsies  
 CC  
 SQ Sequence 15 AA;

Query Match 30.4%; Score 35; DB 2; Length 15;  
 Best Local Similarity 36.4%; Pred. No. 1.5e+02;  
 Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 4 HPTNKHXYLVC 14  
 || : ||::||  
 Db 5 HPQKVTKFMLC 15

RESULT 19  
 AAMS8055  
 ID AAMS8055 standard; peptide; 15 AA.  
 XX  
 AC AAMS8055;

XX 11-AUG-1998 (first entry)

DE Human prostate specific antigen peptide SEQ ID NO:73.

KM Human; prostate specific antigen; PSA; epitope; monoclonal antibody;  
 KW detection; cancer; serine protease.

XX Synthetic.

OS Homo sapiens.

XX MO9810292-A1.

PD 12-MAR-1998.

PF 25-AUG-1997; 97WO-US014909.

XX 06-SEP-1996; 96US-0025404P.

PA (CENZ) CENTOCOR INC.

PI Heavner GA;

DR WPI; 1998-193789/17.

XX Monoclonal antibodies specific for prostate specific antigen - useful,  
 PT e.g. in screening for prostate or breast cancer and especially to  
 PT distinguish between benign prostatic hyperplasia and prostate cancer.

XX Example; Page 60; 84pp; English.

XX The present sequence represents a prostate specific antigen (PSA)  
 CC peptide. Monoclonal antibodies specific for PSA and hybridomas producing  
 CC them have been developed. The antibodies: (a) bind to free PSA; (b) are  
 CC monoclonal antibody 365 binding to amino acids 82-87 of free PSA (LKRRPL)  
 CC or fragment, and (c) are monoclonal antibodies 10, 11, 16 or 22.2 and  
 CC 15.2, 156 or 225 binding to amino acids 139-144 (ESLFLRP) and 55-60  
 CC (SLRFPB) respectively of free and bound PSA, or fragments. The antibodies  
 CC are useful to detect PSA. For detecting free PSA only, an immunoassay  
 CC comprising a solid support with attached labeled monoclonal antibody  
 CC specific for free PSA (especially (b)) and a PSA standard can be used. To  
 CC detect both free and bound PSA, a second solid support with attached  
 CC (differently labelled) monoclonal antibody binding free and bound PSA  
 CC (especially selected from (c)) can be used either with, or in place of,  
 CC the first solid support. The antibodies are useful in cancer screening,  
 CC especially prostate and breast cancer. By obtaining total and free PSA  
 CC values, their ratio can be used to separate prostatic cancer (PCA) from  
 CC benign prostatic hyperplasia (BHP) patients. Measurement of PSA is also  
 CC useful after radical prostatectomy, to predict disease persistence. The  
 CC antibodies allow evaluation of PSA free/total ratio, enabling separation  
 CC of BPH and PCA patients with PSA values 4-10 ng/ml not previously

CC possible by total PSA testing, avoiding biopsies  
 XX  
 SQ Sequence 15 AA;

Query Match 30.4%; Score 35; DB 2; Length 15;  
 Best Local Similarity 36.4%; Pred. No. 1.5e+02;  
 Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 4 HPTNKHXYLVC 14  
 || : ||::||  
 Db 2 HPQKVTKFMLC 12

RESULT 20  
 ADW37502  
 ID ADW37502 standard; peptide; 15 AA.  
 XX  
 AC ADW37502;

XX 10-MAR-2005 (first entry)

DE HLA binding epitope #8252.

KM Virucide; cytostatic; gene therapy; vaccine; epitope; cytotoxic T cell;  
 KW MHC class I; CTL; HTL; A2-restricted cytotoxic lymphocyte; HLA;

XX viral disease; cancer.

XX Unidentified.

PN WO2003040165-A2.

PD 15-MAY-2003.

PF 18-OCT-2001; 2001WO-US051650.

XX 19-OCT-2000; 2000US-0242350P.

PR 20-APR-2001; 2001US-0285624P.

PA (EPI-M) EPI-MONB INC.

PI Sette A, Sidney J, Southwood S;

DR WPI; 2003-441519/41.

XX New composition comprising at least one peptide having allele-specific  
 PT binding motifs for HLA, useful for preventing, treating or diagnosing  
 PT viral diseases and cancer.

PS Claim 1; Page 52-379; 382pp; English.

XX The invention relates to a composition comprising at least one peptide  
 CC having an isolated, prepared epitope selected from any of the sequences  
 CC from 30 lists given in the specification. Also disclosed is a method for  
 CC inducing a cytotoxic T cell response against a pre-selected antigen in a  
 CC patient expressing a specific MHC class I allele by contacting cytotoxic  
 CC T cells from the patient with the composition cited above. The  
 CC composition comprises an epitope that is joined by an amino acid linker.  
 CC The epitope is admixed or joined to a CTL or HTL epitope. The epitope is  
 CC bound to an HLA molecule on the antigen-presenting cell, where when an A2  
 CC -restricted cytotoxic lymphocyte (CTL) is present, a receptor of the CTL  
 CC binds to a complex of the HLA molecule and the epitope. Specifically  
 CC claimed are peptides having allele-specific binding motifs for HLA. The  
 CC compositions and methods are useful for preventing, treating or  
 CC diagnosing viral diseases and cancer. The peptide epitopes are useful as  
 CC diagnostic agents for evaluating immune responses, for making antibodies  
 CC and for evaluating efficacy of a vaccine. Sequences given in ADW37502-1-  
 CC ADW37745 represent epitopes of the invention as given in Tables 2-31.

XX Sequence 15 AA;

Query Match 30.4%; Score 35; DB 7; Length 15;  
 Best Local Similarity 36.4%; Pred. No. 1.5e+02;  
 Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 4 HPTNHHKYLVC 14  
|| : ||: ||  
Db 5 HPQKVTKEFMLC 15

## RESULT 21

ID ADM35209 standard; peptide, 15 AA.

AC ADM35209;

DT 10-MAR-2005 (first entry)

DE HLA binding epitope #5959.

KM Virucide; cytosolic; gene therapy; vaccine; epitope; cytotoxic T cell;  
KM MHC class I; CTL; HTL; A2-restricted cytotoxic lymphocyte; HLA;  
KM viral disease; cancer.

OS Unidentified.

XX WO2003040165-A2.

PD 15-MAY-2003.

PF 18-OCT-2001; 2001WO-US051650.

PR 19-OCT-2000; 2000US-0242350P.

PR 20-APR-2001; 2001US-0285624P.

PA (EPIM-) EPIMMUNE INC.

PI Sette A, Sidney J, Southwood S;

XX WPI; 2003-441519/41.

PT New composition comprising at least one peptide having allele-specific  
PT binding motifs for HLA, useful for preventing, treating or diagnosing  
PT viral diseases and cancer.

XX Claim 1; Page 52-379; 382pp; English.

CC The invention relates to a composition comprising at least one peptide  
CC having an isolated, prepared epitope selected from any of the sequences  
CC from 30 lists given in the specification. Also disclosed is a method for  
CC inducing a cytotoxic T cell response against a pre-selected antigen in a  
CC patient expressing a specific MHC class I allele by contacting cytotoxic  
CC T cells from the patient with the composition cited above. The  
CC composition comprises an epitope that is joined by an amino acid linker.  
CC The epitope is admixed or joined to a CTL or HTL epitope. The epitope is  
CC bound to an HLA molecule on the antigen-presenting cell, where when an A2  
CC -restricted cytotoxic lymphocyte (CTL) is present, a receptor of the CTL  
CC binds to a complex of the HLA molecule and the epitope. Specifically  
CC claimed are peptides having allele-specific binding motifs for HLA. The  
CC compositions and methods are useful for preventing, treating or  
CC diagnosing viral diseases and cancer. The peptide epitopes are useful as  
CC diagnostic agents for evaluating immune responses, for making antibodies  
CC and for evaluating efficacy of a vaccine. Sequences given in ADM29251-  
CC ADM37745 represent epitopes of the invention as given in Tables 2-31.

XX Sequence 15 AA;

Qy Query Match 30.4%; Score 35; DB 7; Length 15;

Best Local Similarity 36.4%; Pred. No. 1.5e+02;  
Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 4 HPTNHHKYLVC 14  
|| : ||: ||  
Db 5 HPQKVTKEFMLC 15

## RESULT 22

ADM33268  
ID ADM33268 standard; peptide, 15 AA.

XX ADM33268;

DT 10-MAR-2005 (first entry)

DE HLA binding epitope #4018.

KM Virucide; cytosolic; gene therapy; vaccine; epitope; cytotoxic T cell;  
KM MHC class I; CTL; HTL; A2-restricted cytotoxic lymphocyte; HLA;  
KM viral disease; cancer.

OS Unidentified.

XX WO2003040165-A2.

PD 15-MAY-2003.

PF 18-OCT-2001; 2001WO-US051650.

PR 19-OCT-2000; 2000US-0242350P.

PR 20-APR-2001; 2001US-0285624P.

PA (EPIM-) EPIMMUNE INC.

PI Sette A, Sidney J, Southwood S;

XX WPI; 2003-441519/41.

PT New composition comprising at least one peptide having allele-specific  
PT binding motifs for HLA, useful for preventing, treating or diagnosing  
PT viral diseases and cancer.

XX Claim 1; Page 52-379; 382pp; English.

CC The invention relates to a composition comprising at least one peptide  
CC having an isolated, prepared epitope selected from any of the sequences  
CC from 30 lists given in the specification. Also disclosed is a method for  
CC inducing a cytotoxic T cell response against a pre-selected antigen in a  
CC patient expressing a specific MHC class I allele by contacting cytotoxic  
CC T cells from the patient with the composition cited above. The  
CC composition comprises an epitope that is joined by an amino acid linker.  
CC The epitope is admixed or joined to a CTL or HTL epitope. The epitope is  
CC bound to an HLA molecule on the antigen-presenting cell, where when an A2  
CC -restricted cytotoxic lymphocyte (CTL) is present, a receptor of the CTL  
CC binds to a complex of the HLA molecule and the epitope. Specifically  
CC claimed are peptides having allele-specific binding motifs for HLA. The  
CC compositions and methods are useful for preventing, treating or  
CC diagnosing viral diseases and cancer. The peptide epitopes are useful as  
CC diagnostic agents for evaluating immune responses, for making antibodies  
CC and for evaluating efficacy of a vaccine. Sequences given in ADM29251-  
CC ADM37745 represent epitopes of the invention as given in Tables 2-31.

XX Sequence 15 AA;

Qy Query Match 30.4%; Score 35; DB 7; Length 15;

Best Local Similarity 36.4%; Pred. No. 1.5e+02;  
Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 4 HPTNHHKYLVC 14  
|| : ||: ||  
Db 5 HPQKVTKEFMLC 15

## RESULT 23

ID ADM33976 standard; peptide, 15 AA.

AC ADM33976;

DT 10-MAR-2005 (first entry)

XX

DE	HLA binding epitope #4726.
XX	
KW	Virucide; cytosstatic; gene therapy; vaccine; epitope; cytotoxic T cell;
KW	MHC class I; CTL; HTLV; A2-restricted cytotoxic lymphocyte; HLA;
KW	viral disease; cancer.
OS	Unidentified.
XX	
PN	WO2003040165-A2.
PN	
PD	15-MAY-2003.
PE	18-OCT-2001; 2001WO-US051650.
PR	19-OCT-2000; 2000US-0242350P.
PR	20-APR-2001; 2001US-0285624P.
PA	(EPIM-) EPIMUNE INC.
PI	Secte A, Sidney J, Southwood S,
DR	WPI; 2003-441519/41.
PT	New composition comprising at least one peptide having allele-specific
PT	binding motifs for HLA, useful for preventing, treating or diagnosing
PT	viral diseases and cancer.
XX	
PS	Claim 1; Page 52-379; 382pp; English.
CC	
CC	The invention relates to a composition comprising at least one peptide
CC	having an isolated, prepared epitope selected from any of the sequences
CC	from 30 lists given in the specification. Also disclosed is a method for
CC	inducing a cytotoxic T cell response against a pre-selected antigen in a
CC	patient expressing a specific MHC class I allele by contacting cytotoxic
CC	T cells from the patient with the composition cited above. The
CC	composition comprises an epitope that is joined by an amino acid linker.
CC	The epitope is admixed or joined to a CTL or HTLV epitope. The epitope is
CC	bound to an HLA molecule on the antigen-presenting cell, where when an A2
CC	-restricted cytotoxic lymphocyte (CTL) is present, a receptor of the CTL
CC	binds to a complex of the HLA molecule and the epitope. Specifically
CC	claimed are peptides having allele-specific binding motifs for HLA. The
CC	compositions and methods are useful for preventing, treating or
CC	diagnosing viral diseases and cancer. The peptide epitopes are useful as
CC	diagnostic agents for evaluating immune responses, for making antibodies
CC	and for evaluating efficacy of a vaccine. Sequences given in ADW29251-
CC	ADW37745 represent epitopes of the invention as given in Tables 2-31.
XX	
SQ	Sequence 15 AA;
DB	
QY	4 HPTNIHKTLVC 14
	:   :
	5 HPOKVTKEMLC 15
Query Match	30.4%; Score 35; DB 7; Length 15;
Best Local Similarity	36.4%; Pred. No. 1.5e+02;
Matches	4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
RESULT 24	
ADN65435	ADN65435 standard; peptide; 15 AA.
XX	
AC	ADN65435;
XX	
DT	01-JUL-2004 (first entry)
XX	
DE	HLA binding peptide #2035.
XX	
KW	cytostatic; hepatotropic; virucide; antiinflammatory; anti-HIV;
KW	gene therapy; vaccine; HLA binding peptide; HTLV epitope; liposome;
KW	prostate specific antigen; prostate specific membrane antigen;
KW	hepatitis B virus antigen; hepatitis C virus antigen;
KW	malignant melanoma antigen; MAGE; Epstein Barr virus; cancer;

KW	prostate cancer; AIDS; renal carcinoma; cervical carcinoma; lymphoma;
XX	chondyroma accuminatum.
XX	
OS	unidentified.
XX	
PN	WO2004032121-A2.
XX	
XX	15-Apr-2004.
PD	
XX	
PF	03-OCT-2003; 2003WO-US031308.
XX	
PR	03-OCT-2002; 2002US-0416207P.
PR	08-OCT-2002; 2002US-0417269P.
XX	
PA	(EPIM-) EPIMMUNE INC.
XX	
PI	Sidney J, Southwood S, Sette A;
XX	
DR	WPI, 2004-347953/32.
XX	
XX	New composition of peptides and nucleic acids capable of binding Major
PT	Histocompatibility Complex molecules, useful for diagnosing, preventing
PT	or treating viral infections or cancer, such as prostate cancer,
PT	hepatitis B or AIDS.
XX	
XX	Claim 1, SEQ ID NO 2035; 186pp; English.
PS	
XX	
CC	The invention relates to a novel composition comprising one or more
CC	peptides or nucleic acids encoding an HLA binding peptide. The
CC	composition further comprises an HLA epitope. It also comprises a spacer
CC	molecule, a carrier, an MHC targeting sequence or a lipid. The peptides
CC	are incorporated as part of a liposome. The peptide is from an antigen
CC	selected from prostate specific antigen (PSA), prostate specific membrane
CC	antigen (PSM), hepatitis B virus (HBV) antigen, hepatitis C virus (HCV)
CC	antigen, malignant melanoma antigen (MAGE), Epstein Barr virus, human
CC	immunodeficiency type-1 (HIV-1), human immunodeficiency type-2 (HIV-2),
CC	Papilloma virus, Lassa virus, Mycobacterium tuberculosis (MT), p53,
CC	murine p53 (mp53), CEA, HER2/neu, and tyrosine kinase related protein
CC	(TRP). The composition is useful for preventing or treating viral
CC	infections or cancer, such as prostate cancer, hepatitis B, hepatitis C,
CC	AIDS, renal carcinoma, cervical carcinoma, lymphoma, CMV or chondyroma
CC	accuminatum. The composition is also be used for diagnosing such diseases.
CC	This sequence represents a peptide of the invention.
XX	
XX	
SQ	Sequence 15 AA;
	Query Match 30.4%; Score 35; DB 8; Length 15;
	Best Local Similarity 36.4%; Pred. No. 1.5e+02; Mismatches 3; Gaps 0;
	Matches 4; Conservative 4; Indels 0;
OY	4 HPTNHHKYLVC 14
	:   :
Db	5 HPQKVTKFMLC 15
RESULT 25	
AAM30783	
ID	AAM30783 standard; peptide; 19 AA.
XX	
XX	AAM30783;
XX	
DT	27-FEB-1998 (first entry)
XX	
DE	Prostate Specific Antigen (PSA) derived peptide ABR15.
XX	
KW	Prostate specific antigen; PSA; immunogenic; human glandular kallikrein;
KW	hK2; antigen; antibody; detection; diagnosis; prostate cancer.
XX	
OS	Synthetic.
OS	Homo sapiens.
XX	
PN	WO9729199-A2.
XX	

PD 14-AUG-1997.  
 XX  
 PF 06-FEB-1997; 97MO-US001911.  
 XX  
 PR 06-FEB-1996; 96US-00595945.  
 XX  
 PA (ABBO ) ABBOTT LAB.  
 XX  
 PI Dowell BL, Bridon DP, Qiu X, Lijja H, Piltanen T, Vihtinen M,  
 PI Petteerson IK,  
 XX WPI, 1997-415352/38.  
 DR  
 PT Prostate Specific Antigen peptide(s) - useful for diagnosis of prostate  
 PT cancer.  
 XX  
 XX Claim 2; Page 10; 42pp; English.  
 XX  
 CC AAM0769-84 are synthetic peptides derived from the prostate specific  
 CC antigen (PSA) sequence. These peptides are identical to a highly  
 CC immunogenic region of PSA, and also comprise one or more amino acids  
 CC identical or non-identical to the amino acid sequence of human glandular  
 CC kallikrein (hK2). The peptides are used as antigens for the production of  
 CC antibodies which are used to detect PSA in a test sample (claimed). This  
 CC is useful for diagnosis of prostate cancer. The peptides enable the  
 CC production of antisera necessary to determine the amount of total PSA,  
 CC free PSA and PSA-AC complex present in a sample and thus improve the  
 CC ability of the clinician to distinguish, e.g., between BPH (benign  
 CC prostatic hyperplasia) and prostatic cancer in a patient  
 CC  
 XX Sequence 19 AA;  
 SQ

Query Match 30.4%; Score 35; DB 2; Length 19;  
 Best Local Similarity 36.4%; Pred. No. 2e+02;  
 Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;  
 QY 4 HPTNTHKYLVC 14  
 ||:|::|  
 Db 9 HPQKVKFMLC 19

RESULT 26  
 AAY31168  
 ID AAY31168 standard; peptide; 20 AA.  
 XX  
 AC AAY31168;  
 XX  
 DT 28-OCT-1999 (first entry)  
 XX  
 DE Human PSA loop peptide PUS 7.  
 XX

Ubiquitin; immunocastration; fusion protein; heat shock protein; epitope;  
 immune response stimulation; vaccine; T cell; viral; infection; cancer;  
 bacterial; parasitic; treatment; gastrointestinal disease; HIV infection;  
 pulmonary infection; respiratory infection; scaffold; anti-self; p1g;  
 steriodogenesis; gamete maturation; prostate; breast; castration; TNF;  
 tumour necrosis factor; septic shock; arthritis; Crohn's disease;  
 inflammatory bowel disease; ulcerative colitis; choriionic gonadotropin;  
 fertility; sperm protein; growth rate; antibody; detection; PSA; human;  
 prostate specific antigen; loop peptide.  
 XX  
 XX Homo sapiens.  
 OS  
 XX  
 XX WO9942472-A1.  
 PN  
 XX  
 XX 26-AUG-1999.  
 PD  
 XX  
 XX 26-JAN-1999; 99MO-US001588.  
 PF  
 XX  
 XX 19-FEB-1998; 98US-00026276.  
 PR  
 XX  
 XX (IGEN-) IGEN INT INC.  
 PA  
 XX

PI Kenten JH, Tramontano A, Pilon AL, Lohnas GL, Roberts SF;  
 XX WPI; 1999-518582/43.  
 DR  
 XX  
 PT Epitope-containing fusion proteins used to generate a highly specific  
 PT immune responses.  
 XX  
 XX Example 2; Page 38; 67pp; English.  
 PS

This invention describes a novel fusion protein, comprising a heat shock  
 CC protein (e.g. ubiquitin), fused to an epitope(s) in a defined manner  
 CC which is useful for the stimulation of a highly specific immune response  
 CC when administered to an animal. The protein of the invention may be post-  
 CC translationally modified (e.g. by the addition of fatty acids to enhance  
 CC immunogenicity). The fusion proteins of the invention can be used as  
 CC vaccines to induce an immune response. When a T cell epitope is attached,  
 CC they can be used for control of viral infections, bacterial infections,  
 CC parasitic infection and cancer. The fusion proteins can be used in  
 CC pharmaceutical compositions for the treatment of gastrointestinal  
 CC diseases, pulmonary infections, respiratory infections, and HIV  
 CC infections. The use of ubiquitin as a scaffold is also useful for the  
 CC presentation and stimulation of anti-self immune responses, e.g.  
 CC generation of anti-gonadotropin releasing hormone antibodies which result  
 CC in the suppression of luteinizing hormone and follicle stimulating  
 CC hormone. This indirectly suppresses steroidogenesis and gamete maturation  
 CC in males and females. This type of anti-self response in humans is useful  
 CC in the treatment of prostate cancer and breast cancer. In livestock, the  
 CC ability to stimulate an anti-self response provides a simple alternative  
 CC to physical castration. Immunocastration of pigs is a better alternative  
 CC to physical castration, as it does not result in any of the detrimental  
 CC side effects associated with physical castration. Other examples of  
 CC diseases and conditions treated with self proteins fused with ubiquitin  
 CC are TNF and its epitopes to modulate septic shock, arthritis,  
 CC inflammatory bowel disease, Crohn's disease, and ulcerative colitis; Ig  
 CC epsilon heavy chain for the control of allergic reactions; choriionic  
 CC gonadotropin for fertility control; and sperm proteins for fertility  
 CC control. A further use of the fusion proteins is as part of a vaccine to  
 CC enhance growth rate and thereby the final weight of the livestock prior  
 CC to shipment to market. In addition, the fusion proteins of the invention  
 CC can be used to detect and identify antibodies from experimental samples.  
 CC This sequence represents a human prostate specific antigen (PSA) peptide  
 CC loop used in the method of the invention  
 CC  
 XX Sequence 20 AA;  
 SQ

Query Match 30.4%; Score 35; DB 2; Length 20;  
 Best Local Similarity 36.4%; Pred. No. 2.1e+02;  
 Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;  
 QY 4 HPTNTHKYLVC 14  
 ||:|::|  
 Db 7 HPQKVKFMLC 17

RESULT 27  
 AAB71939  
 ID AAB71939 standard; peptide; 20 AA.  
 XX  
 AC AAB71939;  
 XX  
 DT 10-MAY-2001 (first entry)  
 XX  
 DE Ubiquitin fusion protein epitope insertion PUS 7.  
 XX  
 XX  
 XX Human; immunostimulant; antiallergic; growth promoting; vaccine;  
 KW heat shock fusion protein; ubiquitin; self-epitope; immunogen;  
 KW male-specific peptide hormone; female-specific peptide hormone;  
 KW prostate specific antigen; PSA.  
 XX  
 XX Homo sapiens.  
 OS  
 XX  
 XX WO200112216-A1.  
 PN  
 XX

PD 22-FEB-2001.  
 XX  
 PF 14-AUG-2000; 2000WO-US022121.  
 XX  
 FR 13-AUG-1999; 99US-00374721.  
 XX  
 PA (PROT-) PROTEINIX CO.  
 XX  
 PI Kanten JH, Roberts S, Lohas G;  
 XX  
 DR WPI; 2001-202829/20.  
 XX  
 PT Novel fusion proteins for stimulating immune response in animals against  
 PT self-antigen, has heat shock protein fused to single or a group of  
 PT epitope-containing segments having identical or non-identical self  
 PT epitopes.  
 XX  
 PS Example 2; Page 38; 94pp; English.  
 XX  
 CC The present sequence is given in an example illustrating an invention  
 CC disclosing self-epitope-containing heat shock fusion proteins. The  
 CC proteins comprise a heat shock protein, preferably ubiquitin, fused to a  
 CC single epitope-containing segment or two or more non-contiguous epitope  
 CC containing segments, each epitope-containing segment comprising one or  
 CC more identical or non-identical self-epitopes. The heat shock fusion  
 CC proteins are useful for stimulating an immune response in an animal.  
 CC especially a pig, directed towards a self-antigen, in particular a male  
 CC or female-specific peptide hormone. The physiological consequence is  
 CC substantially similar to the consequences of surgical castration. The  
 CC proteins are useful for identifying antibodies in experimental or  
 CC diagnostic samples and for reducing levels of a predetermined endogenous  
 CC protein, such as gonadotropin releasing hormone, tumour necrosis factor  
 CC or growth hormone protein. They are also useful for reducing allergic  
 CC responses and for increasing the growth rate of an animal. The proteins  
 CC have a high specific immune response and do not result in detrimental  
 CC side-effects. The present sequence is an antigenic prostate specific  
 CC antigen (PSA) peptide loop  
 XX  
 SQ Sequence 20 AA;  
 XX  
 QY  
 Query Match 30.4%; Score 35; DB 4; Length 20;  
 Best Local Similarity 36.4%; Pred. No. 2.1e+02;  
 Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;  
 DB 4 HPTNTHKYLVC 14  
 7 HPOKVTKFMLC 17  
 XX  
 RESULT 28  
 ADE70892  
 ID ADE70892 standard; peptide; 15 AA.  
 XX  
 AC ADE70892;  
 XX  
 DT 29-JAN-2004 (first entry)  
 XX  
 DE Human 161P2F10B protein-related peptide 4897.  
 XX  
 KW 161P2F10B; cancer; cytostatic; gene therapy; vaccine; human.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2003040340-A2.  
 XX  
 PD 15-MAY-2003.  
 XX  
 PF 07-NOV-2002; 2002WO-US036002.  
 XX  
 PR 07-NOV-2001; 2001US-00005480.  
 XX  
 PR 31-JAN-2002; 2002US-00062109.  
 XX  
 PA (AGEN-) AGENSYS INC.

XX  
 PI Jakobovits A, Raitano AB, Faris M, Hubert RS, Ge W, Morrison KM;  
 PI Morrison RK, Chalilata-Bid PM;  
 XX  
 DR WPI; 2003-441560/41.  
 XX  
 PT A composition for diagnosing, preventing and treating cancer (e.g.  
 PT prostatic, renal or uterine cancer) comprises 161P2F10B polynucleotides  
 PT and polypeptides.  
 XX  
 PS Claim 13; Page 183; 135pp; English.  
 XX  
 CC This invention relates to a novel composition which comprises a substance  
 CC that modulates the status of a novel human protein (161P2F10B) and its  
 CC variants having a sequence of 875 amino acids provided in the  
 CC specification. The protein of the invention is over-expressed in certain  
 CC cancers. The compounds of the invention may have cytostatic activity and  
 CC the sequence of the 161P2F10B protein, and the gene which encodes it, may  
 CC be useful for gene therapy or the development of a vaccine. The  
 CC composition and methods of the invention are useful in diagnosing,  
 CC preventing and treating cancer. The present sequence is the amino acid  
 CC sequence of a peptide which is derived from the sequence of the human  
 CC 161P2F10B protein and which may be used in the development of the  
 CC compounds of the invention.  
 XX  
 SQ Sequence 15 AA;  
 XX  
 QY  
 Query Match 30.0%; Score 34.5; DB 7; Length 15;  
 Best Local Similarity 50.0%; Pred. No. 1.8e+02;  
 Matches 10; Conservative 1; Mismatches 2; Indels 7; Gaps 2;  
 DB 2 IPH-PTNTHKYLVCESVNGG 20  
 1 IPRPTNV-----RSCFEG 14  
 XX  
 RESULT 29  
 ADE70440  
 ID ADE70440 standard; peptide; 15 AA.  
 XX  
 AC ADE70440;  
 XX  
 DT 29-JAN-2004 (first entry)  
 XX  
 DE Human 161P2F10B protein-related peptide 4445.  
 XX  
 KW 161P2F10B; cancer; cytostatic; gene therapy; vaccine; human.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2003040340-A2.  
 XX  
 PD 15-MAY-2003.  
 XX  
 PF 07-NOV-2002; 2002WO-US036002.  
 XX  
 PR 07-NOV-2001; 2001US-00005480.  
 XX  
 PR 31-JAN-2002; 2002US-00062109.  
 XX  
 PA (AGEN-) AGENSYS INC.  
 XX  
 PI Jakobovits A, Raitano AB, Faris M, Hubert RS, Ge W, Morrison KM;  
 PI Morrison RK, Chalilata-Bid PM;  
 XX  
 DR WPI; 2003-441560/41.  
 XX  
 PT A composition for diagnosing, preventing and treating cancer (e.g.  
 PT prostatic, renal or uterine cancer) comprises 161P2F10B polynucleotides  
 PT and polypeptides.  
 XX  
 PS Claim 13; Page 179; 135pp; English.  
 XX  
 CC This invention relates to a novel composition which comprises a substance

CC that modulates the status of a novel human protein (161P2F10B) and its  
 CC variants having a sequence of 875 amino acids provided in the  
 CC specification. The protein of the invention is over-expressed in certain  
 CC cancers. The compounds of the invention may have cytostatic activity and  
 CC be useful for gene therapy or the development of a vaccine. The  
 CC composition and method of the invention are useful in diagnosing,  
 CC preventing and treating cancer. The present sequence is the amino acid  
 CC sequence of a peptide which is derived from the sequence of the human  
 CC 161P2F10B protein and which may be used in the development of the  
 CC compounds of the invention.

CC Sequence 15 AA;

Query Match 30.0%; Score 34.5; DB 7; Length 15;  
 Best Local Similarity 50.0%; Pred. No. 1.8e+02;  
 Matches 10; Conservative 1; Mismatches 2; Indels 7; Gaps 2;

QY 2 IPR-PTNHHKYLVCESVNGG 20  
 ||| |||:  
 1 IPRHPTNV-----ESCPCG 14

RESULT 30

ADN08675  
 ID ADN08675 standard; peptide; 12 AA.

AC ADN08675;

DT 15-JUL-2004 (first entry)

XX Cotton wine stain binding peptide, SEQ ID No 240.

KW tannin; polyphenolic; anthocyanin; tea; wine; stain; fabric; surface;  
 KM enzymatic; ceramic; hair; skin; detergent; cleaning; wine ageing;  
 KM fermentation; reducing; eliminating; astringency; conjugate; bleaching;  
 KM personal care product; cream; lotion; ointment.

XX Unidentified.

PN WO2004033482-A2.

PD 22-APR-2004.

PF 06-OCT-2003; 2003WO-US031776.

PR 08-OCT-2002; 2002US-0417210P.

XX (GENV ) GENENCOR INT INC.

PI Murray CJ, Tijerina P, Van Gaestel FJC,

XX WPI; 2004-340885/31.

PT Novel binding peptide binding to tannin, anthocyanin and phenolic  
 PT compounds, useful for delivering agent to target, and for modifying tea  
 PT or wine stain on fabric or surface chosen from ceramic, glasses, wood,  
 PT paper, skin, hair and plastic.

PS Claim 1; SEQ ID NO 240; 38pp; English.

CC The invention relates to a novel peptide which binds to tannin,  
 CC polyphenolic or anthocyanin compounds. The binding peptide consists  
 CC essentially of any one of 316 amino acid sequences of 5-13 amino acids in  
 CC length or has at least 70% identity to one of the 316 amino acid  
 CC sequences. The binding peptide is useful for delivering an agent to a  
 CC target, which involves conjugating the binding peptide to an agent to  
 CC form a binding peptide conjugate and exposing a target to the binding  
 CC peptide conjugate, where the binding peptide conjugate binds to the  
 CC target. An enzymatic composition comprising the binding peptide is useful  
 CC for modifying a tea or wine stain on a fabric or a surface, which  
 CC involves contacting the surface having tea or wine stain with the  
 CC enzymatic composition. The surface is preferably a ceramic surface, hair

CC or skin. The binding peptide is useful for producing enzymatic  
 CC compositions for use in detergent or cleaning compositions such as for  
 CC removing food stains on fabrics or removing food stains on surfaces such  
 CC as ceramic and teeth. The binding peptide is useful in the wine ageing  
 CC process, where a tannin compound is targeted at the early stage of wine  
 CC fermentation process for reducing or eliminating astringency of tannins  
 CC in the wine. The binding conjugate, combined with a bleaching agent is  
 CC useful for delivering a bleaching agent to stained teeth for bleaching.  
 CC The binding peptide and binding conjugate are useful in personal care  
 CC products such as creams, lotions and ointments. The binding peptide is  
 CC useful for modifying astringency in skin. This sequence represents a  
 CC binding peptide which specifically binds to wine stains on cotton for use  
 CC in the stain removal process of the invention.

CC Sequence 12 AA;

Query Match 29.6%; Score 34; DB 8; Length 12;  
 Best Local Similarity 50.0%; Pred. No. 1.7e+02;  
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 IPRPTNHH 9  
 :|||:|  
 2 MPHATVH 9

RESULT 31

ABR47248  
 ID ABR47248 standard; peptide; 10 AA.

AC ABR47248;

DT 10-JUN-2003 (first entry)

XX Staphylococcus aureus CHIPS-related peptide #2437.

KW CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; C5AR;  
 KM formulated peptide; receptor; FPR; neutrophil; monocyte; endothelial cell;  
 KM inflammation; cardiovascular disease; central nervous system disease;  
 KM gastrointestinal disease; skin disease; genitourinary disease;  
 KM joint disease; respiratory disease; HIV infection; anti-inflammatory;  
 KM cardiac; cerebroprotective; neuroprotective; nootropic; dermatological;  
 KM synecological; immunosuppressive; anti-HIV.

XX Staphylococcus aureus.

OS Synthetic.

XX WO2003006048-A1.

PD 23-JAN-2003.

PF 11-JUL-2001; 2001WO-EP008004.

PR 11-JUL-2001; 2001WO-EP008004.

XX (JARI-) JARI PHARM BV.

PI Van Kessel CPM, Gosselaar-De Haas CJC, Kruijtz JAW;

XX Van Strijp JAG;

XX WPI; 2003-256333/25.

PT Combination of peptides derived from chemotaxis inhibiting protein from  
 PT Staphylococcus aureus (CHIPS) having CHIPS activity, useful in  
 PT prophylaxis and treatment of inflammation, cardiovascular, skin and  
 PT kidney diseases.

PS Example 1; Page 56; 89pp; English.

CC The present invention relates to peptides (ABR44811-ABR47162 and ABR47164  
 CC -ABR4735) derived from the Chemotaxis Inhibitory Protein (CHIPS) from  
 CC Staphylococcus aureus. The peptide fragments are useful in the  
 CC prophylaxis or treatment of diseases or disorders involving the C5a-  
 CC receptor (C5aR) and/or formulated peptide receptor (FPR) or neutrophils,

CC monocytes and endothelial cells or involving acute or chronic  
 CC inflammation reactions. The diseases or disorders include cardiovascular  
 CC disease, disease of the central nervous system, gastrointestinal  
 CC diseases, skin diseases, genitourinary diseases, joint diseases,  
 CC respiratory diseases and HIV infection

XX  
 SQ Sequence 10 AA;

Query Match 28.7%; Score 33; DB 6; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 2e+02; Indels 0; Gaps 0;  
 Matches 5; Conservative 0; Mismatches 0;

QY 3 PPTN 7  
 |||||  
 DB 5 PPTN 9

RESULT 32  
 ADY92058  
 ID ADY92058 standard; peptide; 10 AA.

XX  
 AC ADY92058;  
 XX  
 DT 02-JUN-2005 (first entry)

DE Human tumor-associated antigen LDHC MHC I epitope peptide - SEQ ID 378.

XX tumor-associated antigen, LDHC; lactate dehydrogenase C; gene expression;  
 KM cell death; cell growth; tumor; cancer; neoplasm; cytostatic.

OS Homo sapiens.

PN WO2005026205-A2.

XX 24-MAR-2005.

XX 10-SEP-2004; 2004WO-EP010164.

XX 10-SEP-2003; 2003DE-01041812.

XX (GANY-) GANYMED PHARM AG.

XX Theredi O, Sahlin U, Koslowski M;

XX MPI; 2005-242374/25.

PT Pharmaceutical composition, with an agent to restrict the expression or  
 PT activity of an antigen associated with a tumor, incorporates structured  
 PT nucleic acids.

PS Disclosure; SEQ ID NO 378; 353pp; German.

XX The invention relates to a novel pharmaceutical composition, whereby the  
 CC composition contains an agent which restricts the expression or activity  
 CC of an antigen associated with a tumor and the antigen has a sequence,  
 CC coded by a nucleic acid, where the nucleic acid is selected from SEQ ID  
 CC NOS: 19-21, 54-57, 1-5, 29, 31-33, 37, 39, 40, 62, 63, 70, 74 or 85-88.  
 CC The composition of the invention induces cell death and a reduction of  
 CC cell growth, cell membrane damage or secretion of cytokines. The  
 CC composition may be useful for the identification of differentially  
 CC expressed genes in tumors with combined in silico and wet bench studies.  
 CC The current sequence is that of a human tumor-associated antigen lactate  
 CC dehydrogenase C (LDHC) MHC class I HLA-B\*0702 epitope peptide of the  
 CC invention which stimulates cytotoxic T-lymphocytes in vivo.

XX  
 SQ Sequence 10 AA;

Query Match 28.7%; Score 33; DB 9; Length 10;  
 Best Local Similarity 40.0%; Pred. No. 2e+02; Indels 0; Gaps 0;  
 Matches 4; Conservative 4; Mismatches 2;

QY 4 HPTNKHV 13  
 |||||

DB 1 HPTSGHWII 10

RESULT 33  
 ADX70566  
 ID ADX70566 standard; peptide; 20 AA.

XX  
 AC ADX70566;

XX  
 DT 05-MAY-2005 (first entry)

DE Vaccinia BSR ectodomain peptide, BSR pep#10.

XX vaccine; pox virus infection; virucide; infection;  
 KM variola virus infection; BSR.

XX Vaccinia virus.

OS  
 XX WO2005013918-A2.

XX 17-FEB-2005.

XX 27-FEB-2004; 2004WO-US005903.

XX 28-FEB-2003; 2003US-0451337P.

XX (UNPR-) UNIV PENNSYLVANIA.

PA (NAME-) NAT INST OF HEALTH JAPAN.

PA (COHE/) COHEN G.

PA (EISE/) EISENBERG R J.

PA (WHIT/) WHITEBECK J C.

PA (ALDA/) ALDAR C L.

PA (MOSS/) MOSS B.

PA (LUST/) LUSTIG S.

PA (FOGG/) FOGG C.

XX MPI; 2005-152502/16.

XX

PT New vaccine having a soluble truncated mammalian poxvirus envelope

PT protein or an isolated nucleic acid encoding the protein, useful for

PT preventing and treating a poxvirus infection, in particular a smallpox

PT infection.

XX Example 4; SEQ ID NO 16; 16pp; English.

XX

PS The invention relates to a vaccine comprising a soluble truncated

CC mammalian poxvirus envelope protein or an isolated nucleic acid encoding

CC the protein, and a carrier, where the protein is at least one protein

CC selected from A33Rc, B5Rc, and L1R(185c), or its homolog. The methods and

CC compositions of the present invention are useful for preventing and

CC treating a poxvirus infection, in particular a smallpox infection. The

CC present sequence represents a vaccinia BSR ectodomain peptide.

XX  
 SQ Sequence 20 AA;

Query Match 28.7%; Score 33; DB 9; Length 20;  
 Best Local Similarity 60.0%; Pred. No. 4.5e+02; Indels 0; Gaps 0;  
 Matches 6; Conservative 0; Mismatches 4;

QY 10 KYLVCESVNG 19  
 |||||  
 DB 6 KYFRCEKNG 15

RESULT 34

AAV38258  
 ID AAV38258 standard; peptide; 10 AA.

XX  
 AC AAV38258;

XX 29-SEP-1999 (first entry)

DT HIV-derived HLA-binding peptide.  
 XX



XX Immunogen; HLA; human leukocyte antigen; binding motif; antiviral; MHC;  
 KM major histocompatibility complex; viral infection; anticancer;  
 KM prostate cancer; lymphoma; hepatitis; AIDS; diagnostic; diagnosis.  
 XX Human immunodeficiency virus.  
 XX MO9403205-A1.  
 XX 17-FEB-1994.  
 XX 06-AUG-1993; 93MO-US007421.  
 XX 07-AUG-1992; 92US-00926666.  
 PR 05-MAR-1993; 93US-00027746.  
 XX (CYTE-) CYTEL CORP.  
 PA Kudo RT, Grey HM, Sette A, Cells E;  
 PI WPI, 1994-065403/08.  
 DR Peptide which specifically binds selected MHC allele - used to induce an  
 PT immune response for treatment or prevention of viral infection or cancer,  
 PT or for diagnosis.  
 XX Disclosure, Page 110, 150pp; English.  
 XX The sequence is a specific example of a group of new immunogenic peptides  
 CC having an HLA-A3.2, HLA-A1, HLA-A11 or HLA-A24.1 binding motif. For  
 CC example, the peptides having an HLA-A3.2 binding motif each have 9-10  
 CC residues and contain, from the N-terminus to the C-terminus, (a) a first  
 CC conserved residue selected from L, M, I, V, S, A, T, F, C, G, D and E and  
 CC (b) a second conserved residue of K, R, Y, H or F, where the first and  
 CC second conserved residues are separated by 6-7 residues. The peptides are  
 CC capable of binding selected MHC molecules and inducing an immune  
 CC response. They can be used to treat and/or prevent viral infection and  
 CC cancer, e.g. prostate cancer, lymphoma, hepatitis or AIDS. They can also  
 CC be used to produce antibodies for use as diagnostic or therapeutic  
 CC agents. The peptides can also be used as diagnostic agents  
 CC  
 SQ Sequence 10 AA;  
 Query Match 27.8%; Score 32; DB 2; Length 10;  
 Best Local Similarity 55.6%; Pred. No. 2.9e+02;  
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
 Oy 2 IPHPTNIHK 10  
 ||||| : |  
 Db 2 IPHPAGLKK 10  
 RESULT 35  
 ID AAY45830  
 XX AAY45830 standard; peptide; 10 AA.  
 AC AAY45830;  
 XX 01-DEC-1999 (first entry)  
 DT Immunogenic peptide having a human leukocyte antigen binding motif #441.  
 XX Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA;  
 KM immune response; T cell activation; major histocompatibility complex;  
 KM cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer;  
 KM prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;  
 KM vaccine; immunisation.  
 XX Synthetic.  
 OS Homo sapiens.  
 XX MO9445954-A1.  
 XX

PD 16-SEP-1999.  
 XX 13-MAR-1998; 98MO-US005039.  
 XX 13-MAR-1998; 98MO-US005039.  
 PR (BPIW-) BPIW INC.  
 PA Sette A, Kudo RT, Sidney J, Cells E, Grey HM, Southwood S;  
 PI WPI, 1999-551214/46.  
 DR New immunogenic peptides with HLA binding motif, useful in treatment and  
 PT diagnosis of cancers and viral diseases.  
 XX Claim 1; Page 44; 150pp; English.  
 XX AAY45390 to AAY48214 represent specifically claimed immunogenic peptides  
 CC having a human major histocompatibility complex (MHC) Class I (also known  
 CC as human leukocyte antigen (HLA)) binding motif. The immunogenic peptides  
 CC can bind to a specific HLA allele (i.e. HLA-A subtypes HLA-A2.1, A1, A3.2  
 CC or A24.1 or HLA-B or C) and induce a cytotoxic T cell response against  
 CC the antigen from which the peptide is derived. Cytotoxic T lymphocytes  
 CC (CTLs) which destroy antigen-bearing cells are normally induced by an  
 CC antigen in the form of a peptide fragment bound to a HLA molecule, rather  
 CC than the intact foreign antigen itself, and are particularly important in  
 CC tumour rejection and in fighting viral infections. The peptides are  
 CC therefore useful therapeutically to treat or prevent viral infections and  
 CC cancers in mammals (especially humans) e.g. prostate cancer, hepatitis B  
 CC and C, AIDS, and renal carcinoma. They can be administered as vaccines to  
 CC elicit an immune response in individuals susceptible or otherwise at risk  
 CC of viral infection or cancer, or used to treat chronic or acute  
 CC conditions. They are also useful diagnostically, and can be used to  
 CC induce a cytotoxic T cell response, by contacting a cytotoxic T cell with  
 CC the peptide e.g. to produce CTLs ex vivo for infusion back into a  
 CC patient. The polypeptides encoding the immunogenic peptides are also  
 CC useful therapeutically and for immunisation as above  
 CC  
 SQ Sequence 10 AA;  
 Query Match 27.8%; Score 32; DB 2; Length 10;  
 Best Local Similarity 55.6%; Pred. No. 2.9e+02;  
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
 Oy 2 IPHPTNIHK 10  
 ||||| : |  
 Db 2 IPHPAGLKK 10  
 RESULT 36  
 ID ABP14809  
 XX ABP14809 standard; peptide; 10 AA.  
 AC ABP14809;  
 XX 11-SEP-2003 (revised)  
 DT 15-JUL-2002 (first entry)  
 XX HIV A03 super motif pol peptide #183.  
 XX HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu;  
 KM vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen;  
 KM vaccine; HIV infection; immunisation; virucide.  
 OS Human immunodeficiency virus 1.  
 XX MO200124810-A1.  
 XX 12-APR-2001.  
 PD 05-OCT-2000; 2000MO-US027766.  
 PF 05-OCT-1999; 99US-00412863.  
 PR

XX (EPIM-) EPIMUNE INC.  
 XX  
 XX Sette A, Sidney J, Southwood S, Livingston BD, Cheesnut R;  
 PI Baker DM, Celis E, Kubo RT, Grey HM;  
 XX  
 XX WPI; 2001-354887/37.  
 DR  
 XX  
 PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)  
 PT peptide groups, useful for vaccinating against HIV-1.  
 XX  
 XX Claim 32; Page 171; 448pp; English.  
 PS  
 XX  
 CC The present invention describes a composition (I) comprising a prepared  
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid  
 CC sequence selected from 51 defined amino acid sequences (ABL25347 to  
 CC ABP25397). (I) has virucide activity and can be used in vaccines. (I) may  
 CC be used for immunising subjects against HIV-1 infections. The use of  
 CC group-based vaccines has several advantages over traditional vaccines,  
 CC particularly when compared to the use of whole antigens in vaccine  
 CC compositions. There is evidence that the immune response to whole  
 CC antigens is directed largely toward variable regions of the antigen,  
 CC allowing for immune escape due to mutations. The groups for inclusion in  
 CC an group-based vaccine may be selected from conserved regions of viral or  
 CC tumour-associated antigens, which therefore reduces the likelihood of  
 CC escape mutants. Furthermore, immunosuppressive groups that may be present  
 CC in whole antigens can be avoided with the use of group-based vaccines. An  
 CC additional advantage of an group-based vaccine approach is the ability to  
 CC combine selected groups (CTL and HTL), and further, to modify the  
 CC composition of the groups, achieving, for example, enhanced  
 CC immunogenicity. Accordingly, the immune response can be modulated, as  
 CC appropriate, for the target disease. Similar engineering of the response  
 CC is not possible with traditional approaches. ABP1501 to ABP25412  
 CC represent peptide sequences used in the exemplification of the present  
 CC invention. (Updated on 11-SEP-2003 to standardise OS field)  
 CC  
 XX  
 SQ Sequence 10 AA;  
 XX  
 Query Match 27.8%; Score 32; DB 4; Length 10;  
 Best Local Similarity 55.6%; Pred. No. 2.9e+02;  
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
 QY 2 IPHPTNIHK 10  
 DB 2 IPHPAGLKK 10  
 XX  
 RESULT 37  
 ABJ15141  
 ID ABJ15141 standard; peptide; 10 AA.  
 XX  
 AC ABJ15141;  
 XX  
 DT 02-JAN-2003 (first entry)  
 XX  
 DB Immunogenic HIV peptide #1.  
 XX  
 KM HIV; gene therapy; vaccine; immunogenic HIV peptide;  
 KM cytotoxic T lymphocyte; HIV infection.  
 XX  
 OS Human immunodeficiency virus.  
 OS  
 PN WO200269691-A2.  
 XX  
 PD 12-SEP-2002.  
 XX  
 PP 01-MAR-2002; 2002WO-US006314.  
 XX  
 PR 01-MAR-2001; 2001US-0272565P.  
 XX  
 PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 PA (UYBR-) UNIV BROWN RES FOUND.  
 XX

PI Menicholl JM, Bond K, Sriwanthana B, Pau C, Degroot A;  
 XX  
 DR WPI; 2002-750429/81.  
 XX  
 PT New immunogenic HIV peptide having one or more epitopes immunoreactive  
 PT with cytotoxic T lymphocytes, useful for diagnosing, treating and  
 PT monitoring HIV infection in humans.  
 XX  
 XX  
 PS Claim 6; Page 42; 65pp; English.  
 XX  
 CC The invention comprises immunogenic HIV peptides which contain one or  
 CC more epitopes that are immunoreactive with cytotoxic T lymphocytes from  
 CC an HIV-positive individual. The immunogenic HIV peptides of the invention  
 CC are useful for diagnosing, treating and monitoring HIV infection. The  
 CC present amino acid sequence represents an immunogenic HIV peptide of the  
 CC invention  
 CC  
 XX  
 SQ Sequence 10 AA;  
 XX  
 Query Match 27.8%; Score 32; DB 5; Length 10;  
 Best Local Similarity 55.6%; Pred. No. 2.9e+02;  
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
 QY 2 IPHPTNIHK 10  
 DB 2 IPHPAGLKK 10  
 XX  
 RESULT 38  
 ABJ15176  
 ID ABJ15176 standard; peptide; 10 AA.  
 XX  
 AC ABJ15176;  
 XX  
 DT 02-JAN-2003 (first entry)  
 XX  
 DE Immunogenic HIV peptide #36.  
 XX  
 KM HIV; gene therapy; vaccine; immunogenic HIV peptide;  
 KM cytotoxic T lymphocyte; HIV infection.  
 XX  
 OS Human immunodeficiency virus.  
 OS  
 PN WO200269691-A2.  
 XX  
 PD 12-SEP-2002.  
 XX  
 PP 01-MAR-2002; 2002WO-US006314.  
 XX  
 PR 01-MAR-2001; 2001US-0272565P.  
 XX  
 PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 PA (UYBR-) UNIV BROWN RES FOUND.  
 XX  
 PI Menicholl JM, Bond K, Sriwanthana B, Pau C, Degroot A;  
 XX  
 DR WPI; 2002-750429/81.  
 XX  
 PT New immunogenic HIV peptide having one or more epitopes immunoreactive  
 PT with cytotoxic T lymphocytes, useful for diagnosing, treating and  
 PT monitoring HIV infection in humans.  
 XX  
 XX  
 PS Claim 6; Page 43; 65pp; English.  
 XX  
 CC The invention comprises immunogenic HIV peptides which contain one or  
 CC more epitopes that are immunoreactive with cytotoxic T lymphocytes from  
 CC an HIV-positive individual. The immunogenic HIV peptides of the invention  
 CC are useful for diagnosing, treating and monitoring HIV infection. The  
 CC present amino acid sequence represents an immunogenic HIV peptide of the  
 CC invention  
 CC  
 XX  
 SQ Sequence 10 AA;  
 XX

Query Match 27.8%; Score 32; DB 5; Length 10;  
 Best Local Similarity 55.6%; Pred. No. 2.9e+02;  
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 IHPPTNIHK 10  
 ||||| :  
 DB 1 IHPHAGLKK 9

## RESULT 39

ABU070353  
 ID ABU070353 standard; peptide; 10 AA.

XX ABU070353;  
 XX

DT 23-OCT-2003 (revised)  
 DT 05-JUN-2003 (first entry)

XX Human immunodeficiency virus 1 (HIV1) vaccine candidate peptide #671.

XX KM Human immunodeficiency virus; HIV; vaccine; immunological excipient;  
 KM anti-HIV immune response; T cell response;  
 KW viral multiplication inhibitor; chronic viraemia; AIDS.

XX Human immunodeficiency virus 1.

OS US2002182222-A1.

XX PD 05-DEC-2002.

XX PF 26-OCT-2001; 2001US-00055524.

XX PR 10-JUL-1998; 98US-0092346P.

XX PR 08-JAN-1999; 99US-0115145P.

XX PR 23-APR-1999; 99US-0130677P.

XX PR 09-JUL-1999; 99US-00351036.

XX PA (GROO/) GROOT A D.

XX PI Groot AD;

XX DR WPI; 2003-352642/33.

XX PT New vaccine comprising human immunodeficiency virus (HIV) vaccine  
 PT candidate peptides, useful as antigens for raising anti-HIV immune  
 PT responses, such as T cell responses, and for inducing antibodies and  
 PT impairing viral multiplication.

XX PS Claim 1; Fig 9; 32pp; English.

XX CC The invention describes a vaccine comprising a human immunodeficiency  
 CC virus (HIV) vaccine candidate peptide containing an amino acid sequence  
 CC selected from 669 amino acid sequences given in the specification, in an  
 CC immunological excipient. The HIV vaccine peptides are useful as antigens  
 CC for raising anti-HIV immune responses, such as T cell responses, and for  
 CC inducing antibodies that react with HIV-1 and impairing viral  
 CC multiplication in vivo. These antibodies reduce viral multiplication  
 CC during any initial acute infection with HIV-1 and minimise chronic  
 CC viraemia or progression leading to AIDS. This is the amino acid sequence  
 CC of a human immunodeficiency virus 1 (HIV1) vaccine candidate peptide.  
 CC (Updated on 23-OCT-2003 to standardise OS field)

XX SQ Sequence 10 AA;

Query Match 27.8%; Score 32; DB 6; Length 10;

Best Local Similarity 55.6%; Pred. No. 2.9e+02;  
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 IHPPTNIHK 10  
 ||||| :  
 DB 2 IHPHAGLKK 10

RESULT 40  
 ABU69777  
 ID ABU69777 standard; peptide; 10 AA.

XX ABU69777;  
 XX

DT 23-OCT-2003 (revised)  
 DT 05-JUN-2003 (first entry)

XX Human immunodeficiency virus 1 (HIV1) vaccine candidate peptide #95.

XX KM Human immunodeficiency virus; HIV; vaccine; immunological excipient;  
 KM anti-HIV immune response; T cell response;  
 KW viral multiplication inhibitor; chronic viraemia; AIDS.

XX Human immunodeficiency virus 1.

OS US2002182222-A1.

XX PD 05-DEC-2002.

XX PF 26-OCT-2001; 2001US-00055524.

XX PR 10-JUL-1998; 98US-0092346P.

XX PR 08-JAN-1999; 99US-0115145P.

XX PR 23-APR-1999; 99US-0130677P.

XX PR 09-JUL-1999; 99US-00351036.

XX PA (GROO/) GROOT A D.

XX PI Groot AD;

XX DR WPI; 2003-352642/33.

XX PT New vaccine comprising human immunodeficiency virus (HIV) vaccine  
 PT candidate peptides, useful as antigens for raising anti-HIV immune  
 PT responses, such as T cell responses, and for inducing antibodies and  
 PT impairing viral multiplication.

XX PS Claim 1; Page 13; 32pp; English.

XX CC The invention describes a vaccine comprising a human immunodeficiency  
 CC virus (HIV) vaccine candidate peptide containing an amino acid sequence  
 CC selected from 669 amino acid sequences given in the specification, in an  
 CC immunological excipient. The HIV vaccine peptides are useful as antigens  
 CC for raising anti-HIV immune responses, such as T cell responses, and for  
 CC inducing antibodies that react with HIV-1 and impairing viral  
 CC multiplication in vivo. These antibodies reduce viral multiplication  
 CC during any initial acute infection with HIV-1 and minimise chronic  
 CC viraemia or progression leading to AIDS. This is the amino acid sequence  
 CC of a human immunodeficiency virus 1 (HIV1) vaccine candidate peptide.  
 CC (Updated on 23-OCT-2003 to standardise OS field)

XX SQ Sequence 10 AA;

Query Match 27.8%; Score 32; DB 6; Length 10;

Best Local Similarity 55.6%; Pred. No. 2.9e+02;  
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 IHPPTNIHK 10  
 ||||| :  
 DB 2 IHPHAGLKK 10

## RESULT 41

ABU69799  
 ID ABU69799 standard; peptide; 10 AA.

XX ABU69799;  
 XX

DT 23-OCT-2003 (revised)  
 DT 05-JUN-2003 (first entry)

XX

DE Human immunodeficiency virus 1 (HIV1) vaccine candidate peptide #117.  
 XX  
 XX Human immunodeficiency virus; HIV; vaccine; immunological excipient;  
 KW anti-HIV immune response; T cell response;  
 KW viral multiplication inhibitor; chronic viraemia; AIDS.  
 XX  
 OS Human immunodeficiency virus 1.  
 XX  
 PN US2002182222-A1.  
 PD  
 XX 05-DEC-2002.  
 PD  
 XX  
 PF 26-OCT-2001; 2001US-00055524.  
 XX  
 XX 10-JUL-1998; 98US-0092346P.  
 PR 08-JAN-1999; 99US-0115145P.  
 PR 23-APR-1999; 99US-0130677P.  
 PR 09-JUL-1999; 99US-00351036.  
 XX  
 PA (GROO/) GROOT A D.  
 XX  
 PI Groot AD;  
 XX  
 DR WPI; 2003-352642/33.  
 XX  
 PT New vaccine comprising human immunodeficiency virus (HIV) vaccine  
 PT candidate peptides, useful as antigens for raising anti-HIV immune  
 PT responses, such as T cell responses, and for inducing antibodies and  
 PT impairing viral multiplication.  
 XX  
 XX Claim 1; Page 14; 32pp; English.  
 XX  
 CC The invention describes a vaccine comprising a human immunodeficiency  
 CC virus (HIV) vaccine candidate peptide containing an amino acid sequence  
 CC selected from 669 amino acid sequences given in the specification, in an  
 CC immunological excipient. The HIV vaccine peptides are useful as antigens  
 CC for raising anti-HIV immune responses, such as T cell responses, and for  
 CC inducing antibodies that react with HIV-1 and impairing viral  
 CC multiplication in vivo. These antibodies reduce viral multiplication  
 CC during any initial acute infection with HIV-1 and minimise chronic  
 CC viraemia or progression leading to AIDS. This is the amino acid sequence  
 CC of a human immunodeficiency virus 1 (HIV1) vaccine candidate peptide.  
 CC (Updated on 23-OCT-2003 to standardise OS field)  
 XX  
 SQ Sequence 10 AA;  
 XX  
 XX  
 Query Match 27.8%; Score 32; DB 6; Length 10;  
 Best Local Similarity 55.6%; Pred. No. 2.9e+02;  
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
 QY 2 IPHPTNIHK 10  
 ||||| : |  
 Db 2 IPHPAGLKK 10  
 XX  
 RESULT 42  
 ABU69801  
 ID ABU69801 standard; peptide; 10 AA.  
 XX  
 AC ABU69801;  
 XX  
 DT 23-OCT-2003 (revised)  
 DT 05-JUN-2003 (first entry)  
 XX  
 DE Human immunodeficiency virus 1 (HIV1) vaccine candidate peptide #119.  
 XX  
 XX Human immunodeficiency virus; HIV; vaccine; immunological excipient;  
 KW anti-HIV immune response; T cell response;  
 KW viral multiplication inhibitor; chronic viraemia; AIDS.  
 XX  
 OS Human immunodeficiency virus 1.  
 XX  
 PN US2002182222-A1.

XX  
 PD 05-DEC-2002.  
 PD  
 XX 26-OCT-2001; 2001US-00055524.  
 PF  
 XX 10-JUL-1998; 98US-0092346P.  
 PR 08-JAN-1999; 99US-0115145P.  
 PR 23-APR-1999; 99US-0130677P.  
 PR 09-JUL-1999; 99US-00351036.  
 XX  
 PA (GROO/) GROOT A D.  
 XX  
 PI Groot AD;  
 XX  
 DR WPI; 2003-352642/33.  
 XX  
 PT New vaccine comprising human immunodeficiency virus (HIV) vaccine  
 PT candidate peptides, useful as antigens for raising anti-HIV immune  
 PT responses, such as T cell responses, and for inducing antibodies and  
 PT impairing viral multiplication.  
 XX  
 XX Claim 1; Page 14; 32pp; English.  
 XX  
 CC The invention describes a vaccine comprising a human immunodeficiency  
 CC virus (HIV) vaccine candidate peptide containing an amino acid sequence  
 CC selected from 669 amino acid sequences given in the specification, in an  
 CC immunological excipient. The HIV vaccine peptides are useful as antigens  
 CC for raising anti-HIV immune responses, such as T cell responses, and for  
 CC inducing antibodies that react with HIV-1 and impairing viral  
 CC multiplication in vivo. These antibodies reduce viral multiplication  
 CC during any initial acute infection with HIV-1 and minimise chronic  
 CC viraemia or progression leading to AIDS. This is the amino acid sequence  
 CC of a human immunodeficiency virus 1 (HIV1) vaccine candidate peptide.  
 CC (Updated on 23-OCT-2003 to standardise OS field)  
 XX  
 SQ Sequence 10 AA;  
 XX  
 XX  
 Query Match 27.8%; Score 32; DB 6; Length 10;  
 Best Local Similarity 55.6%; Pred. No. 2.9e+02;  
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
 QY 2 IPHPTNIHK 10  
 ||||| : |  
 Db 1 IPHPAGLKK 9  
 XX  
 RESULT 43  
 ABU69729  
 ID ABU69729 standard; peptide; 10 AA.  
 XX  
 AC ABU69729;  
 XX  
 DT 23-OCT-2003 (revised)  
 DT 05-JUN-2003 (first entry)  
 XX  
 DE Human immunodeficiency virus 1 (HIV1) vaccine candidate peptide #47.  
 XX  
 XX Human immunodeficiency virus; HIV; vaccine; immunological excipient;  
 KW anti-HIV immune response; T cell response;  
 KW viral multiplication inhibitor; chronic viraemia; AIDS.  
 XX  
 OS Human immunodeficiency virus 1.  
 XX  
 PN US2002182222-A1.  
 PD  
 XX 05-DEC-2002.  
 PD  
 XX 26-OCT-2001; 2001US-00055524.  
 PF  
 XX 10-JUL-1998; 98US-0092346P.  
 PR 08-JAN-1999; 99US-0115145P.  
 PR 23-APR-1999; 99US-0130677P.  
 PR 09-JUL-1999; 99US-00351036.

XX (GROO/) GROOT A D.  
 PA Groot AD,  
 XX WPI; 2003-352642/33.  
 DR  
 XX New vaccine comprising human immunodeficiency virus (HIV) vaccine  
 PT candidate peptides, useful as antigens for raising anti-HIV immune  
 PT responses, such as T cell responses, and for inducing antibodies and  
 PT impacting viral multiplication.  
 XX  
 PS Claim 1; Page 13; 32pp; English.  
 XX  
 CC The invention describes a vaccine comprising a human immunodeficiency  
 CC virus (HIV) vaccine candidate peptide containing an amino acid sequence  
 CC selected from 669 amino acid sequences given in the specification, in an  
 CC immunological excipient. The HIV vaccine peptides are useful as antigens  
 CC for raising anti-HIV immune responses, such as T cell responses, and for  
 CC inducing antibodies that react with HIV-1 and impacting viral  
 CC multiplication in vivo. These antibodies reduce viral multiplication  
 CC during any initial acute infection with HIV-1 and minimise chronic  
 CC viraemia or progression leading to AIDS. This is the amino acid sequence  
 CC of a human immunodeficiency virus 1 (HIV1) vaccine candidate peptide.  
 CC (Updated on 23-OCT-2003 to standardise OS field)  
 XX  
 SQ Sequence 10 AA;  
 SO  
 Query Match 27.8%; Score 32; DB 6; Length 10;  
 Best Local Similarity 55.6%; Pred. No. 2.9e+02;  
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
 QY 2 IPHPNTNKH 10  
 Db 1 IPHPAGLKK 9  
 RESULT 44  
 ADD96334  
 ID ADD96334 standard; peptide; 10 AA.  
 AC ADD96334;  
 XX  
 DT 29-JAN-2004 (first entry)  
 XX  
 DE HIV-1 cross-clade candidate peptide #119.  
 XX  
 KW HIV-1; cross-clade candidate peptide; HIV clade;  
 KM major histocompatibility complex; MHC; human leukocyte antigen; HLA;  
 KM T-cell activation; HIV positive patient; HIV infection; anti-HIV.  
 XX  
 OS Human immunodeficiency virus 1.  
 PN US2003180314-A1.  
 XX  
 PD 25-SEP-2003.  
 XX  
 PF 22-JUL-2002; 2002US-00200708.  
 XX  
 PR 10-JUL-1998; 98US-0092346P.  
 PR 08-JAN-1999; 99US-0115145P.  
 PR 23-APR-1999; 99US-0130677P.  
 PR 09-JUL-1999; 99US-00351036.  
 XX  
 PA (DEGR/) DEGROOT A.  
 PI Degroot A;  
 XX  
 DR WPI; 2003-852210/79.  
 XX  
 PT New cross-clade HIV candidate peptide that binds a human major  
 PT histocompatibility complex binding matrix motif or activates T-cells from  
 PT HIV positive patients, useful for preventing or treating HIV infection.

XX Example 3; SEQ ID NO 119; 146pp; English.  
 PS  
 XX The present invention relates to HIV-1 cross-clade candidate peptides  
 CC comprising a sequence of about 8-50 amino acids, the sequence having  
 CC complete, sequential sequence identity with a partial HIV-1 amino acid  
 CC sequence that is absolutely conserved across at least 2 clades of HIV.  
 CC The HIV-1 cross-clade candidate peptides possess at least one of the  
 CC biological properties selected from (i) the ability to bind a human MHC  
 CC histocompatibility complex (MHC) binding matrix motif for a human MHC  
 CC allele, (ii) the ability to bind MHC human leukocyte antigen (HLA) in the  
 CC T2 in vitro peptide binding assay, and (iii) the ability to activate T-  
 CC cells from HIV positive patients in at least one in vitro assay. The  
 CC invention also discloses a pharmaceutical composition comprising the  
 CC above peptide, and methods for the production and use of the cross-clade  
 CC peptides. The composition and methods are useful in preventing or  
 CC treating HIV infection. The present sequence represents a HIV-1 cross-  
 CC clade candidate peptide.  
 XX  
 SQ Sequence 10 AA;  
 SO  
 Query Match 27.8%; Score 32; DB 7; Length 10;  
 Best Local Similarity 55.6%; Pred. No. 2.9e+02;  
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
 QY 2 IPHPNTNKH 10  
 Db 1 IPHPAGLKK 9  
 RESULT 45  
 ADD96886  
 ID ADD96886 standard; peptide; 10 AA.  
 AC ADD96886;  
 XX  
 DT 29-JAN-2004 (first entry)  
 XX  
 DE HIV-1 cross-clade candidate peptide #671.  
 XX  
 KW HIV-1; cross-clade candidate peptide; HIV clade;  
 KM major histocompatibility complex; MHC; human leukocyte antigen; HLA;  
 KM T-cell activation; HIV positive patient; HIV infection; anti-HIV.  
 XX  
 OS Human immunodeficiency virus 1.  
 PN US2003180314-A1.  
 XX  
 PD 25-SEP-2003.  
 XX  
 PF 22-JUL-2002; 2002US-00200708.  
 XX  
 PR 10-JUL-1998; 98US-0092346P.  
 PR 08-JAN-1999; 99US-0115145P.  
 PR 23-APR-1999; 99US-0130677P.  
 PR 09-JUL-1999; 99US-00351036.  
 XX  
 PA (DEGR/) DEGROOT A.  
 PI Degroot A;  
 XX  
 DR WPI; 2003-852210/79.  
 XX  
 PT New cross-clade HIV candidate peptide that binds a human major  
 PT histocompatibility complex binding matrix motif or activates T-cells from  
 PT HIV positive patients, useful for preventing or treating HIV infection.  
 XX  
 PS Example 2; SEQ ID NO 671; 146pp; English.  
 XX  
 CC The present invention relates to HIV-1 cross-clade candidate peptides  
 CC comprising a sequence of about 8-50 amino acids, the sequence having  
 CC complete, sequential sequence identity with a partial HIV-1 amino acid  
 CC sequence that is absolutely conserved across at least 2 clades of HIV.

CC The HIV-1 cross-clade candidate peptides possess at least one of the  
CC biological properties selected from (i) the ability to bind a human major  
CC histocompatibility complex (MHC) binding matrix motif for a human MHC  
CC allele, (ii) the ability to bind MHC human leukocyte antigen (HLA) in the  
CC T2 in vitro peptide binding assay, and (iii) the ability to activate T-  
CC cells from HIV positive patients in at least one in vitro assay. The  
CC invention also discloses a pharmaceutical composition comprising the  
CC above peptide, and methods for the production and use of the cross-clade  
CC peptides. The composition and methods are useful in preventing or  
CC treating HIV infection. The present sequence represents a HIV-1 cross-  
CC clade candidate peptide.

CC Sequence 10 AA;

QY Query Match 27.8%; Score 32; DB 7; Length 10;  
Best Local Similarity 55.6%; Pred. No. 2.9e+02;  
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
DB 2 IPHPTNIHK 10  
2 IPHPAGLKK 10

RESULT 46  
ADD96262  
ID ADD96262 standard; peptide; 10 AA.

AC ADD96262;

DT 29-JAN-2004 (first entry)

DE HIV-1 cross-clade candidate peptide #47.

KW HIV-1, cross-clade candidate peptide; HIV clade;  
KW major histocompatibility complex; MHC; human leukocyte antigen; HLA;  
KW T-cell activation; HIV positive patient; HIV infection; anti-HIV.

OS Human immunodeficiency virus 1.

XX US2003180314-A1.

PD 25-SEP-2003.

PF 22-JUL-2002; 2002US-00200708.

PR 10-JUL-1998; 98US-0092346P.

PR 08-JAN-1999; 99US-0115145P.

PR 23-APR-1999; 99US-0130677P.

PR 09-JUL-1999; 99US-00351036.

PA (DEGR/) DEGROOT A.

PI Degroot A;

DR WPI; 2003-852210/79.

PT New cross-clade HIV candidate peptide that binds a human major  
PT histocompatibility complex binding matrix motif or activates T-cells from  
PT HIV positive patients, useful for preventing or treating HIV infection.

XX Example 3; SEQ ID NO 47; 146pp; English.

CC The present invention relates to HIV-1 cross-clade candidate peptides  
CC comprising a sequence of about 8-50 amino acids, the sequence having  
CC complete, sequential sequence identity with a partial HIV-1 amino acid  
CC sequence that is absolutely conserved across at least 2 clades of HIV.  
CC The HIV-1 cross-clade candidate peptides possess at least one of the  
CC biological properties selected from (i) the ability to bind a human major  
CC histocompatibility complex (MHC) binding matrix motif for a human MHC  
CC allele, (ii) the ability to bind MHC human leukocyte antigen (HLA) in the  
CC T2 in vitro peptide binding assay, and (iii) the ability to activate T-  
CC cells from HIV positive patients in at least one in vitro assay. The  
CC invention also discloses a pharmaceutical composition comprising the

CC above peptide, and methods for the production and use of the cross-clade  
CC peptides. The composition and methods are useful in preventing or  
CC treating HIV infection. The present sequence represents a HIV-1 cross-  
CC clade candidate peptide.

CC Sequence 10 AA;

QY Query Match 27.8%; Score 32; DB 7; Length 10;  
Best Local Similarity 55.6%; Pred. No. 2.9e+02;  
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
DB 2 IPHPTNIHK 10  
1 IPHPAGLKK 9

RESULT 47  
ADD96332  
ID ADD96332 standard; peptide; 10 AA.

AC ADD96332;

DT 29-JAN-2004 (first entry)

DE HIV-1 cross-clade candidate peptide #117.

KW HIV-1, cross-clade candidate peptide; HIV clade;  
KW major histocompatibility complex; MHC; human leukocyte antigen; HLA;  
KW T-cell activation; HIV positive patient; HIV infection; anti-HIV.

OS Human immunodeficiency virus 1.

XX US2003180314-A1.

PD 25-SEP-2003.

PF 22-JUL-2002; 2002US-00200708.

PR 10-JUL-1998; 98US-0092346P.

PR 08-JAN-1999; 99US-0115145P.

PR 23-APR-1999; 99US-0130677P.

PR 09-JUL-1999; 99US-00351036.

PA (DEGR/) DEGROOT A.

PI Degroot A;

DR WPI; 2003-852210/79.

PT New cross-clade HIV candidate peptide that binds a human major  
PT histocompatibility complex binding matrix motif or activates T-cells from  
PT HIV positive patients, useful for preventing or treating HIV infection.

XX Example 3; SEQ ID NO 117; 146pp; English.

CC The present invention relates to HIV-1 cross-clade candidate peptides  
CC comprising a sequence of about 8-50 amino acids, the sequence having  
CC complete, sequential sequence identity with a partial HIV-1 amino acid  
CC sequence that is absolutely conserved across at least 2 clades of HIV.  
CC The HIV-1 cross-clade candidate peptides possess at least one of the  
CC biological properties selected from (i) the ability to bind a human major  
CC histocompatibility complex (MHC) binding matrix motif for a human MHC  
CC allele, (ii) the ability to bind MHC human leukocyte antigen (HLA) in the  
CC T2 in vitro peptide binding assay, and (iii) the ability to activate T-  
CC cells from HIV positive patients in at least one in vitro assay. The  
CC invention also discloses a pharmaceutical composition comprising the  
CC above peptide, and methods for the production and use of the cross-clade  
CC peptides. The composition and methods are useful in preventing or  
CC treating HIV infection. The present sequence represents a HIV-1 cross-  
CC clade candidate peptide.

CC Sequence 10 AA;

Query Match 27.8%; Score 32; DB 7; Length 10;  
 Best Local Similarity 55.6%; Pred. No. 2.9e+02;  
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 IHPPTNIRK 10  
 |||||  
 :  
 Db 2 IHPHAGLKK 10

## RESULT 48

ADD96310  
 ID ADD96310 standard; peptide; 10 AA.

XX  
 AC ADD96310;

XX  
 DT 29-JUN-2004 (first entry)

XX  
 DE HIV-1 cross-clade candidate peptide #95.

XX  
 KM HIV-1, cross-clade candidate peptide; HIV clade;

XX  
 KM major histocompatibility complex; MHC; human leukocyte antigen; HLA;

XX  
 OS T-cell activation; HIV positive patient; HIV infection; anti-HIV.

XX  
 OS Human immunodeficiency virus 1.

XX  
 PN US2003180314-A1.

XX  
 PD 25-SEP-2003.

XX  
 PF 22-JUL-2002; 2002US-00200708.

XX  
 PR 10-JUL-1998; 98US-0092346P.

XX  
 PR 08-JAN-1999; 98US-0115145P.

XX  
 PR 23-APR-1999; 99US-0130677P.

XX  
 PR 09-JUL-1999; 99US-00351036.

XX  
 PA (DEGR/) DEGROOT A.

XX  
 PI Degroot A;

XX  
 DR WPI; 2003-852210/79.

XX  
 PT New cross-clade HIV candidate peptide that binds a human major

XX  
 PT histocompatibility complex binding matrix motif or activates T-cells from

XX  
 PT HIV positive patients; useful for preventing or treating HIV infection.

XX  
 PS Example 3; SEQ ID NO 95; 146pp; English.

XX  
 CC The present invention relates to HIV-1 cross-clade candidate peptides

XX  
 CC comprising a sequence of about 8-50 amino acids, the sequence having

XX  
 CC complete, sequential sequence identity with a partial HIV-1 amino acid

XX  
 CC sequence that is absolutely conserved across at least 2 clades of HIV.

XX  
 CC The HIV-1 cross-clade candidate peptides possess at least one of the

XX  
 CC biological properties selected from (i) the ability to bind a human major

XX  
 CC histocompatibility complex (MHC) binding matrix motif for a human MHC

XX  
 CC allele, (ii) the ability to bind MHC human leukocyte antigen (HLA) in the

XX  
 CC T2 in vitro peptide binding assay, and (iii) the ability to activate T-

XX  
 CC cells from HIV positive patients in at least one in vitro assay. The

XX  
 CC invention also discloses a pharmaceutical composition comprising the

XX  
 CC above peptide, and methods for the production and use of the cross-clade

XX  
 CC peptide. The composition and methods are useful in preventing or

XX  
 CC treating HIV infection. The present sequence represents a HIV-1 cross-

XX  
 CC clade candidate peptide.

XX  
 CC Sequence 10 AA;

XX  
 SQ

XX  
 Query Match 27.8%; Score 32; DB 7; Length 10;

XX  
 Best Local Similarity 55.6%; Pred. No. 2.9e+02;

XX  
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

XX  
 QY 2 IHPPTNIRK 10

XX  
 |||||

XX  
 : 1

XX  
 Db 2 IHPHAGLKK 10

## RESULT 49

ABG75542  
 ID ABG75542 standard; peptide; 14 AA.

XX  
 AC ABG75542;

XX  
 DT 17-APR-2003 (first entry)

XX  
 DE Human sperm acrosomal protein (ACRP) dinucleotide repeat translation #2.

XX  
 KM Polymorphic repeat; tandem repeat; sperm acrosomal protein; ACRP;

XX  
 KM polymorphic marker prediction of ubiquitous simple sequences; POMPOUS;

XX  
 KM Rep-X; human; genetic disease; drug-treatment; Machado-Joseph;

XX  
 KM Haw River syndrome; Huntington's disease; fragile-X syndrome;

XX  
 KM Friedrich's ataxia; myotonic dystrophy; hyperandrogenaemia;

XX  
 KM spinal atrophy; bulbar atrophy; spinocerebellar ataxia.

XX  
 OS Homo sapiens.

XX  
 PN US6472154-B1.

XX  
 PD 29-OCT-2002.

XX  
 PF 31-DEC-1999; 99US-00475947.

XX  
 PR 31-DEC-1999; 99US-00475947.

XX  
 PA (TEXA ) UNIV TEXAS SYSTEM.

XX  
 PI Garner HR, Wren JD, Minna JD, Fondon JW;

XX  
 DR WPI; 2003-208818/20.

XX  
 PT Identifying a candidate polymorphic repeat within a coding sequence, for

XX  
 PT understanding or treating genetic disease, comprises detecting tandem

XX  
 PT repeats in a target coding sequence and scoring the repeats for

XX  
 PT polymorphic probability.

XX  
 PS Example; Col 12; 588pp; English.

XX  
 CC The invention discloses a method for identifying a candidate polymorphic

XX  
 CC repeat within a coding sequence (expressed sequence tag, EST), which

XX  
 CC comprises detecting tandem repeats in a target coding sequence, scoring

XX  
 CC the repeats for polymorphic probability and generating a dataset

XX  
 CC correlating the repeats with polymorphic probability to identify a

XX  
 CC candidate polymorphic repeat. The computational methods (polymorphic

XX  
 CC marker prediction of ubiquitous simple sequences, POMPOUS, and Rep-X) are

XX  
 CC useful for identifying and detecting candidate polymorphic repeats in

XX  
 CC human genes, which can be used to understand, treat or eliminate genetic

XX  
 CC diseases, predispositions or adverse drug-treatment reactions. Examples

XX  
 CC of diseases linked to nucleotide repeats are Machado-Joseph, Haw River

XX  
 CC syndrome, Huntington's disease, fragile-X syndrome, Friedrich's ataxia,

XX  
 CC myotonic dystrophy, hyperandrogenaemia, spinal and bulbar atrophy and

XX  
 CC spinocerebellar ataxia. The sequence presented is the translated product

XX  
 CC of one reading frame of a polymorphic dinucleotide repeat within the 3'

XX  
 CC terminus of the human sperm acrosomal protein (ACRP) coding sequence

XX  
 CC Sequence 14 AA;

XX  
 SQ

XX  
 Query Match 27.8%; Score 32; DB 6; Length 14;

XX  
 Best Local Similarity 100.0%; Pred. No. 4.3e+02;

XX  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX  
 QY 13 VCESVN 18

XX  
 |||||

XX  
 : 9

XX  
 Db 4 VCESVN 9

XX  
 RESULT 50

XX  
 ADP53446

XX  
 ID ADP53446 standard; peptide; 14 AA.

XX	ADP53446;
AC	
DT	12-FEB-2004 (first entry)
XX	
DE	MCPc 603 antibody CDR2 mutant peptide amino acid sequence 7.
XX	
KW	walk-through mutagenesis; prototype amino acid; prototype nucleotide;
KW	mutant polypeptide production; MCPc 603,
KM	complementarity determining region; CDR; heavy chain; CDR2; mutant;
KM	muEIn.
OS	unidentified.
OS	Synthetic.
XX	
PN	WO2003089671-A1.
XX	
PD	30-OCT-2003.
PF	16-APR-2003; 2003WO-US011935.
XX	
PR	17-APR-2002; 2002US-0373686P.
XX	
PA	(CREA/) CREA R.
PA	(CAPV/) CAPPUCCIILI G.
PI	Crea R, Capuccilli G;
XX	
DR	WPI; 2003-854132/79.
XX	
PT	Walk-through mutagenesis of a nucleic acid encoding a polypeptide, useful
PT	for producing mutant polypeptides comprising synthesizing oligonucleotides
PT	comprising a nucleotide sequence for each target region of a prototype
PT	amino acid.
XX	
PS	Example; Fig 6; 40pp; English.
XX	
CC	This invention relates to a novel method of walk-through mutagenesis of a
CC	nucleic acid encoding a polypeptide which comprises synthesizing a
CC	mixture of oligonucleotides comprising a nucleotide sequence for each
CC	target region of a prototype amino acid, where each oligonucleotide
CC	contains, at each sequence position in the target region, a prototype
CC	nucleotide for synthesis of the prototype amino acid, or a predetermined
CC	nucleotide that is useful for synthesis of the predetermined amino
CC	acid. The method is useful in producing mutant polypeptides in which the
CC	overall presence of the predetermined amino acid is limited to one or two
CC	positions per mutated polypeptide, leaving the remaining amino acids in
CC	the targeted region intact or as close as possible to the prototype
CC	sequence. The invention was exemplified using the three complementarity
CC	determining regions (CDRs) of the heavy chain of the monoclonal antibody
CC	MCPc 603.
XX	
XX	
SO	Sequence 14 AA;
Query Match	27.8%; Score 32; DB 7; Length 14;
Best Local Similarity	55.6%; Pred NO. 4.3e+02;
Matches 5; Conservative	1; Mismatches 3; Indels 0; Gaps 0;
OY	4 HPTNIHKYL 12      :      :
DB	4 HPTQHHDVV 12
RESULT 51	
ID ADT41277	standard; peptide; 14 AA.
XX	
AC	ADT41277;
XX	
DT	30-DEC-2004 (first entry)
XX	
DE	hsARS virus peptide, SEQ ID 2265.
XX	

KM	Vitruccide; Severe Acute Respiratory Syndrome; SARS; vaccine.
XX	
OS	SARS coronavirus.
XX	
PN	W02004085650-A1.
XX	
PD	07-OCT-2004.
XX	
PF	24-MAR-2004; 2004MO-CN000246.
XX	
PR	24-MAR-2003; 2003US-0457031P.
XX	
PR	26-MAR-2003; 2003US-0457730P.
XX	
PR	02-APR-2003; 2003US-0459931P.
XX	
PR	03-APR-2003; 2003US-0460357P.
XX	
PR	08-APR-2003; 2003US-0461265P.
XX	
PR	14-APR-2003; 2003US-0462805P.
XX	
PR	23-APR-2003; 2003US-0464886P.
XX	
PR	25-APR-2003; 2003US-0465738P.
XX	
PR	14-MAY-2003; 2003US-0470935P.
XX	
PA	(UHK-) UNIV HONG KONG.
XX	
P1	Chan K, Guan Y, Nicholls JM, Peiris JSM, Poon L, Yuan K;
PI	Leung FC;
XX	
DR	WPI, 2004-737326/72.
XX	
PT	New nucleic acid molecule encoding nucleocapsid- or spike-gene protein of
XX	a human Severe Acute Respiratory Syndrome (hSARS) virus, useful for
PT	diagnosing and treating SARS.
XX	
PS	Example; SEQ ID NO 2265; 200pp; English.
XX	
CC	The present invention relates to novel human Severe Acute Respiratory
XX	Syndrome (hSARS) viral nucleic acid and protein sequences derived from a
CC	hSARS virus having China Center for Type Culture Collection Deposit
XX	Accession No. CCTCC-V200303. The present invention also relates to novel
CC	nucleic acid molecules (I; ADT41483 or ADT41485) encoding a nucleocapsid-
XX	(N) or spike (S)-gene protein of a hSARS virus. Also disclosed are
CC	methods for detecting the presence of a N- or S-gene of the hSARS virus
XX	or of the protein in a biological sample and identifying a subject
CC	infected with the hSARS virus. The hSARS virus, nucleic acid and protein
XX	sequences are useful as vaccines for diagnosing or treating SARS. They
CC	are also useful in clinical and scientific research applications. The
XX	hSARS virus genome (ADT39027) was obtained and the amino acid sequences
CC	of all three reading frames were deduced from the complementary strand.
XX	ADT40120 is the full-length protein encoded by the first reading frame of
CC	the complementary strand and ADT40121-ADT40601 are the peptides from the
XX	first reading frame protein. ADT40602 is the full-length protein encoded
CC	by the second reading frame of the complementary strand and ADT40603-
XX	ADT40976 are the peptides from the second reading frame protein. ADT40977
CC	is the full-length protein encoded by the third reading frame of the
XX	complementary strand and ADT40978-ADT41482 are the peptides from the
CC	third reading frame protein.
XX	
SEQ	Sequence 14 AA;
QY	Query Match 27.8%; Score 32; DB 8; Length 14;
DB	Best Local Similarity 83.3%; Pred.No. 4.3e+02;
Matches	5; Conservative 0; Mismatches 1; Indels 0; Gaps 0
QY	4 HPTNIH 9
DB	9 HPTTIH 14
RESULT 52	
ADS80692	
ID	ADS80692 standard; protein; 14 AA.
AC	ADS80692;
XX	
DT	30-DEC-2004 (first entry)



```

XX DE SARS virus complementary DNA strand reading frame 3 protein #300.
XX KM vlnuclde; vaccine; detection; severe acute respiratory syndrome;
XX KM real-time quantitative polymerase chain reaction; SARS.
XX OS SARS coronavirus.
XX PN MO2004085455-A1.
XX PD 07-OCT-2004.
XX PF 24-MAR-2004; 2004MO-CN000247.
XX PR 24-MAR-2003; 2003US-0457031P.
XX PR 26-MAR-2003; 2003US-0457730P.
XX PR 02-APR-2003; 2003US-0459931P.
XX PR 03-APR-2003; 2003US-0460357P.
XX PR 08-APR-2003; 2003US-0461265P.
XX PR 14-APR-2003; 2003US-0462805P.
XX PR 23-APR-2003; 2003US-0464886P.
XX PR 05-MAY-2003; 2003US-0468139P.
XX PR 16-MAY-2003; 2003US-0471200P.
XX PA (UYHK-) UNIV HONG KONG.
XX PI Chan K, Guan Y, Nicholls JM, Petris JSM, Poon L, Yuen K;
XX DR WPI, 2004-737292/72.
XX PT New isolated nucleic acid molecule useful for detecting, treating,
XX PT ameliorating, or preventing the virus causing severe acute respiratory
XX PT syndrome in humans using a real-time quantitative polymerase chain
XX PT reaction assay.
XX PS Example; SEQ ID NO 2265; 183bp; English.
XX CC The invention relates to an isolated nucleic acid molecule consisting
XX CC essentially of, and/or hybridizes under stringent conditions to a fully
XX CC defined nucleotide sequence of 16-25 base pairs (bp); SEQ ID NO: 2471-
XX CC 2476), or its complement. The methods and compositions of the present
XX CC invention are useful for the detection of the virus causing Severe Acute
XX CC Respiratory Syndrome (SARS) in humans using a real-time quantitative
XX CC polymerase chain reaction (PCR) assay. They can also be used in treating,
XX CC ameliorating, manging or preventing SARS. This sequence corresponds to a
XX CC partial SARS protein sequence from the complementary reading frame 3.
XX SQ Sequence 14 AA;

Query Match          27.8%; Score 32; DB 8; Length 14;
Best Local Similarity 83.3%; Pred. No. 4.3e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 HPTNIH 9
   |||||
Db 9 HPTTII 14

RESULT 53
ADT38807
ID ADT38807 standard; peptide; 14 AA.
XX AC ADT38807;
XX DT 30-DEC-2004 (first entry)
XX DE hSARS virus peptide; SEQ ID 2265.
XX KM vlnuclde; Severe Acute Respiratory Syndrome; SARS; vaccine.
XX OS SARS coronavirus.
XX PN MO2004085633-A1.

```

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XX PD 07-OCT-2004.
XX PF 24-MAR-2004; 2004MO-CN000248.
XX PR 24-MAR-2003; 2003US-0457031P.
XX PR 26-MAR-2003; 2003US-0457730P.
XX PR 02-APR-2003; 2003US-0459931P.
XX PR 03-APR-2003; 2003US-0460357P.
XX PR 08-APR-2003; 2003US-0461265P.
XX PR 14-APR-2003; 2003US-0462805P.
XX PR 23-APR-2003; 2003US-0464886P.
XX PA (UYHK-) UNIV HONG KONG.
XX PI Chan K, Guan Y, Nicholls JM, Petris JSM, Poon L, Yuen K;
XX PI Leung FC;
XX DR WPI, 2004-728736/71.
XX PT New isolated human severe acute respiratory syndrome (hSARS) virus,
XX PT useful as vaccine for diagnosing or treating SARS or in clinical and
XX PT scientific research applications.
XX PS Example; SEQ ID NO 2265; 176bp; English.
XX CC The present invention relates to novel human Severe Acute Respiratory
XX CC Syndrome (hSARS) viral nucleic acid and protein sequences derived from a
XX CC hSARS virus having China Center for Type Culture Collection Deposit
XX CC Accession No. CCTCC-V200303. The hSARS virus, nucleic acid and protein
XX CC sequences are useful as vaccines for diagnosing or treating SARS. They
XX CC are also useful in clinical and scientific research applications. The
XX CC hSARS virus genome (ADT36557) was obtained and the amino acid sequences
XX CC of all three reading frames were deduced from the complementary strand.
XX CC ADT37650 is the full-length protein encoded by the first reading frame of
XX CC the complementary strand and ADT37651-ADT38131 are the peptides from the
XX CC first reading frame protein. ADT38132 is the full-length protein encoded
XX CC by the second reading frame of the complementary strand and ADT38133-
XX CC ADT38506 are the peptides from the second reading frame protein. ADT38507
XX CC is the full-length protein encoded by the third reading frame of the
XX CC complementary strand and ADT38508-ADT39012 are the peptides from the
XX CC third reading frame protein.
XX SQ Sequence 14 AA;

Query Match          27.8%; Score 32; DB 8; Length 14;
Best Local Similarity 83.3%; Pred. No. 4.3e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 HPTNIH 9
   |||||
Db 9 HPTTII 14

RESULT 54
AAW85207
ID AAW85207 standard; peptide; 15 AA.
XX AC AAW85207;
XX DT 16-FEB-1999 (first entry)
XX DE Helper T-cell peptide derived from a POL protein.
XX KM Helper T-cell peptide; human leucocyte antigen; HLA; DR4w4; DR1; DR7;
XX KM cytotoxic T lymphocyte; CTL; hepatitis; autoimmune disease;
XX KM acquired immune deficiency syndrome; malaria; cancer;
XX KM allograft rejection; allergy; Lyme disease; hepatitis;
XX KM post-streptococcal endocarditis; glomerulonephritis;
XX KM food hypersensitivity.
XX OS Synthetic.
XX PN Human immunodeficiency virus 1.

```

XX WO9832456-A1.  
PN 30-JUL-1998.  
XX  
XX 23-JAN-1998; 98WO-US001373.  
XX  
XX 23-JAN-1997; 97US-0036713P.  
PR 07-FEB-1997; 97US-0037432P.  
XX  
XX (EPTM-) EPIMUNE INC.  
XX  
XX Sette A, Sidney J, Southwood S;  
PI WPI; 1998-427679/36.  
XX  
XX Composition containing peptide that induces cytotoxic T lymphocyte  
PT response, and helper peptide - can bind to human leucocyte antigen  
PT alleles, used to treat or prevent cancers, parasitic infections and  
PT autoimmune disease.  
XX  
XX Claim 11; Page 38; 51pp; English.  
XX  
XX AAW85138-283 represent helper T-cell peptides, which can bind to the  
CC human leucocyte antigens (HLA) DR4w4, DR1 and DR7. The peptides are used  
CC in the course of the invention. The specification describes peptides that  
CC that induce a cytotoxic T lymphocyte (CTL) response, and T-helper  
CC peptides, that are used together to generate a CTL response for the  
CC treatment or prevention of viral, fungal, bacterial or parasitic  
CC infections (e.g. hepatitis, acquired immune deficiency syndrome or  
CC malaria) or cancer (e.g. renal or cervical carcinoma, lymphoma, prostate  
CC cancer or condyloma acuminatum). Helper T-cell peptides may be used alone  
CC to induce a helper T cell response, e.g. in cases of autoimmune disease,  
CC allograft rejection, allergy, Lyme disease, hepatitis, post-streptococcal  
CC endocarditis, glomerulonephritis and food hypersensitivity  
XX  
SQ Sequence 15 AA;  
XX  
Query Match 27.8%; Score 32; DB 2; Length 15;  
Best Local Similarity 55.6%; Pred. No. 4.7e+02;  
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
QY 2 IPHPTNIHK 10  
| | | | |  
| | | | |  
DB 6 IPHPAGLKK 14  
XX  
RESULT 55  
ABP24655  
ID ABP24655 standard; peptide; 15 AA.  
XX  
XX ABP24655;  
AC  
XX  
XX 11-SEP-2003 (revised)  
DT 15-JUL-2002 (first entry)  
XX  
XX HIV DR super motif pol peptide #22.  
DE  
XX HIV, HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu;  
KW vif; tat; cytoxic T lymphocyte; CTL; immune response; epitope; antigen;  
KW vaccine; HIV infection; immunisation; virucide.  
XX  
XX Human immunodeficiency virus 1.  
OS  
XX  
XX WO200124810-A1.  
PN  
XX  
XX 12-APR-2001.  
PD  
XX  
XX 05-OCT-2000; 2000WO-US027766.  
PF  
XX  
XX 05-OCT-1999; 99US-00412863.  
PR  
XX  
XX (EPTM-) EPIMUNE INC.  
PA

XX Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;  
PI Baker DM, Celis E, Kudo RT, Grey HM;  
XX  
XX WPI; 2001-354887/37.  
XX  
XX Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)  
PT peptide groups, useful for vaccinating against HIV-1.  
XX  
XX Claim 32; Page 374; 448pp; English.  
XX  
XX The present invention describes a composition (I) comprising a prepared  
CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid  
CC sequence selected from 51 defined amino acid sequences (ABL25347 to  
CC ABP25397). (I) has virucide activity and can be used in vaccines. (I) may  
CC be used for immunising subjects against HIV-1 infections. The use of  
CC group-based vaccines has several advantages over traditional vaccines,  
CC particularly when compared to the use of whole antigens in vaccine  
CC compositions. There is evidence that the immune response to whole  
CC antigens is directed largely toward variable regions of the antigen,  
CC allowing for immune escape due to mutations. The groups for inclusion in  
CC an group-based vaccine may be selected from conserved regions of viral or  
CC tumour-associated antigens, which therefore reduces the likelihood of  
CC escape mutants. Furthermore, immunosuppressive groups that may be present  
CC in whole antigens can be avoided with the use of group-based vaccines. An  
CC additional advantage of an group-based vaccine approach is the ability to  
CC combine selected groups (CTL and HTL), and further, to modify the  
CC composition of the groups, achieving, for example, enhanced  
CC immunogenicity. Accordingly, the immune response can be modulated, as  
CC appropriate, for the target disease. Similar engineering of the response  
CC is not possible with traditional approaches. ABP1501 to ABP25412  
CC represent peptide sequences used in the exemplification of the present  
CC invention. (Updated on 11-SEP-2003 to standardise OS field)  
XX  
SQ Sequence 15 AA;  
XX  
Query Match 27.8%; Score 32; DB 4; Length 15;  
Best Local Similarity 55.6%; Pred. No. 4.7e+02;  
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
QY 2 IPHPTNIHK 10  
| | | | |  
| | | | |  
DB 6 IPHPAGLKK 14  
XX  
RESULT 56  
ADN14050  
ID ADN14050 standard; peptide; 15 AA.  
XX  
XX ADN14050;  
AC  
XX  
XX 17-JUN-2004 (first entry)  
DT  
XX  
XX HIV helper T cell epitope #17.  
DE  
XX  
XX HIV; antigen; epitope; T cell; MHC; major histocompatibility complex;  
KW CTL; cytotoxic T lymphocyte; HIV infection; cancer; tuberculosis; tumour;  
KW hepatitis; melanoma; breast cancer; Hodgkin lymphoma;  
KW nasopharyngeal carcinoma; vaccine; immune response; hyaluronic acid; HA;  
KW CD8+ T cell; CD4+ T cell; viral infection; bacterial infection;  
KW fungal infection; parasitic infection.  
XX  
XX Human immunodeficiency virus 1.  
OS  
XX  
XX US2003049253-A1.  
PN  
XX  
XX 13-MAR-2003.  
PD  
XX  
XX 05-FEB-2002; 2002US-00062710.  
PF  
XX  
XX 08-AUG-2001; 2001US-0310498P.  
PR  
XX  
XX (LIFO/) LI F Q.  
PA

PA	(CHUY// CHU Y.
PA	(QIU/) QIU J.
PI	
PI	Lf FO, Chu Y, Qiu J,
DR	WPI, 2003-540464/51.
XX	
PT	Modulating an immune system response to an antigen in a mammal, comprises
PT	administering a particle-free therapeutic comprising a hyaluronic acid
PT	polymer analogue covalently linked to a peptide that comprises a T cell
PT	epitope.
PS	Disclosure, Page 12; 23pp; English.
XX	
CC	The invention relates to modulating an immune system response to an
CC	antigen in a mammal comprising administering to the mammal a particle-
CC	free therapeutic comprising a hyaluronic acid (HA) polymer analogue
CC	covalently linked to at least one peptide that comprises a T cell epitope
CC	recognised by a major histocompatibility complex molecule of the mammal.
CC	The T cell epitope comprises a sequence of at least about eight amino
CC	acids of the antigen. Also included are a method of improving major
CC	histocompatibility complex (MHC) presentation of a T cell epitope of an
CC	antigen in a mammal (comprising administering to the mammal the
CC	conjugate). The T cell epitope is recognised by a major
CC	histocompatibility complex (MHC) class I molecule and by a CD8+ T cell of
CC	the mammal, or an MHC class II molecule and a CD4+ T cell of the mammal.
CC	The immune system response comprises a cytotoxic T lymphocyte, a CD4+T
CC	cell, or an antibody that recognises the antigen. The immune system
CC	response to the antigen is increased after administration of the
CC	conjugate, where the antigen is an antigen of a pathogenic agent or a
CC	tumour cell. The immune system response to the antigen is decreased after
CC	administration of the conjugate, where the antigen is an antigen of a
CC	tissue or organ transplanted to the mammal. The composition and methods
CC	are useful for modulating, i.e. enhancing or diminishing, an immune
CC	system response to an antigen in a mammal. The composition is also useful
CC	for improving major histocompatibility complex presentation of a T cell
CC	epitope of an antigen in a mammal. The polymeric hyaluronic acid
CC	conjugates are useful as peptide vaccines against an antigen, a
CC	pathogenic agent such as viral, bacterial, fungal or parasitic protein,
CC	or a tumour cell) in a mammal. The peptide vaccine compositions are
CC	useful for treating or preventing diseases associated with any of the
CC	antigens above e.g. HIV infection, cancer, tuberculosis, hepatitis,
CC	melanoma, breast cancer, Hodgkin's lymphoma and nasopharyngeal carcinoma.
CC	The peptide vaccine compositions of the present invention do not require
CC	additional adjuvants, but still induce a stronger cell-mediated response
CC	than peptide vaccines of the prior art. The present sequence is an HIV-1
CC	derived epitope suitable for the vaccine of the invention.
XX	
SQ	Sequence 15 AA;
Query Match	27.8%; Score 32; DB 7; Length 15;
Best Local Similarity	55.6%; Pred. NO. 4.7e+02;
Matches	5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
OY	2 IPHPTNIHK 10       : :
DB	7 IPHPAGLKK 15
RESULT 57	
ID	ADW36336
ID	ADW36336 standard; peptide; 15 AA.
XX	
AC	ADW36336;
XX	
DT	10-MAR-2005 (first entry)
XX	
DE	HLA binding epitope #7086.
XX	
KX	Viralicide, cytotaxtic, gene therapy; vaccine; epitope, cytotoxic T cell;
KX	MHC class I; CTL; HTLV, A2-restricted cytotoxic lymphocyte; HLA;
KX	viral disease; cancer.
XX	

**OS** Unidentified.  
**PX** WO2003040165-A2.

**PN**

**XX** 15-MAY-2003.

**PP**

**PR** 18-OCT-2001; 2001WO-US051650.

**PS**

**PT** 19-OCT-2000; 2000US-0242350P.

**PI** 20-APR-2001; 2001US-0285624P.

**DR** (EPM-) EPRIMMUNE INC.

**DZ**

**SU** Sette A, Sidney J, Southwood S;  
WPL; 2003-441519/41.

**TN**

**TT** New composition comprising at least one peptide having allele-specific  
binding motifs for HLA, useful for preventing, treating or diagnosing  
viral diseases and cancer.

**VN**

**ZI** Claim 1; Page 52-379; 382pp; English.

The invention relates to a composition comprising at least one peptide  
having an isolated, prepared epitope selected from any of the sequences  
from 30 lists given in the specification. Also disclosed is a method for  
inducing a cytotoxic T cell response against a pre-selected antigen in a  
patient expressing a specific MHC class I allele by contacting cytotoxic  
T cells from the patient with the composition cited above. The  
composition comprises an epitope that is joined by an amino acid linker.  
The epitope is admixed or joined to a CTL or HTL epitope. The epitope is  
bound to an HLA molecule on the antigen-presenting cell, where when an Az  
restricted cytotoxic lymphocyte (CTL) is present, a receptor of the CTL  
binds to a complex of the HLA molecule and the epitope. Specifically  
claimed are peptides having allele-specific binding motifs for HLA. The  
compositions and methods are useful for preventing, treating or  
diagnosing viral diseases and cancer. The peptide epitopes are useful as  
diagnostic agents for evaluating immune responses, for making antibodies  
and for evaluating efficacy of a vaccine. Sequences given in ADW29251-  
ADW37745 represent epitopes of the invention as given in Tables 2-31.

**XO** Sequence 15 AA;

**Query Match**                27.8%, Score 32; DB 7; Length 15;  
**Best Local Similarity**     55.6%; Pred. No. 4.7e+02;  
**Matches**      5; Conservative    1; Mismatches    3; Indels          0; Gaps          0;

**OY**                2 IPHPTNIHK 10  
                 |||| : |

**DB**                6 IPHDGGLKK 14

**RESULT 58**

**ID** ADV22436 standard; peptide; 15 AA.

**AC** ADV22436;

**DT** 10-MAR-2005 (first entry)

**DE** HIV-1 Pol protein, immunogenic peptide #63.

**KV** Vaccine; virucide; antigen; autoimmune disease; infection;  
immune modulation; cancer; neoplasm; cytostatic; melanoma; lung tumor;  
breast tumor; uterine cervix tumor; prostatic cancer; colon tumor;  
pancreas tumor; stomach tumor; bladder tumor; kidney tumor;  
hodgkin's lymphoma.

**OS** Human immunodeficiency virus 1.

**WO** WO2004108753-A1.

**PD** 16-DEC-2004.

```

XX 10-JUN-2004; 2004WO-AU000775.
PF
XX
XX 10-JUN-2003; 2003AU-00902875.
PR
XX 25-MAR-2004; 2004AU-00901589.
PR
XX (UYME ) UNIV MELBOURNE.
PA
XX
XX Kent SU;
PI
XX WPI; 2005-031657/03.
DR
XX
XX Use of at least one set of peptides in the preparation of a medicament
PT for modulating an immune response, and for treating cancer or yeast,
PT viral, bacterial, protozoal and mycoplasma infections.
XX
XX Disclosure; SEQ ID NO 856; 645bp; English.
XX
XX The invention relates to the use of at least one set of peptides in the
CC preparation of a medicament for modulating an immune response, where
CC individual peptides of a respective set comprise different portions of an
CC amino acid sequence corresponding to a single polypeptide of interest and
CC display partial sequence identity or similarity to at least one other
CC peptide of the same set of peptides (i.e. they are overlapping). Also
CC included are an antigen-presenting cell which has been contacted with the
CC peptides above and thus presents the peptides, a population of such
CC antigen-presenting cells, a process for producing antigen-presenting
CC cells for modulating an immune response to a polypeptide of interest, a
CC method for producing antigen-specific lymphocytes, a composition
CC comprising at least one set of the peptides (and a carrier and/or
CC diluent), a method for administering an immune response to a polypeptide of
CC interest comprising administering to a patient in need at least one set
CC of the peptides, a method for treatment and/or prophylaxis of a disease
CC or condition associated with the presence of a polypeptide of interest
CC and a composition of matter for modulating an immune response in a
CC subject to a target antigen. The polypeptide of interest is also a
CC disease- or condition-associated polypeptide that is a polypeptide
CC produced by a pathogenic organism or a cancer, and produced by a
CC pathogenic organism selected from yeast, viruses, bacteria, helminths,
CC protozoans and mycoplasmas. The disease- or condition-associated
CC polypeptide is produced by a cancer selected from melanoma, lung cancer,
CC breast cancer, cervical cancer, prostate cancer, colon cancer, pancreatic
CC cancer, stomach cancer, bladder cancer, kidney cancer, post transplant
CC lymphoproliferative disease (PTLD) or Hodgkin's lymphoma. The uncultured
CC antigen-presenting cells or their precursors are useful in the
CC preparation of a medicament for the treatment of a disease or condition
CC in a subject, which disease or condition is associated with the presence
CC of aberrant expression of a target antigen, where the antigen-presenting
CC cells or their precursors have not been subjected to activating
CC conditions but have been contacted with an antigen that corresponds to
CC the target antigen to express a processed or modified form of the antigen
CC for presentation to the subject's immune system. The present sequence is
CC one of a set of overlapping immunogenic peptides derived from an HIV-1
CC protein.
XX
XX Sequence 15 AA;
SQ
XX
XX Query Match 27.8%; Score 32; DB 9; Length 15;
XX Best Local Similarity 55.6%; Pred. No. 4.7e+02;
XX Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
XX
XX 2 IPHPTIHK 10
XX | | | | : |
XX 1 IPHPAGLTK 9
XX
XX RESULT 59
XX ADV22435
XX ID ADV22435 standard; peptide; 15 AA.
XX AC ADV22435;
XX XX
XX 10-MAR-2005 (first entry)
DT

```

```

XX DE HIV-1 Pol protein, immunogenic peptide #62.
XX
XX Vaccine; virucide; antigen; autoimmune disease; infection;
XX immune modulation; cancer; neoplasm; cytostatic; melanoma; lung tumor;
XX breast tumor; uterine cervix tumor; prostatic cancer; colon tumor;
XX pancreas tumor; stomach tumor; bladder tumor; kidney tumor;
XX hodgkin's lymphoma.
XX
XX Human immunodeficiency virus 1.
XX
XX WO2004108753-A1.
XX
XX 16-DEC-2004.
XX
XX 10-JUN-2004; 2004WO-AU000775.
XX
XX 10-JUN-2003; 2003AU-00902875.
XX
XX 25-MAR-2004; 2004AU-00901589.
XX
XX (UYME ) UNIV MELBOURNE.
XX
XX Kent SU;
XX
XX WPI; 2005-031657/03.
XX
XX Use of at least one set of peptides in the preparation of a medicament
PT for modulating an immune response, and for treating cancer or yeast,
PT viral, bacterial, protozoal and mycoplasma infections.
XX
XX Disclosure; SEQ ID NO 855; 645bp; English.
XX
XX The invention relates to the use of at least one set of peptides in the
CC preparation of a medicament for modulating an immune response, where
CC individual peptides of a respective set comprise different portions of an
CC amino acid sequence corresponding to a single polypeptide of interest and
CC display partial sequence identity or similarity to at least one other
CC peptide of the same set of peptides (i.e. they are overlapping). Also
CC included are an antigen-presenting cell which has been contacted with the
CC peptides above and thus presents the peptides, a population of such
CC antigen-presenting cells, a process for producing antigen-presenting
CC cells for modulating an immune response to a polypeptide of interest, a
CC method for producing antigen-specific lymphocytes, a composition
CC comprising at least one set of the peptides (and a carrier and/or
CC diluent), a method for administering an immune response to a polypeptide of
CC interest comprising administering to a patient in need at least one set
CC of the peptides, a method for treatment and/or prophylaxis of a disease
CC or condition associated with the presence of a polypeptide of interest
CC and a composition of matter for modulating an immune response in a
CC subject to a target antigen. The polypeptide of interest is also a
CC disease- or condition-associated polypeptide that is a polypeptide
CC produced by a pathogenic organism or a cancer, and produced by a
CC pathogenic organism selected from yeast, viruses, bacteria, helminths,
CC protozoans and mycoplasmas. The disease- or condition-associated
CC polypeptide is produced by a cancer selected from melanoma, lung cancer,
CC breast cancer, cervical cancer, prostate cancer, colon cancer, pancreatic
CC cancer, stomach cancer, bladder cancer, kidney cancer, post transplant
CC lymphoproliferative disease (PTLD) or Hodgkin's lymphoma. The uncultured
CC antigen-presenting cells or their precursors are useful in the
CC preparation of a medicament for the treatment of a disease or condition
CC in a subject, which disease or condition is associated with the presence
CC of aberrant expression of a target antigen, where the antigen-presenting
CC cells or their precursors have not been subjected to activating
CC conditions but have been contacted with an antigen that corresponds to
CC the target antigen to express a processed or modified form of the antigen
CC for presentation to the subject's immune system. The present sequence is
CC one of a set of overlapping immunogenic peptides derived from an HIV-1
CC protein.
XX
XX Sequence 15 AA;
SQ
XX
XX Query Match 27.8%; Score 32; DB 9; Length 15;
XX Best Local Similarity 55.6%; Pred. No. 4.7e+02;
XX

```

Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 IHPPTNIHK 10  
 |||||  
 Db 5 IHPHAGLKK 13

RESULT 60  
 AD124615  
 ID AD124615 standard; peptide; 17 AA.  
 XX  
 AC AD124615;  
 XX  
 DT 22-APR-2004 (first entry)  
 XX  
 DE HIV-1 HLA class I restricted CTL peptide epitope SegID 32.  
 XX  
 KM immunogenic; epitope; HIV-1 infection; Human Leukocyte Antigen; HLA;  
 KM cytotoxic T lymphocyte; CTL; vaccine; immunostimulant; virucidal.  
 XX  
 OS Human immunodeficiency virus 1.  
 XX  
 PN US2004001845-A1.  
 XX  
 PD 01-JAN-2004.  
 XX  
 PF 20-MAY-2003; 2003US-00442909.  
 XX  
 PR 20-MAY-2002; 2002US-0382120P.  
 XX  
 PA (ALTE/) ALTEFLD M.  
 PA (YDXX/) YU X.  
 PA (WALK/) WALKER B D.  
 PA (ADDO/) ADDO M.  
 XX  
 PI Altfeld M, Yu X, Walker BD, Addo M;  
 XX  
 DR WPI, 2004-098245/10.  
 XX  
 PT New immunogenic composition, useful in eliciting an immune response and  
 PT in treating human immunodeficiency virus, comprises an HLA class I  
 PT restricted HIV-1 polypeptide..  
 XX  
 PS Disclosure; SEQ ID NO 32; 18pp; English.  
 CC This invention relates to novel immunogenic compositions that contain HIV  
 CC -1 epitopes and represent early targets in a naturally occurring response  
 CC against HIV-1 infection. Specifically, these epitopes contain a Human  
 CC Leukocyte Antigen (HLA) class I restricted HIV-1 peptide that is  
 CC recognized by cytotoxic T lymphocytes (CTLs). The present invention  
 CC describes a method of using these peptides to stimulate an HIV-specific  
 CC immune response, such that these peptide compositions can be used to as a  
 CC highly immunogenic HIV-1 vaccine. Accordingly, these compositions that  
 CC exhibit immunostimulant and virucidal activities can also be used to  
 CC treat an HIV-1 infection. This peptide sequence is an HIV-1 peptide  
 CC epitope of the invention.  
 CC  
 XX  
 SQ Sequence 17 AA;  
 XX  
 Query Match 27.8%; Score 32; DB 8; Length 17;  
 Best Local Similarity 55.6%; Pred. No. 5.4e+02;  
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 IHPPTNIHK 10  
 |||||  
 Db 8 IHPHAGLKK 16

RESULT 61  
 ADC89725  
 ID ADC89725 standard; peptide; 20 AA.  
 XX  
 AC ADC89725;

XX  
 DT 01-JAN-2004 (first entry)  
 XX  
 DE Cotton fibre transcription factor 4-4 probable peptide #1.  
 XX  
 KM Cotton; fibre; transcription factor; 4-4; rac13; plant; fibre phenotype;  
 KM pigment biosynthesis pathway.  
 XX  
 OS Gossypium hirsutum.  
 XX  
 PN US2003106089-A1.  
 XX  
 PD 05-JUN-2003.  
 XX  
 PF 31-OCT-2002; 2002US-00285649.  
 XX  
 PR 07-JUN-1995; 95US-00480178.  
 PR 07-JUN-1996; 96MO-US009897.  
 PR 03-DEC-1997; 97US-00984099.  
 XX  
 PA (MGBR/) MGBRIDE K.  
 PA (STAL/) STALKER D M.  
 PA (PEAR/) PEAR J R.  
 PA (PERE/) PEREZ-GRAU L.  
 XX  
 PI McBride K, Stalker DM, Pear JR, Perez-Grau L;  
 XX  
 DR WPI; 2003-801255/75.  
 DR N-PSDB; ADC89723, ADC89724.  
 XX  
 PT New DNA sequence comprising a cotton fiber transcriptional factor and an  
 PT open reading frame of a protein of interest, for modifying fiber  
 PT phenotype in a cotton plant.  
 XX  
 PS Disclosure; SEQ ID NO 9; 63pp; English.  
 CC The invention relates to a DNA sequence comprising a cotton fibre  
 CC transcriptional factor and an open reading frame (orf) encoding a protein  
 CC of interest, operably joined in the direction of transcription, where the  
 CC transcription factor is selected from the 4-4 and rac13 promoter  
 CC sequences. Also included are a DNA construct comprising a promoter for  
 CC transcription in a plant cell the construct above, a plant cell  
 CC comprising the construct, a plant comprising the cell, modifying fibre  
 CC phenotype in a cotton plant (comprising: transforming a plant cell with  
 CC DNA comprising a construct for expression of a protein in a pigment  
 CC biosynthesis pathway, where the construct expresses operably joined  
 CC components: a transcriptional initiation region functional in cells of  
 CC the plant tissue; and an open reading frame encoding a protein of  
 CC interest; and a transcriptional termination region functional in cells of  
 CC the plant tissue, where the plant tissue comprises a substrate of the  
 CC protein and growing the plant cell to produce a plant comprising the  
 CC tissue, where the protein reacts with the substrate to produce the  
 CC pigment), a recombinant DNA construct comprising a cotton tissue  
 CC transcriptional sequence appearing as ADC89725 or ADC89731 and an  
 CC isolated DNA encoding sequence appearing as ADC89737 and ADC89728, being  
 CC the 4-4 and Rac13 cDNAs. The construct is used in a method for modifying  
 CC fibre phenotype in a cotton plant. The construct is also used as a  
 CC molecular probe. The present sequence is probably a transcription factor  
 CC 4-4 promoter cassette peptide, although the authors do not refer to the  
 CC sequence explicitly in the specification.  
 CC  
 XX  
 SQ Sequence 20 AA;  
 XX  
 Query Match 27.8%; Score 32; DB 7; Length 20;  
 Best Local Similarity 42.9%; Pred. No. 6.5e+02;  
 Matches 6; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 2 IHPPTNIHKYVCE 15  
 :|||:|  
 Db 6 LPFPPTTKCLTSD 19

RESULT 62

AAW79123  
 ID AAW79123 standard; peptide; 8 AA.  
 AC AAW79123;  
 DT 27-AUG-2003 (revised)  
 DT 18-NOV-1998 (first entry)  
 XX  
 DE Peptide obtained by oligomerisation of a minimal motif.  
 XX  
 KM Fusion protein; stabilising polypeptide; proteolytic degradation;  
 KM resistance; half-life; autoimmune disease; inflammation; nitro drug;  
 KM IkappaB regulator protein; inflammatory bowel disease; in vivo imaging;  
 KM nitroreductase protein; enzyme therapy; prodrug therapy; protease;  
 KM cancer; pathological condition.  
 XX  
 OS Human herpesvirus 4.  
 XX  
 PN WO9822577-A1.  
 XX  
 PD 28-MAY-1998.  
 XX  
 PP 17-NOV-1997; 97WO-IB001508.  
 XX  
 XX 15-NOV-1996; 96US-0030986P.  
 PR 25-JUN-1997; 97US-0048945P.  
 XX  
 XX (MASU/) MASUCCI M G.  
 PA  
 PI Masucci MG;  
 PI  
 DR WPI; 1998-312463/27.  
 XX  
 PT New fusion proteins resistant to proteolytic degradation - comprising a  
 PT core protein with a stabilising polypeptide comprising a peptide sequence  
 PT containing glycine repeats.  
 XX  
 PS Disclosure; Page 73; 120pp; English.  
 XX  
 CC Sequences shown in AAW79110 to AAW79125 are obtained by oligomerisation  
 CC of a selected minimal motif by complementary oligonucleotides. The  
 CC invention provides a method for increasing the resistance of a core  
 CC protein to proteolytic degradation that comprises linking or inserting  
 CC onto or into the core protein a stabilising polypeptide of formula  
 CC ((Gly)(X)(Gly)(Z)n where Gly, Glyb, Glyc are 1-6 sequential Gly  
 CC residues and X, Y, Z are Ala, Ser, Val, Ile, Leu, Met, Phe, Pro or Thr  
 CC and n can be anything between 1-66. X, Y and Z need not be identical from  
 CC n repeat to n repeat. Alternatively a nucleic acid encoding a stabilising  
 CC polypeptide can be linked onto or inserted into a nucleic acid encoding a  
 CC core protein. The fusion proteins of the invention are more resistant to  
 CC degradation by proteases and, thus, have a longer half-life than the  
 CC unfused core protein. The products can be used for treating autoimmune  
 CC diseases, cancer and inflammation. In particular, the core protein may be  
 CC an IkappaB regulator protein for the treatment of inflammatory bowel  
 CC disease, or a nitroreductase protein which can activate nitro drugs in  
 CC enzyme/prodrug therapy to treat cancer or other pathological conditions.  
 CC The fusion proteins can also be used in diagnostic methods such as in  
 CC vivo imaging. (Updated on 27-AUG-2003 to correct OS field.)  
 XX  
 SQ Sequence 8 AA;  
 Query Match 27.0%; Score 31; DB 2; Length 8;  
 Best Local Similarity 71.4%; Pred. No. 2e+06;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 8 IHRYLVC 14  
 DB 1 IHRYLRC 7  
 RESULT 63  
 AAP50408  
 ID AAP50408 standard; protein; 12 AA.

XX  
 AC AAP50408;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 20-JAN-1992 (first entry)  
 XX  
 DE Human leukemic virus antigen.  
 XX  
 KM Adult T-cell Leukaemia virus; ATL; diagnosis.  
 XX  
 OS Synthetic.  
 XX  
 PN JP60067432-A.  
 XX  
 PD 17-APR-1985.  
 XX  
 PP 22-SEP-1983; 83JP-00176079.  
 XX  
 PR 22-SEP-1983; 83JP-00176079.  
 XX  
 PA (SAKA-) OTSUKA PHARM CO LTD.  
 PA (GANK-) GAN KANKYU-KAI ZH.  
 XX  
 DR WPI; 1985-130934/22.  
 XX  
 PT Human leukemic virus antibody prodn. - by dosing mammal with immune  
 PT antigen comprising complex of carrier and peptide.  
 XX  
 PS Claim 1; Page 171; 20pp; Japanese.  
 XX  
 CC Antigenic peptides may be used to form peptide-carrier complex, allowing  
 CC Abs to be raised, useful in the diagnosis of infection by the adult T-  
 CC cell leukaemia virus. (Updated on 25-MAR-2003 to correct PA field.)  
 XX  
 SQ Sequence 12 AA;  
 Query Match 27.0%; Score 31; DB 1; Length 12;  
 Best Local Similarity 83.3%; Pred. No. 5.3e+02;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 2 IHPTN 7  
 DB 1 IHPTN 6  
 RESULT 64  
 ADQ15533  
 ID ADQ15533 standard; peptide; 12 AA.  
 XX  
 AC ADQ15533;  
 XX  
 DT 07-OCT-2004 (first entry)  
 XX  
 DE Targeting peptide for Pseudomonas #6.  
 XX  
 KM Antimicrobial peptide; targeting peptide; microbial infection;  
 KM mucosal surface; mouth; vagina; gastrointestinal tract;  
 KM oesophageal tract; Staphylococcus mutans infection;  
 KM Candida albicans infection; Helicobacter pylori infection;  
 KM Campylobacter jejuni infection; Vibrio cholerae infection;  
 KM Salmonella infection; Shigella infection; Escherichia coli infection.  
 XX  
 OS Synthetic.  
 XX  
 PN US2004137482-A1.  
 XX  
 PD 15-JUL-2004.  
 XX  
 PP 12-NOV-2003; 2003US-00706391.  
 XX  
 PR 20-AUG-1999; 99US-00378577.  
 PR 19-JUL-2001; 2001US-00910358.  
 PR 14-FEB-2002; 2002US-00077624.

XX (ECKE/) ECKERT R.  
 PA (OIFR/) OI F.  
 PA (SHIW/) SHI W.  
 PA (ANDE/) ANDERSON M H.  
 XX  
 PI Eckert R, OI F, Shi W, Anderson MH;  
 DR WPI, 2004-542706/52.  
 XX  
 PT Composition used for treating microbial infections on mucosal surface  
 PT e.g. mouth, vagina, gastrointestinal tract or esophageal tract comprises  
 PT targeting group and antimicrobial peptide group.  
 XX  
 PS Claim 37; SEQ ID NO 29; 44pp; English.  
 XX  
 CC The invention relates to a composition comprising a targeting group and  
 CC an antimicrobial peptide group. The targeting group is coupled to the  
 CC antimicrobial peptide group and recognises a target microbial organism.  
 CC The composition has an antimicrobial effect on the target microbial  
 CC organism. Also included are a method of treating a target microbial  
 CC organism infection (by administering the composition), and the targeting  
 CC peptide that specifically binds to the microorganism). The targeting  
 CC group is coupled to the C-terminus of the antimicrobial peptide moiety,  
 CC preferably of novipirin G10. The targeting group and the antimicrobial  
 CC peptide group are fused via a peptide linker to form a fusion peptide.  
 CC The composition is useful for treating a microbial infection e.g. on the  
 CC mucosal surface of the mouth, vagina, gastrointestinal tract or  
 CC oesophagagel tract, such as S. mutans infection in a mouth, a Candida  
 CC albicans infection in the vagina and a gastrointestinal infection  
 CC selected from Helicobacter pylori infection, Campylobacter jejuni  
 CC infection, Vibrio cholerae infection, Salmonella infection, Shigella  
 CC infection and Escherichia coli infection. The present sequence is  
 CC bacterial targeting peptide suitable for use in the composition of the  
 CC invention.  
 CC  
 SQ Sequence 12 AA;  
 XX  
 XX  
 Query Match 27.0%; Score 31; DB 8; Length 12;  
 Best Local Similarity 57.1%; Pred. No. 5.3e+02;  
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 QY 3 PHPTNIH 9  
 ||| |  
 Db 2 PHPHKVN 8  
 RESULT 65  
 AAP40114  
 ID AAP40114 standard; protein; 13 AA.  
 XX  
 AC AAP40114;  
 XX  
 DT 27-AUG-2003 (revised)  
 DT 25-MAR-2003 (revised)  
 DT 01-FEB-1992 (first entry)  
 XX  
 DE Sequence of human leukaemia virus-related peptide number 3.  
 XX  
 KM Human leukaemia virus; adult T-cell leukaemia virus; lymphoma;  
 KM cutaneous T-cell lymphoma; immunoblast; diagnosis.  
 XX  
 OS Human T-cell leukemia virus.  
 XX  
 FH Key  
 FH Modified-site 1 Location/Qualifiers  
 FT /label= OTHER  
 FT /note= "Hydrogen atom or a group of the formula, H-Tyr-  
 FT in which Tyr moiety may be labelled with radioactive  
 FT iodine"  
 FT Modified-site 13  
 FT /label= Val-OH  
 XX

PN EP107053-A.  
 XX  
 PD 02-MAY-1984.  
 XX  
 PK 23-SEP-1983; 83EP-00109481.  
 PP  
 XX 30-SEP-1982; 82JP-00171313.  
 PR 07-JAN-1983; 83JP-00001495.  
 PR 16-FEB-1983; 83JP-00025233.  
 PR 23-FEB-1983; 83JP-00030096.  
 XX  
 PA (SAKA ) OTSUKA PHARM CO LTD.  
 PA (NICA-) JAPAN FOUND CANCER RES.  
 PA (GANK-) GAN KENKIU-KAI ZH.  
 XX  
 XX Yoshida M, Sugano H, Shimizu F, Tachikawa T, Ikei N, Noda A;  
 PI Hashimura E, Imagawa K;  
 XX  
 DR WPI, 1984-115670/19.  
 XX  
 XX Antibody of human leukaemia virus related peptide - useful in diagnosis  
 PT of leukaemia and lymphoma and in affinity chromatography.  
 PT  
 XX  
 PS Claim 6(3); Page 75; 86pp; English.  
 XX  
 CC The inventors claim HTLV-related peptides and antibodies obtd. after  
 CC admin. of an antigen consisting of one of the peptides as happen, bound  
 CC to a carrier. The specific antibodies are useful for purification of  
 CC virus-associated proteins, and in immunological measurements related to  
 CC the proteins. (Updated on 25-MAR-2003 to correct PA field.) (Updated on  
 CC 27-AUG-2003 to correct OS field.)  
 CC  
 SQ Sequence 13 AA;  
 XX  
 XX  
 Query Match 27.0%; Score 31; DB 1; Length 13;  
 Best Local Similarity 83.3%; Pred. No. 5.8e+02;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 2 IPHPN 7  
 ||| |  
 Db 2 IPHPKN 7  
 RESULT 66  
 ABG61667  
 ID ABG61667 standard; peptide; 15 AA.  
 XX  
 AC ABG61667;  
 XX  
 DT 13-AUG-2002 (first entry)  
 XX  
 DE Human HGPBMY7 peptide modulator #5.  
 XX  
 KM G protein-coupled receptor; HGPBMY7; spinal chord; ligand library;  
 KM spinal chord-related disorder; breast cancer; neoplastic disease;  
 KM brain disorder; leukaemia; myeloma; immunological disorder;  
 KM cholelcytitis; Grave's disease; osteoarthritis; asthma;  
 KM neurological disorder; dementia; depression; Alzheimer's disease;  
 KM Down's syndrome; epilepsy; intracellular calcium level; NFAT;  
 KM nuclear factor activator of transcription element.  
 XX  
 OS Synthetic.  
 XX  
 XX WO200226823-A2.  
 PN  
 XX  
 PD 04-APR-2002.  
 XX  
 XX 26-SEP-2001; 2001WO-US030351.  
 PF  
 XX 27-SEP-2000; 2000US-0235731P.  
 PR 14-FEB-2001; 2001US-0268580P.  
 PR 28-AUG-2001; 2001US-0315423P.  
 XX





KM immune modulation; cancer; neoplasm; cytostatic; melanoma; lung tumor;  
 KM breast tumor; uterine cervix tumor; prostatic cancer; colon tumor;  
 KM pancreas tumor; stomach tumor; bladder tumor; kidney tumor;  
 KM Hodgkin's lymphoma.  
 XX  
 OS Bimlan immunodeficiency virus SIWmac; isolate 236.  
 PN MO2004108753-A1.  
 XX  
 PD 16-DEC-2004.  
 XX  
 PF 10-JUN-2004; 2004MO-AU000775.  
 XX  
 PR 10-JUN-2003; 2003AU-00902875.  
 PR 25-MAR-2004; 2004AU-00901589.  
 XX  
 PA (UTME ) UNIT MELBOURNE.  
 XX  
 PI Kent SJ;  
 XX  
 DR WPI; 2005-031657/03.  
 XX  
 PT Use of at least one set of peptides in the preparation of a medicament  
 PT for modulating an immune response, and for treating cancer or yeast,  
 PT viral, bacterial, protozoal and mycoplasma infections.  
 XX  
 PS Example 4, SEQ ID NO 201, 645bp, English.  
 XX  
 XX The invention relates to the use of at least one set of peptides in the  
 CC preparation of a medicament for modulating an immune response, where  
 CC individual peptides of a respective set comprise different portions of an  
 CC amino acid sequence corresponding to a single polypeptide of interest and  
 CC display partial sequence identity or similarity to at least one other  
 CC peptide of the same set of peptides (i.e. they are overlapping). Also  
 CC included are an antigen-presenting cell which has been contacted with the  
 CC peptides above and thus presents the peptides, a population of such  
 CC antigen-presenting cells, a process for producing antigen-presenting  
 CC cells for modulating an immune response to a polypeptide of interest, a  
 CC method for producing antigen-specific lymphocytes, a composition  
 CC comprising at least one set of the peptides (and a carrier and/or  
 CC diluent), a method for modulating an immune response to a polypeptide of  
 CC interest comprising administering to a patient in need at least one set  
 CC of the peptides, a method for treatment and/or prophylaxis of a disease  
 CC or condition associated with the presence of a polypeptide of interest  
 CC and a composition of matter for modulating an immune response in a  
 CC subject to a target antigen. The polypeptide of interest is also a  
 CC disease- or condition-associated polypeptide that is a polypeptide  
 CC produced by a pathogenic organism or a cancer, and produced by a  
 CC pathogenic organism selected from yeast, viruses, bacteria, helminths,  
 CC protozoans and mycoplasmas. The disease- or condition-associated  
 CC polypeptide is produced by a cancer selected from melanoma, lung cancer,  
 CC breast cancer, cervical cancer, prostate cancer, colon cancer, pancreatic  
 CC cancer, stomach cancer, bladder cancer, kidney cancer, post transplant  
 CC lymphoproliferative disease (PTLD) or Hodgkin's lymphoma. The uncutlured  
 CC antigen-presenting cells or their precursors are useful in the  
 CC preparation of a medicament for the treatment of a disease or condition  
 CC in a subject, which disease or condition is associated with the presence  
 CC of aberrant expression of a target antigen, where the antigen-presenting  
 CC cells or their precursors have not been subjected to activating  
 CC conditions but have been contacted with an antigen that corresponds to  
 CC the target antigen to express a processed or modified form of the antigen  
 CC for presentation to the subject's immune system. The present sequence is  
 CC one of a set of overlapping immunogenic peptides derived from an SIV  
 CC protein.  
 CC  
 XX  
 SO Sequence 15 AA;  
 XX  
 Query Match 27.0%; Score 31; DB 9; Length 15;  
 Best Local Similarity 55.6%; Pred. No. 6.8e+02;  
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
 QY 2 IPHPNIIHK 10  
 ||||| : |

DB 2 IPHPAGIAK 10  
 RESULT 69  
 AAAY90148  
 ID AAAY90148 standard; peptide; 16 AA.  
 XX  
 AC AAAY90148;  
 XX  
 DT 06-AUG-2003 (revised)  
 DT 21-SEP-2000 (first entry)  
 XX  
 DE Ligand epitope for UPAR #3.  
 XX  
 XX Ligand epitope; UPAR; urokinase-type plasminogen activator receptor;  
 KM adenovirus; hexon HVR5 loop; hexon HI loop; peripheral artery disease;  
 KM recombinant adenovirus vector; tumor; restenosis; gene therapy; asthma;  
 KM smooth muscle cell proliferation inhibitor; coronary artery disease;  
 KM obesity; neurodegenerative disease; infection; autoimmune disease; HIV;  
 KM thrombosis; diabetes; tropism-modified virus.  
 XX  
 OS Synthetic.  
 XX  
 PN MO200012738-A1.  
 XX  
 PD 09-MAR-2000.  
 XX  
 PF 27-AUG-1999; 99MO-IB001524.  
 XX  
 PR 27-AUG-1998; 98US-0098028P.  
 XX  
 PA (AVERT ) AVENTIS PHARMA SA.  
 XX  
 PI Vigne E, Dedieu J, Latra M, Yeh P, Perricaudet M;  
 XX  
 DR WPI; 2000-256653/22.  
 XX  
 PT Urokinase-type plasminogen activator receptor (UPAR)-targeted adenovirus  
 PT vectors having modified hexon HVR5 and HI loops and modified fiber  
 PT proteins useful for targeted gene therapy to treat cancer or restenosis.  
 XX  
 PS Claim 14; Page 69; 128bp; English.  
 XX  
 XX This sequence represents a ligand epitope for UPAR, and is used as a  
 CC targeting sequence. The invention relates to an adenovirus from which at  
 CC least a part of the hexon HVR5 or HI loop is replaced with a binding  
 CC peptide, or targeting sequence, flanked by connecting amino acid spacers,  
 CC to functionally display its binding specificity at the capsid surface.  
 CC The invention also relates to a recombinant adenovirus vector where a  
 CC binding peptide, or targeting sequence, is connected to the C-terminus of  
 CC the fiber by a connecting spacer, or linker, so as to functionally  
 CC display its binding specificity at the capsid surface. The adenovirus or  
 CC recombinant adenovirus vector can be used to preferentially express a  
 CC gene in a target cell, especially a cell that expresses a UPAR. The  
 CC targeted adenovirus vector preferably comprises a heterologous gene  
 CC encoding a gene for treatment of a tumor or restenosis. The targeted  
 CC adenovirus vector is useful for gene therapy treatment of a disease, and  
 CC for manufacturing a medicine used in gene therapy treatment of a disease.  
 CC The viruses can also be used to inhibit smooth muscle cell proliferation,  
 CC to treat peripheral artery diseases, coronary artery diseases, obesity,  
 CC neurodegenerative diseases, infections, autoimmune diseases, asthma, HIV,  
 CC thrombosis, and diabetes. The viruses are particularly targeted against a  
 CC urokinase-type plasminogen activator receptor (UPAR). The adenoviruses  
 CC are tropism-modified without adversely impacting productivity of the  
 CC vectors. (Updated on 06-AUG-2003 to correct OS field.)  
 CC  
 XX  
 SO Sequence 16 AA;  
 XX  
 Query Match 27.0%; Score 31; DB 3; Length 16;  
 Best Local Similarity 45.5%; Pred. No. 7.4e+02;  
 Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
 QY 2 IPHPNIIHKYL 12

Db 4 MPHSLNFSQYL 14

RESULT 70

AA66562 standard; peptide; 17 AA.

AA66562;

25-MAR-2003 (revised)

11-AUG-1995 (first entry)

uPAR-binding peptide #8 isolated from random peptide library.

Random peptide library; fusion protein; filamentous phage; M13; gene III; E.coli; bioactive peptide; target substrate; false positive.

Synthetic.

MO9428424-A1.

08-DEC-1994.

19-MAY-1994; 94WO-US005591.

28-MAY-1993; 93US-00069352.

(CHIR ) CHIRON CORP.

Doyle MV;

WPI; 1995-023023/03.

Identifying cpds. with specific binding affinity - comprises contacting candidate cpds. with target mol. on at least 2 different substrates, ' esp. to identify bioactive peptide(s) '.

Example 5; Page 14; 26pp; English.

Peptides AAR6554-63 are examples of peptides able to bind to the urokinase plasminogen activator receptor (uPAR). The peptides are isolated from a peptide library constructed by inserting the oligonucleotides AAQ79693-4 into the phage M13 construct M13P67. The oligonucleotides are inserted in the newly created KpnI and BglI sites (see AAQ79697-700) at the start of the M13 gene III coding sequence in M13P67. The oligonucleotides generate a random library of peptides when expressed as fusion protein with the gene III product. The library of peptides produced can be used to identify bioactive peptides e.g. by binding the peptides to two or more target substrates. This reduces the chances of false positives. (Updated on 25-MAR-2003 to correct PN field.)

Sequence 17 AA;

Query Match 27.0%; Score 31; DB 2; Length 17;

Best Local Similarity 45.5%; Pred. No. 7.9e+02;

Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 IHPPTNIHXYL 12

Db 4 MPHSLNFSQYL 14

RESULT 71

AA67550 standard; peptide; 17 AA.

AA67550;

25-MAR-2003 (revised)

04-JUL-1995 (first entry)

Antagonist (1) of human urokinase-type plasminogen activator receptor.

XX uPA; urokinase-type plasminogen activator; amino-terminal fragment; ATF; treatment; metastasis; inappropriate angiogenesis; inhibitor;

KW chronic inflammation; Kaposi's sarcoma; diabetic retinopathy;

KW rheumatoid arthritis.

Synthetic.

Key Location/Qualifiers

Modified-site 1 /note= "amidated residue"

WO9428014-A2.

08-DEC-1994.

19-MAY-1994; 94WO-US005684.

28-MAY-1993; 93US-00061514.

(CHIR ) CHIRON CORP.

Rosenberg S, Doyle MV;

WPI; 1995-022708/03.

Peptide inhibitors of urokinase receptor activity - used in compns. to treat e.g. metastasis, chronic inflammation, Kaposi's sarcoma or rheumatoid arthritis.

Claim 1; Page 36; 39pp; English.

AA67550-74 are peptide inhibitors of human urokinase-type plasminogen activator receptor (huPAR). The ability of the peptides to bind huPA ATP (amino terminal fragment, residues 1-135) was measured in an assay performed at 100 pM ATP, 0.3 micrograms/mL su PAR (soluble uPAR) in 200 microL. This peptide had an affinity of 0.015 microm for su PAR. The peptides were synthesised by recombinant DNA techniques using oligonucleotides encoding random peptides (eg. see AAQ79086-87). M13P67 was used to generate the random peptide library and 50-90% of the phage generated contg. the plasmid contained a 69 bp insert at the 5' end of gene III. An alanine and glutamic acid dipeptide were included because the residues corresponding to the first 2 residues of the amino terminus of the wild type mature gene III protein of M13, and may facilitate CC producing fusion proteins. (See also AAQ79088-89). (Updated on 25-MAR-2003 to correct PN field.)

Sequence 17 AA;

Query Match 27.0%; Score 31; DB 2; Length 17;

Best Local Similarity 45.5%; Pred. No. 7.9e+02;

Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 IHPPTNIHXYL 12

Db 4 MPHSLNFSQYL 14

RESULT 72

AA67568 standard; peptide; 17 AA.

AA67568;

18-DEC-1998 (first entry)

Clone 20 peptide.

Urokinase plasminogen activator; uPA; receptor; uPAR; inhibitor; cyclic; antagonist; treatment; disease; unregulated expression; tumour; invasive; metastasis; angiogenesis; proteolytic; contraceptive; gene therapy.

Synthetic.

XX	PN	WO9846731-A1.
XX	PD	22-OCT-1998.
XX	PF	14-APR-1998; 98WO-EP002178.
XX	PR	11-APR-1997; 97EP-00106024.
XX	PA	(BOE) BOEHRINGER MANNHEIM GMBH.
XX	P1	Kessler H, Graeff H, Schmitt M, Magdolen V, Wilhelm OG, Riemer C;
XX	P1	Bueggle M, Koppitz M, Koenig B, Weidle U,
XX	DR	WPI; 1998-568721/48.
XX	PT	New antagonistic peptides derived from urokinase plasminogen activator -
XX	PT	with high affinity for the urokinase receptor, particularly for treatment
XX	PT	of tumours.
XX	PS	Example 2; Page 13; 27pp; German.
XX	CC	This peptide is used in a method to produce cyclic peptides which inhibit
XX	CC	urokinase plasminogen activator (UPA) binding to its receptor (UPAR). The
XX	CC	peptides have the formula X1-(X2)n-X3-X4-K(R)-X5-X6-I-X7-W-(X8)m where X1-
XX	CC	X8 = any aminocarboxylic acid, n and m are each 0 or 1; K, Y, F, I and W
XX	CC	= aminocarboxylic acids with the side chains of, respectively, Lys, Tyr,
XX	CC	Phe, Ile and Trp, the monomers are linked via CONRI or NRICO, and RI =
XX	CC	hydrogen, methyl or ethyl. The peptides may also contain D-form residues.
XX	CC	Such novel peptides can be used in the treatment of diseases involving
XX	CC	expression of UPA or UPAR, especially tumours where they reduce
XX	CC	invasiveness, metastasis and angiogenesis, but more generally wherever
XX	CC	inhibition of the proteolytic activity of UPA is required, e.g.
XX	CC	arthritis, inflammation, osteoporosis, retinopathy and also for
XX	CC	contraception. The peptides are administered orally or parenterally at
XX	CC	0.1-50 (preferably 1-20) mg/kg/day. Cyclic and D-amino acid containing
XX	CC	peptides have better affinity for UPAR than known compounds and are more
XX	CC	resistant to degradation
XX	SQ	Sequence 17 AA;
OY	Query Match	27.0%; Score 31; DB 2; Length 17;
OY	Best Local Similarity	45.5%; Pred. No. 7.9e+02;
OY	Matches 5; Conservative	2; Mismatches 4; Indels 0; Gaps 0;
DB	2 IPHPNINHYL 12	:      :
DB	4 MPHSLNFSOYL 14	:
RESULT 73		
AAW76564		
AAW76564	standard; peptide; 17 AA.	
AC	AAW76564;	
DT	18-DEC-1998 (first entry)	
DE	Clone 20 peptide.	
XX	Urokinase plasminogen activator; uPA; receptor; uPAR; inhibitor; cyclic;	
XX	antagonist; treatment; disease; unregulated expression; tumour; invasive;	
XX	metastasis; angiogenesis; proteolytic; contraception; gene therapy;	
XX	targeting vehicle.	
OS	Synthetic.	
PN	WO9846632-A2.	
PD	22-OCT-1998.	
PF	14-APR-1998; 98WO-EP002179.	

PR	11-APR-1997;	97EP-00106024.
XX	(WILE-) WILEX BIOTECHNOLOGY GMBH.	
PA	Kessler H, Graeff H, Schmitt M, Magdolen V, Wilhelm OG, Riemer C;	
PI	Buerzgle M;	
XX	WPI, 1998-568669/48.	
DR	New antagonistic peptide(s) derived from urokinase plasminogen activator	
PT	- have high affinity for urokinase receptor, particularly for treatment	
XX	of tumours.	
PS	Example 2; Page 15, 30pp; German.	
CC	This peptide is used in a method which produces cyclic peptides having a	
CC	nine-membered ring in which at least two of the ring-forming amino acids	
CC	are derived from the 22-28 amino acid region of urokinase plasminogen	
CC	activator (UPA). The peptides may also contain D-form residues. Such	
CC	peptides have the formula X21-X22-X23-X24-X25-X26-X27-X28-X29-(X30)n-(Y)m	
CC	where X21-X30 are amino acids, Y = spacer, m and n are each 0 or 1,	
CC	whereas are linked via N-R1-CO or CO-N-R1, R1 = hydrogen, methyl or	
CC	ethyl groups, with a bridge between X21 and X29. The novel peptides are	
CC	UPA antagonists (they inhibit binding of UPA to its receptor, UPAR) so	
CC	are useful for treating diseases involving unregulated expression of UPA	
CC	or UPAR, especially tumours where they reduce invasiveness, metastasis	
CC	and angiogenesis. They can act more generally wherever inhibition of the	
CC	proteolytic activity of UPA is required, e.g. arthritis, inflammation,	
CC	osteoporosis, retinopathy and also for contraception. They can	
CC	additionally act as targeting vehicles (liposomes or viral vectors) for	
CC	UPAR-expressing cells, e.g. for delivering diagnostic markers or	
CC	therapeutic agents, including nucleic acids for gene therapy. Cyclic and	
CC	D-amino acid containing peptides have better affinity for UPAR than known	
CC	compounds and its derivatives are more resistant to degradation	
XX	Sequence 17 AA:	
SQ		
OY	2 IPHEPTNHHKYL 12	
	:     :	
DB	4 MPHSLNFSQYL 14	
Query Match	27.0%; Score 31; DB 2; Length 17;	
Best Local Similarity	45.5%; Pred. No. 7.9e+02;	
Matches	5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;	
RESULT 74		
AAAY79011		
ID	AAAY79011 standard; peptide; 17 AA.	
XX		
AC	AAAY79011;	
DT	05-JUN-2000 (first entry)	
DE	Urokinase receptor antagonist peptide AB78.	
XX		
KW	Antagonist; urokinase plasminogen activator; UPA; UPAR; cancer; plasmin;	
KW	myeloid leukemia; urokinase plasminogen activator receptor; plasminogen;	
KW	malignant glioma gastric cancer; proteolysis.	
XX		
OS	Synthetic.	
XX		
PN	WO200001802-A2.	
PD	13-JAN-2000.	
PP	01-JUL-1999; 99WO-DK000377.	
XX		
PR	01-JUL-1998; 98DK-00000874.	
XX		
PA	(CANC-) CANCERFORSKNINGSPONDET AF 1989.	
Pt	Pjong M, Ostergaard S, Holm A, Holst-Hansen C, Stephens RW;	

PI Dano K;  
 XX  
 DR MPI; 2000-171009/15.  
 XX  
 PT New peptides that antagonize the urokinase receptor, used for treating  
 XX cancer by preventing localized conversion of plasminogen to plasmin.  
 XX  
 PS Example 1; Page 51; 75pp; English.  
 XX  
 CC This sequence represents a urokinase receptor (UPAR) antagonist peptide.  
 CC The peptide inhibits the binding interaction between human urokinase  
 CC plasminogen activator (uPA) and its cell surface receptor (UPAR).  
 CC Preventing uPA binding to uPAR, reduces the ability of uPA to convert  
 CC plasminogen to plasmin, this results in a reduction of localised  
 CC proteolysis caused by plasmin. The peptides of the invention are used to  
 CC treat cancer, particularly acute myeloid leukaemia, malignant gliomas and  
 CC gastric cancer  
 XX  
 SQ Sequence 17 AA;  
 XX  
 Query Match 27.0%; Score 31; DB 3; Length 17;  
 Best Local Similarity 45.5%; Pred. No. 7.9e+02;  
 Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
 QY 2 IPHPTNIHKYL 12  
 :||| :|||  
 Db 4 MPHSLNFSQYL 14  
 RESULT 75  
 AAB17140  
 ID AAB17140 standard; peptide; 17 AA.  
 XX  
 AC AAB17140;  
 XX  
 DT 31-OCT-2000 (first entry)  
 XX  
 DE UKR antagonist peptide sequence SEQ ID NO:196.  
 XX  
 KW Modified peptide; therapeutic agent; fusion; Fc domain; cancer;  
 KW autoimmune disease; cytostatic; antiaesthetic; thrombolytic; VEGF;  
 KW immunosuppressive; EPO; TPO; CTLA4; mmetic; IL-1; TNF; antagonist; MMP;  
 KW inhibitor; erythropoietin; thrombopoietin; interleukin 1;  
 KW cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;  
 KW vascular endothelial growth factor; matrix metalloproteinase; asthma;  
 KW thrombosis; pharmaceutical.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200024782-A2.  
 XX  
 PD 04-MAY-2000.  
 XX  
 PF 25-OCT-1999; 99WO-US025044.  
 XX  
 PR 23-OCT-1998; 98US-0105371P.  
 XX  
 PR 22-OCT-1999; 99US-00428082.  
 XX  
 PA (AMGE-) AMGEN INC.  
 XX  
 PI Felge U, Liu C, Cheetham J, Boone TC;  
 XX  
 DR MPI; 2000-350702/30.  
 XX  
 PT Novel composition of matter comprising an Fc domain and pharmacologically  
 XX active peptides, useful for treating cancer and autoimmune diseases.  
 XX  
 PS Claim 39; Page 261; 608pp; English.  
 XX  
 CC The present invention describes composition of matter (I) comprising an  
 CC Fc domain, pharmacologically active peptides, and linkers. Where (I) is:  
 CC (X1)a-P1-(X2)b, where: P1 = an Fc domain; X1 and X2 = are each  
 CC independently selected from -(L1)-C-P1, -(L1)-C-P1-(L2)-d-P2, -(L1)-C-P1-

CC (L2)-d-P2-(L3)-e-P\*3, or -(L1)-C-P1-(L2)-d-P2-(L3)-e-P3-(L4)-f-P4 where P1, P2,  
 CC P3, and P4 = are each independently sequences of pharmacologically active  
 CC peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b,  
 CC c, d, e, and f = are each independently 0 or 1, provided that at least 1  
 CC of a and b is 1. The composition can have cytostatic, antiaesthetic,  
 CC thrombolytic and immunosuppressive activities. DNA, vectors and host  
 CC cells from the present invention can be used for producing pharmaceutical  
 CC compositions. The compositions are useful for treating cancer, asthma,  
 CC thrombosis, or autoimmune diseases. The use of an Fc domain (rather than  
 CC a Fc domain) can provide a longer half-life or incorporate functions  
 CC such as Fc receptor binding, protein A binding, complement fixation, and  
 CC possibly placental transfer. AA69443 to AA69526 and AA6955 to  
 CC AA69803 represent nucleotide and amino acid sequences used in the  
 CC exemplification of the present invention  
 XX  
 SQ Sequence 17 AA;  
 XX  
 Query Match 27.0%; Score 31; DB 3; Length 17;  
 Best Local Similarity 45.5%; Pred. No. 7.9e+02;  
 Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
 QY 2 IPHPTNIHKYL 12  
 :||| :|||  
 Db 4 MPHSLNFSQYL 14  
 RESULT 76  
 AAY90149  
 ID AAY90149 standard; peptide; 17 AA.  
 XX  
 AC AAY90149;  
 XX  
 DT 06-AUG-2003 (revised)  
 XX  
 DT 21-SEP-2000 (first entry)  
 XX  
 DE Ligand epitope for UPAR #4.  
 XX  
 KW Ligand epitope; UPAR; urokinase-type plasminogen activator receptor;  
 KW adenovirus; hexon HRV5 loop; hexon HI loop; peripheral artery disease;  
 KW recombinant adenovirus vector; tumour; restenosis; gene therapy; asthma;  
 KW smooth muscle cell proliferation inhibitor; coronary artery disease;  
 KW obesity; neurodegenerative disease; infection; autoimmune disease; HIV;  
 KW thrombosis; diabetes; tropism-modified virus.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200012738-A1.  
 XX  
 PD 09-MAR-2000.  
 XX  
 PF 27-AUG-1999; 99WO-1B001524.  
 XX  
 PR 27-AUG-1998; 98US-0098028P.  
 XX  
 PA (AVENTIS PHARMA SA.  
 XX  
 PI Vigne E, Dedieu J, Latta M, Yeh P, Perricaudet M;  
 XX  
 DR MPI; 2000-256653/22.  
 XX  
 PT Urokinase-type plasminogen activator receptor (UPAR)-targeted adenovirus  
 XX vectors having modified hexon HRV5 and HI loops and modified fiber  
 XX proteins useful for targeted gene therapy to treat cancer or restenosis.  
 XX  
 PS Claim 14; Page 69; 128pp; English.  
 XX  
 CC This sequence represents a ligand epitope for UPAR, and is used as a  
 CC targeting sequence. The invention relates to an adenovirus from which at  
 CC least a part of the hexon HRV5 or HI loop is replaced with a binding  
 CC peptide, or targeting sequence, flanked by connecting amino acid spacers,  
 CC to functionally display its binding specificity at the capsid surface.  
 CC The invention also relates to a recombinant adenovirus vector where a  
 CC binding peptide, or targeting sequence, is connected to the C-terminus of

CC the fiber by a connecting spacer, or linker, so as to functionally  
CC display its binding specificity at the capid surface. The adenovirus or  
CC recombinant adenovirus vector can be used to preferentially express a  
CC gene in a target cell, especially a cell that expresses a UPAR. The  
CC targeted adenovirus vector preferably comprises a heterologous gene  
CC encoding a gene for treatment of a tumour or restenosis. The targeted  
CC adenovirus vector is useful for gene therapy treatment of a disease, and  
CC for manufacturing a medicine used in gene therapy treatment of a disease.  
CC The viruses can also be used to inhibit smooth muscle cell proliferation,  
CC to treat peripheral artery diseases, coronary artery diseases, obesity,  
CC neurodegenerative diseases, infections, autoimmune diseases, asthma, HIV,  
CC thrombosis, and diabetes. The viruses are particularly targeted against a  
CC urokinase-type plasminogen activator receptor (UPAR). The adenoviruses  
CC are tropism-modified without adversely impacting productivity of the  
CC vectors. (Updated on 06-AUG-2003 to correct OS field.)  
CC  
XX  
SQ Sequence 17 AA;  
Query Match 27.0%; Score 31; DB 3; Length 17;  
Best Local Similarity 45.5%; Pred. No. 7.9e+02;  
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
QY 2 IHPPTNIHKYL 12  
: || | : ||  
DB 4 MPHSLNPSQYL 14  
RESULT 77  
AAB74578 standard; peptide; 17 AA.  
ID AAB74578  
XX AAB74578;  
AC  
XX  
DT 05-JUN-2001 (first entry)  
XX  
XX Context-dependent functional entity recognition domain #2.  
DE  
XX  
XX Context-dependent functional entity; efficacy enhancement; inflammation;  
KM selective recognition domain; thrombogenic potential; cancer; infection;  
KM arthritis; atherosclerosis; burn.  
OS  
XX Synthetic.  
OS  
XX MO200125413-A1.  
PN  
XX 12-APR-2001.  
PD  
XX 04-OCT-2000; 2000MO-US027794.  
PF  
XX 04-OCT-1999; 99US-00411067.  
PR  
XX (NUVA-) NUVAS LLC.  
PA  
XX  
PI Houston LL;  
PI  
XX WPI; 2001-258295/26.  
DR  
XX  
XX Enhancing the efficacy of active and diagnostic agents and treating  
PT pathological conditions in a subject by administering the agent with a  
PT context-dependent functional entity, useful for treating e.g. malignant  
PT neoplasms.  
PS  
XX Claim 10; Page 39; 49pp; English.  
XX  
XX The present invention describes a method of enhancing the efficacy of an  
CC agent by coadministering the agent and a context-dependent functional  
CC entity. The latter comprises a substructure with thrombogenic potential  
CC and a selective recognition domain. This is useful in the treatment of  
CC cancer, arthritis, infections, neovascular glaucoma, inflammatory  
CC conditions, dermatitis, endometriosis, atherosclerosis, vascular  
CC restenosis and conditions associated with granuloma tissues, such as  
CC burns and pyogenic granuloma. The present sequence is an example of a  
CC recognition domain for use in the invention

XX  
SQ Sequence 17 AA;  
Query Match 27.0%; Score 31; DB 4; Length 17;  
Best Local Similarity 45.5%; Pred. No. 7.9e+02;  
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
QY 2 IHPPTNIHKYL 12  
: || | : ||  
DB 4 MPHSLNPSQYL 14  
RESULT 78  
AAB73284 standard; peptide; 17 AA.  
ID AAB73284  
XX  
XX AAB73284;  
AC  
XX  
DT 05-APR-2002 (first entry)  
XX  
XX UTR antagonist peptide SEQ ID NO:196.  
DE  
XX  
XX Modified peptide; mimetic; Fc domain; fusion; immunoglobulin G; IgG; EPO;  
KM erythropoietin; TPO; tumour necrosis factor alpha inhibitor;  
KM TNF-alpha inhibitor; interleukin 1 antagonist; IL-1 antagonist; TMP;  
KM TPO mimetic peptide; EPO mimetic peptide; BMP; VEGF antagonist;  
KM MMP inhibitor; antiinflammatory; antitumour; immunosuppressive;  
KM cytostatic; antineumatic; antiarthritis; antidiabetic; ophthalmological;  
KM antihaemic; anorectic; antifertility; haemostatic; dermatological;  
KM neuroprotective; inflammatory disease; autoimmune disease; tumour growth;  
KM cancer; rheumatoid arthritis; diabetic retinopathy; infertility; obesity;  
KM sleep disorder; neurological degenerative disease; anaemia;  
KM thrombocytopaenia; metastatic tumour; systemic lupus erythematosus;  
KM Fanconi's syndrome.  
XX  
XX Homo sapiens.  
OS  
XX Synthetic.  
OS  
XX MO200183525-A2.  
PN  
XX 08-NOV-2001.  
PD  
XX  
XX 02-MAY-2001; 2001MO-US014310.  
PF  
XX  
XX 03-MAY-2000; 2000US-00563286.  
PR  
XX (AMGE-) AMGEN INC.  
PA  
XX  
PI Feige U, Liu C, Cheetham JC, Boone TC, Guada JM;  
PI  
XX WPI; 2002-130313/17.  
DR  
XX  
XX Novel vehicle-peptide molecule or its multimers useful for treating  
PT inflammatory and autoimmune diseases, cancer, rheumatoid arthritis,  
PT diabetic retinopathy, obesity, sleep disorders and infertility.  
PT  
XX  
XX Claim 39; Page 57; 176pp; English.  
XX  
XX The present invention describes a vehicle-peptide molecule (I) or its  
CC multimers. (I) can have antiinflammatory, antitumour, immunosuppressive,  
CC cytostatic, antineumatic, antiarthritis, antidiabetic, ophthalmological,  
CC antianaemic, anorectic, antifertility, haemostatic, dermatological and  
CC neuroprotective activities. (I) can be used as a therapeutic or  
CC prophylactic agent as well as for screening purposes. (I) is useful for  
CC diagnosing diseases characterised by dysfunction of their associated  
CC protein of interest, for identifying normal or abnormal proteins of  
CC interest, as a part of diagnostic kit to detect the presence of their  
CC proteins of interest in a biological sample. Additionally, (I) is useful  
CC for treating inflammatory and autoimmune diseases, tumour growth, cancer,  
CC rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders,  
CC infertility, and neurological degenerative diseases. (I), comprising EPO-  
CC mimetic compounds are useful for treating disorders characterised by low  
CC red blood cell levels such as anaemia. The TPO-mimetic comprising

CC compounds are useful for treating conditions that involve an existing  
CC megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet  
CC deficiency, such as thrombocytopenia, aplastic anemia, metastatic  
CC tumor which result in thrombocytopenia, systemic lupus erythematosus,  
CC and Fanconi's syndrome. ABB72409 to ABB73426 and ABL33695 to ABL35777  
CC represent amino acid and nucleic acid sequences used in the  
CC exemplification of the present invention  
SQ Sequence 17 AA;

Query Match 27.0%; Score 31; DB 5; Length 17;  
Best Local Similarity 45.5%; Pred. No. 7.9e+02;  
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 IHPHTIHKYL 12  
: || | : ||  
Db 4 MHSLSNFSQYL 14

RESULT 79  
ADG25913  
ID ADG25913 standard; peptide; 17 AA.  
AC ADG25913;  
XX  
XX  
DT 26-FEB-2004 (first entry)  
XX  
XX  
DE INPIONCH03 protein sequence - exon 27.  
XX  
XX  
KM INPIONCH03; INPIONCH04; PKD/REJ cation channel; cardiovascular disease;  
KM heart arrhythmia; angina; neurological disorder; psychiatric disorder;  
KM Alzheimer's disease; Huntington's disease; diabetes; dermatitis;  
KM pulmonary disease; asthma; cystic fibrosis; mucous membrane disorders;  
KM COPD; rhinitis; leukema; ocular disease; glaucoma; retinopathy;  
KM immune disorder; renal disease; polycystic kidney disease;  
KM fertility disorder; testosterone-related disorder; cancer;  
KM gastrointestinal disorders; developmental disorder;  
KM muscle tone-related disease; vascular muscle disorder; migraine;  
KM pre-eclampsia; hypertension; cardiac arrhythmia;  
KM bladder muscle tone disorder; urinary incontinence;  
KM urinary tract infection.  
XX  
XX  
OS unidentified.  
XX  
XX  
PN WO2003089469-A2.  
XX  
XX  
PD 30-OCT-2003.  
XX  
XX  
PF 16-APR-2003; 2003WO-GB001655.  
XX  
XX  
PR 16-APR-2002; 2002GB-00008707.  
XX  
XX  
PA (INPH-) INPHARMATICA LTD.  
XX  
XX  
PI Lobley AE, Michalovich D, Allen KE, Reynolds L, Pierron VN;  
PI Allen JM;  
XX  
XX  
DR WPI: 2003-845523/78.  
DR N-PsDB; ADG25912.  
XX  
XX  
PT New polypeptide of the PKD/REJ family of cation channels, useful for  
PT preparing a composition for diagnosing, treating or preventing e.g.,  
PT hypertension, angina or psychiatric disorders.  
XX  
XX  
PS Claim 1, SEQ ID NO 54; 104pp; English.  
XX  
XX  
CC The invention comprises the amino acid and coding sequence of two  
CC proteins (INPIONCH03 and INPIONCH04) which are members of the PKD/REJ  
CC family of cation channels. The proteins of the invention are useful for  
CC preparing a composition for diagnosing, treating or preventing:  
CC cardiovascular disease (e.g. heart arrhythmia and angina), neurological  
CC and psychiatric disorders (e.g. Alzheimer's disease and Huntington's  
CC disease), diabetes, dermatitis, pulmonary disease, asthma, cystic

CC fibrosis, mucous membrane disorders, COPD, rhinitis, leukaemia, ocular  
CC disease, glaucoma, retinopathy, immune disorder, renal disease,  
CC polycystic kidney disease, fertility disorders, testosterone-related  
CC disorders, cancer, gastrointestinal disorders, developmental disorders,  
CC diseases related to muscle tone, including vascular muscle disorders such  
CC as migraine, pre-eclampsia, hypertension and cardiac arrhythmia/s; and  
CC bladder muscle tone disorders (e.g. urinary incontinence and urinary  
CC tract infection). The present amino acid sequence represents an  
XX INPIONCH03 polypeptide of the invention.  
SQ Sequence 17 AA;

Query Match 27.0%; Score 31; DB 7; Length 17;  
Best Local Similarity 62.5%; Pred. No. 7.9e+02;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DIPHTNI 8  
: || | |  
Db 10 DLPHPBAI 17

RESULT 80  
ADJ73438  
ID ADJ73438 standard; peptide; 17 AA.  
AC ADJ73438;  
XX  
XX  
DT 06-MAY-2004 (first entry)  
XX  
XX  
DE Somatostatin (or cortistatin) mimetic peptide sequence SeqID 894.  
XX  
XX  
KM mimetic; CDR mimetibody; gene therapy; transgenic; immune;  
KM cardiovascular; infectious; malignant; neurological disease; anaemia;  
KM immunomodulator; cardiac; antimicrobial; cytostatic; neuroprotective;  
KM somatostatin; cortibatin.  
XX  
XX  
OS Synthetic.  
XX  
XX  
PN WO2003084477-A2.  
XX  
XX  
PD 16-OCT-2003.  
XX  
XX  
PF 24-MAR-2003; 2003WO-US009139.  
XX  
XX  
PR 29-MAR-2002; 2002US-0368791P.  
XX  
XX  
PA (CENZ) CENTOCOR INC.  
XX  
XX  
PI Heavner GA, Knight DM, Scallion BJ, Grayeb J;  
PI WPI: 2003-804237/75.  
XX  
XX  
DR WPI: 2003-804237/75.  
XX  
XX  
PT New CDR mimetibody comprising a portion of a heavy or light chain  
PT variable region comprising human framework or ligand binding region,  
PT useful for preparing a composition for treating e.g., immune,  
PT cardiovascular or neurologic disease.  
XX  
XX  
PS Disclosure, SEQ ID NO 894; 97pp; English.  
XX  
XX  
CC This invention relates to novel mammalian CDR mimetibodies, specific  
CC portions or variants thereof. Specifically, it refers to an antibody  
CC fragment where a protein has been inserted into, or replaces a portion  
CC of, one or more CDR regions, such that each CDR mimetibody comprises at  
CC least one portion of a heavy chain or light chain variable region, which  
CC itself comprises at least one human framework region and at least one  
CC ligand binding region (LBR). The present invention describes human  
CC mimetibodies, including modified immunoglobulins and cleavage products  
CC that can be useful in gene therapy and the generation of transgenic  
CC plants and animals. Furthermore, the CDR mimetibody is useful for  
CC preparing compositions for modulating, treating or reducing the symptoms  
CC of immune, cardiovascular, infectious, malignant and/or neurologic  
CC diseases, as well as anaemia. Accordingly, they exhibit immunomodulator,  
CC cardiac, antimicrobial, cytostatic and neuroprotective activities. This

CC peptide sequence is an somatostatin mimetic peptide sequence used to make  
CC a mimetibody of the invention.

XX Sequence 17 AA;

SO

Query Match 27.0%; Score 31; DB 7; Length 17;  
Best Local Similarity 45.5%; Pred. No. 7.9e+02;  
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY

2 IHPHTNHKYL 12  
: || | : ||  
4 MPHSLNFSQYL 14

DB

#### RESULT 81

ADJ53072  
ID ADJ53072 standard; peptide; 17 AA.

XX

ADJ53072;

XX

06-MAY-2004 (first entry)

XX

CHI deleted mimetibody-related peptide SegID894.

XX

CHI deleted mimetibody; immunosuppressive; cardiovascular; cardiac;  
hypotensive; neuroprotective; nootropic; antibacterial; virocidic;  
fungicide; gene therapy; immune disorder; cardiovascular disease;  
arrhythmia; hypertension; heart failure; neurodegenerative;  
multiple sclerosis; dementia; Alzheimer's disease; anaemia;  
cancerous condition; infectious disease; bacterial infection;  
viral infection; fungal infection.

XX

Unidentified.

OS

Synthetic.

XX

WO2004002417-A2.

XX

08-JAN-2004.

XX

27-JUN-2003; 2003WO-US020347.

XX

28-JUN-2002; 2002US-0392431P.

XX

(CENZ ) CENTOOR INC.

XX

Heavner GA, Knight DM, Ghrayeb J, Scallion BJ, Nesspor TC;  
Kutoloeki KA;

XX

WPI; 2004-082870/08.

XX

New CHI-deleted mimetibody polypeptides and nucleic acids, useful for  
modulating, treating, alleviating, preventing an immune, cardiovascular,  
PT or neurodegenerative disease or disorder, anemia, cancer, or infectious  
PT diseases.

XX

Claim 3; SEQ ID NO 894; 129pp; English.

XX

This invention relates to CHI deleted mimetibodies (and the DNA sequences  
CC which encode them), compositions, methods and uses. The invention may be  
CC useful for the development of compounds with an immunosuppressive,  
CC cardiovascular, cardiac, hypotensive, neuroprotective, nootropic,  
CC antibacterial, virocidic or fungicide activity. In addition, the disclosed  
CC sequences may prove useful for gene therapy. The CHI-deleted mimetibody  
CC is useful for diagnosing or treating a disease condition in a cell,  
CC tissue, organ or animal, specifically for modulating, treating,  
CC alleviating, preventing the incidence or reducing the symptoms of an  
CC immune, cardiovascular (for example arrhythmia, hypertension or heart  
CC failure), or neurodegenerative (for example multiple sclerosis, dementia  
CC or Alzheimer's disease) diseases or disorders, anaemia, cancerous  
CC conditions, or infectious diseases (for example bacterial, viral or  
CC fungal infection). The present sequence is that of a peptide which may be  
CC used during the creation of a mimetibody of the invention.

SO Sequence 17 AA;

XX

Query Match 27.0%; Score 31; DB 8; Length 17;  
Best Local Similarity 45.5%; Pred. No. 7.9e+02;  
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY

2 IHPHTNHKYL 12  
: || | : ||  
4 MPHSLNFSQYL 14

DB

#### RESULT 82

ADJ52033  
ID ADJ52033 standard; peptide; 17 AA.

XX

ADJ52033;

XX

06-MAY-2004 (first entry)

XX

CHI deleted mimetibody-related peptide SegID894.

XX

CHI deleted mimetibody; osteopathic; cardiovascular-Gen;  
dermatological-Gen; auditory; endocrine-Gen; gastrointestinal-Gen;  
gynaecological-Gen; hepatotropic; haemostatic; immunomodulator;  
antiallergic; muscular-Gen; cytostatic; antiinflammatory; neuroleptic;  
ophthalmological; nephrotropic; respiratory-Gen; tumour necrosis factor;  
TNF; cytokine; bone disorder; joint disorder; cardiovascular disorder;  
dental disorder; oral disorder; dermatological disorder; ear disorder;  
nose disorder; throat disorder; endocrine disorder; metabolic disorder;  
gastrointestinal disorder; gynaecological disorder; hepatic disorder;  
obstetric disorder; haematologic disorder; immunological disorder;  
allergic disorder; infectious disorder; musculoskeletal disorder;  
oncological disorder; neurological disorder; nutritional disorder;  
ophthalmologic disorder; pediatric disorder; psychiatric disorder;  
renal disorder; pulmonary disorder.

XX

Unidentified.

OS

Synthetic.

XX

WO2004002424-A2.

XX

08-JAN-2004.

XX

30-JUN-2003; 2003WO-US020495.

XX

28-JUN-2002; 2002US-0392431P.

XX

19-SEP-2002; 2002US-0412144P.

XX

(CENZ ) CENTOOR INC.

XX

Heavner GA, Knight DM, Ghrayeb J, Scallion BJ, Nesspor TC;  
Kutoloeki KA;

XX

WPI; 2004-082872/08.

XX

New CHI deleted mimetibody polypeptide and nucleic acid, useful for  
PT diagnosing, preventing or treating cardiovascular, dermatologic,  
PT endocrine, gastrointestinal, gynecologic, infectious, neurologic and  
PT nutritional disorders.

XX

Claim 15; SEQ ID NO 894; 123pp; English.

XX

This invention relates to CHI deleted mimetibodies (and the DNA sequences  
CC which encode them), compositions, methods and uses. The invention may be  
CC useful for the development of compounds with an osteopathic,  
CC cardiovascular-Gen, dermatological-Gen, auditory, endocrine-Gen,  
CC gastrointestinal-Gen, gynaecological-Gen, hepatotropic, haemostatic,  
CC immunomodulator, antiallergic, muscular-Gen, cytostatic,  
CC antiinflammatory, neuroleptic, ophthalmological, nephrotropic or  
CC respiratory-Gen activity acting as a tumour necrosis factor (TNF)-  
CC modulator or cytokine-agonist. The methods and compositions of the  
CC present invention are useful for the diagnosis, prevention and/or  
CC treatment of diseases or conditions associated with aberrant expression

CC or activity of the CH1 deleted mimetibody, such as a bone or joint,  
 CC cardiovascular, dental or oral, dermatological, ear, nose or throat,  
 CC endocrine, metabolic, gastrointestinal, gynaecological, hepatic,  
 CC obstructive, haematologic, immunological, allergic, infectious,  
 CC musculoskeletal, oncological, neurological, nutritional, ophthalmologic,  
 CC pediatric, psychiatric, renal or pulmonary disorders. The present  
 CC sequence is that of a peptide which may be used during the creation of a  
 CC mimetibody of the invention.

XX  
 SQ Sequence 17 AA;

Query Match 27.0%; Score 31; DB 8; Length 17;  
 Best Local Similarity 45.5%; Pred. No. 7.9e+02;  
 Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 IHPPTNIHKYL 12  
 :|||:|:  
 Db 4 MPHSLNFSQYL 14

RESULT 83

ABB39967  
 ID ABB39967 standard; peptide; 18 AA.

AC ABB39967;

DT 04-FEB-2002 (first entry)

DE Peptide #7473 encoded by human foetal liver single exon probe.

KW Human; foetal liver; gene expression; single exon nucleic acid probe.

OS Homo sapiens.

PN WO200157277-A2.

PD 09-AUG-2001.

PF 30-JAN-2001; 2001WO-US000669.

PR 04-FEB-2000; 2000US-0180312P.

PR 26-MAY-2000; 2000US-0207456P.

PR 30-JUN-2000; 2000US-00608408.

PR 03-AUG-2000; 2000US-00632366.

PR 21-SEP-2000; 2000US-0234687P.

PR 27-SEP-2000; 2000US-0236359P.

PR 04-OCT-2000; 2000GB-00024263.

PA (MOLE-) MOLECULAR DYNAMICS INC.

PI Penn SG, Hanzel DK, Chen W, Rank DR;

DR WPI; 2001-483447/52.

PT Human genome-derived single exon nucleic acid probes useful for analyzing

PS gene expression in human fetal liver.

PS Claim 27; SEQ ID NO 32602; 639bp + Sequence Listing; English.

XX The invention relates to a single exon nucleic acid probe for measuring  
 CC human gene expression in a sample derived from human foetal liver. The  
 CC single exon nucleic acid probes may be used for predicting, measuring and  
 CC displaying gene expression in samples derived from human fetal liver. The  
 CC present sequence is a peptide encoded by a single exon nucleic acid probe  
 CC of the invention. Note: The sequence data for this patent did not form  
 CC part of the printed specification, but was obtained in electronic format  
 CC directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 18 AA;

Query Match 27.0%; Score 31; DB 4; Length 18;  
 Best Local Similarity 44.4%; Pred. No. 8.5e+02;  
 Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 6 TNIHKYIWC 14  
 :|||:|:  
 Db 9 SHIHVFLIC 17

RESULT 84

AAM33587  
 ID AAM33587 standard; protein; 18 AA.

AC AAM33587;

DT 17-OCT-2001 (first entry)

DE Peptide #7624 encoded by probe for measuring placental gene expression.

KW Probe; microarray; human; placenta; antenatal diagnosis;

OS genetic disorder.

PN WO200157272-A2.

PD 09-AUG-2001.

PF 30-JAN-2001; 2001WO-US000663.

PR 04-FEB-2000; 2000US-0180312P.

PR 26-MAY-2000; 2000US-0207456P.

PR 30-JUN-2000; 2000US-00608408.

PR 03-AUG-2000; 2000US-00632366.

PR 21-SEP-2000; 2000US-0234687P.

PR 27-SEP-2000; 2000US-0236359P.

PR 04-OCT-2000; 2000GB-00024263.

PA (MOLE-) MOLECULAR DYNAMICS INC.

PI Penn SG, Hanzel DK, Chen W, Rank DR;

DR WPI; 2001-488897/53.

PT Human genome-derived single exon nucleic acid probes useful for analyzing

PS gene expression in human placenta.

PS Claim 27; SEQ ID NO 33856; 654bp; English.

XX The present invention relates to single exon nucleic acid probes (SENPs;  
 CC see A131315-A157546). The present sequence is a peptide encoded by one  
 CC such probe. The probes are useful for producing a microarray for  
 CC predicting, measuring and displaying gene expression in samples derived  
 CC from human placenta. The probes are useful for antenatal diagnosis of  
 CC human genetic disorders

XX Sequence 18 AA;

Query Match 27.0%; Score 31; DB 4; Length 18;  
 Best Local Similarity 44.4%; Pred. No. 8.5e+02;  
 Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 6 TNIHKYIWC 14  
 :|||:|:  
 Db 9 SHIHVFLIC 17

RESULT 85

AAM73385  
 ID AAM73385 standard; protein; 18 AA.

AC AAM73385;

DT 06-NOV-2001 (first entry)

DE Human bone marrow expressed probe encoded protein SEQ ID NO: 33691.



XX Human; bone marrow expressed exon; gene expression analysis; probe;  
KM microarray; cancer; leukemia; lymphoma; myeloma.  
XX  
OS Homo sapiens.  
XX  
PN WO200157276-A2.  
XX  
PD 09-AUG-2001.  
XX  
PF 30-JAN-2001; 2001WO-US000668.  
XX  
PR 04-FEB-2000; 2000US-0180312P.  
PR 26-MAY-2000; 2000US-0207456P.  
PR 30-JUN-2000; 2000US-00608408.  
PR 03-AUG-2000; 2000US-00632366.  
PR 21-SEP-2000; 2000US-0234687P.  
PR 27-SEP-2000; 2000US-0236359P.  
PR 04-OCT-2000; 2000GB-00024263.  
XX  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
XX  
PI Penn SG, Hanzel DK, Chen W, Rank DR;  
XX  
DR WPI; 2001-488900/53.  
XX  
XX Human genome-derived single exon nucleic acid probes useful for analyzing  
PT gene expression in human bone marrow.  
XX  
PS Example 4; SEQ ID NO 33691; 658pp + Sequence Listing; English.  
XX  
CC The present invention provides a number of single exon nucleic acid  
CC probes which are derived from genomic sequences expressed in the human  
CC bone marrow. They can be used to measure gene expression in bone marrow  
CC samples, which may enable the improved diagnosis and treatment of cancers  
CC such as lymphoma, leukemia and myeloma. The present sequence is a  
CC protein encoded by one of the probes of the invention  
XX  
SQ Sequence 18 AA;  
XX  
Query Match 27.0%; Score 31; DB 4; Length 18;  
Best Local Similarity 44.4%; Pred. No. 8.5e+02;  
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;  
QY 6 TNHRYLVC 14  
Db :||:|:  
9 SHIHVPLIC 17  
XX  
RESULT 86  
AAM60712  
ID AAM60712 standard; protein; 18 AA.  
XX  
AC AAM60712;  
XX  
DT 05-NOV-2001 (first entry)  
XX  
DE Human brain expressed single exon probe encoded protein SEQ ID NO: 32817.  
XX  
KM Human; brain expressed exon; gene expression analysis; probe; microarray;  
KM Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer.  
XX  
OS Homo sapiens.  
XX  
PN WO200157275-A2.  
XX  
PD 09-AUG-2001.  
XX  
PF 30-JAN-2001; 2001WO-US000667.  
XX  
PR 04-FEB-2000; 2000US-0180312P.  
PR 26-MAY-2000; 2000US-0207456P.  
PR 30-JUN-2000; 2000US-00608408.

PR 03-AUG-2000; 2000US-00632366.  
PR 21-SEP-2000; 2000US-0234687P.  
PR 27-SEP-2000; 2000US-0236359P.  
PR 04-OCT-2000; 2000GB-00024263.  
XX  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
XX  
PI Penn SG, Hanzel DK, Chen W, Rank DR;  
XX  
DR WPI; 2001-483446/52.  
XX  
XX Single exon nucleic acid probes for analyzing gene expression in human  
PT brain.  
XX  
PS Example 4; SEQ ID NO 32817; 650pp + Sequence Listing; English.  
XX  
CC The present invention provides a number of single exon nucleic acid  
CC probes which are derived from genomic sequences expressed in the human  
CC brain. They can be used to measure gene expression in brain cell samples,  
CC which may enable the diagnosis and improved treatment of nervous system  
CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,  
CC epilepsy and cancers. The present sequence is a protein encoded by one of  
CC the probes of the invention  
XX  
SQ Sequence 18 AA;  
XX  
Query Match 27.0%; Score 31; DB 4; Length 18;  
Best Local Similarity 44.4%; Pred. No. 8.5e+02;  
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;  
QY 6 TNHRYLVC 14  
Db :||:|:  
9 SHIHVPLIC 17  
XX  
RESULT 87  
ABG55102  
ID ABG55102 standard; peptide; 18 AA.  
XX  
AC ABG55102;  
XX  
DT 25-FEB-2003 (first entry)  
XX  
DE Human liver peptide, SEQ ID NO 33750.  
XX  
KM Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia;  
KM hypercholesterolaemia; coronary heart disease.  
XX  
OS Homo sapiens.  
XX  
PN WO200157273-A2.  
XX  
PD 09-AUG-2001.  
XX  
PF 30-JAN-2001; 2001WO-US000664.  
XX  
PR 04-FEB-2000; 2000US-0180312P.  
PR 26-MAY-2000; 2000US-0207456P.  
PR 30-JUN-2000; 2000US-00608408.  
PR 03-AUG-2000; 2000US-00632366.  
PR 21-SEP-2000; 2000US-0234687P.  
PR 27-SEP-2000; 2000US-0236359P.  
PR 04-OCT-2000; 2000GB-00024263.  
XX  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
XX  
PI Penn SG, Hanzel DK, Chen W, Rank DR;  
XX  
DR WPI; 2001-488980/53.  
XX  
PT Human genome-derived single exon nucleic acid probes useful for analyzing  
PT gene expression in human adult liver.  
XX

PS Claim 27; SEQ ID NO 33750; 658bp; English.  
 CC The invention relates to a single exon nucleic acid probe (SENP) (1) for  
 CC measuring human gene expression in a sample derived from human adult  
 CC liver, comprising one of 13109 defined nucleotide sequences given in the  
 CC specification (or complements/ fragments). The probe hybridizes at high  
 CC stringency to a nucleic acid molecule expressed in the human adult liver.  
 CC (1) may be used for predicting, measuring and displaying gene expression  
 CC in samples derived from human adult liver. The genes identified may be  
 CC involved in genetic liver diseases such as cirrhosis,  
 CC hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is  
 CC associated with coronary heart disease. ABG47348-ABG5930 represent human  
 CC liver single exon encoded peptides of the invention. Note: The sequence  
 CC information for this patent does not appear in the printed specification  
 CC but was obtained in electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 18 AA;

Query Match 27.0%; Score 31; DB 4; Length 18;  
 Best Local Similarity 44.4%; Pred. No. 8.5e+02;  
 Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 6 TNHRYLVC 14  
 :||:|:  
 DB 9 SHHVFLLIC 17

RESULT 88

ABG43239  
 ID ABG43239 standard; peptide; 18 AA.

XX ABG43239;

DT 19-AUG-2002 (first entry)

XX Human peptide encoded by genome-derived single exon probe SEQ ID 32904.

KW Human; single exon probe; asthma; lung cancer; COPD; ILD;  
 KW chronic obstructive pulmonary disease; interstitial lung disease;  
 KW familial idiopathic pulmonary fibrosis; neurofibromatosis;  
 KW tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;  
 KW Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;  
 KW pulmonary histiocytosis; lymphangioleiomyomatosis; Karsenger syndrome;  
 KW pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;  
 KW primary ciliary dyskinesia; pulmonary hypertension;  
 KW hyaline membrane disease.

XX Homo sapiens.

PN WO200186003-A2.

XX 15-NOV-2001.

PF 30-JAN-2001; 2001WO-US000665.

PR 04-FEB-2000; 2000US-0180312P.

PR 26-MAY-2000; 2000US-0207456P.

PR 30-JUN-2000; 2000US-00608408.

PR 03-AUG-2000; 2000US-0063366P.

PR 21-SEP-2000; 2000US-0234687P.

PR 27-SEP-2000; 2000US-0236359P.

PR 04-OCT-2000; 2000GB-00024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2002-114183/15.

PT Spatially-addressable set of single exon nucleic acid probes, used to  
 PF measure gene expression in human lung samples.

PS Claim 27; SEQ ID NO 32904; 634bp; English.

XX The invention relates to a spatially-addressable set of single exon  
 CC nucleic acid probes for measuring gene expression in a sample derived  
 CC from human lung comprising single exon nucleic acid probes having one of  
 CC 12614 nucleic acid sequences mentioned in the specification, or their  
 CC complements or the 12387 open reading frames derived from the 12614  
 CC probes. Also included are a microarray comprising the novel set of probes  
 CC; the novel set of probes which hybridizes at high stringency to a nucleic  
 CC acid expressed in the human lung; measuring gene expression in a sample  
 CC derived from human lung; comprising (a) contacting the array with a  
 CC collection of detectably labeled nucleic acids derived from human lung  
 CC mRNA, and (b) measuring the label detectably bound to each probe of the  
 CC array; identifying exons in a eukaryotic genome, comprising (a)  
 CC algorithmically predicting at least one exon from genomic sequences of  
 CC the eukaryote; and (b) detecting specific hybridisation of detectably  
 CC labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,  
 CC having a fragment identical to the predicted exon, the probe is included  
 CC in the above mentioned microarray; assigning exons to a single gene,  
 CC comprising (a) identifying exons from genomic sequence by the method  
 CC above and (b) measuring the expression of each of the exons in several  
 CC tissues and/or cell types using hybridisation to a single exon  
 CC microarray having a probe with the exon, where a common pattern of  
 CC expression of the exons in the tissues and/or cell types indicates that  
 CC the exons should be assigned to a single gene; a peptide comprising one  
 CC of 12011 sequences, mentioned in the specification, or encoded by the  
 CC probes/open reading frames (ORF). The probes are used for gene expression  
 CC analysis, and for identifying exons in a gene, particularly using human  
 CC lung derived mRNA and for the study of lung diseases such as asthma, lung  
 CC cancer, chronic obstructive pulmonary disease (COPD), interstitial lung  
 CC disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis,  
 CC tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-  
 CC Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary  
 CC histiocytosis, lymphangioleiomyomatosis, pulmonary alveolar proteinosis,  
 CC Karsenger syndrome, fibrocystic pulmonary dysplasia, primary ciliary  
 CC dyskinesia, pulmonary hypertension and hyaline membrane disease. The  
 CC present sequence is a peptide/protein encoded by a single exon probe of  
 CC the invention. Note: The sequence data for this patent did not form part  
 CC of the printed specification, but was obtained in electronic format  
 CC directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 18 AA;

Query Match 27.0%; Score 31; DB 5; Length 18;  
 Best Local Similarity 44.4%; Pred. No. 8.5e+02;  
 Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 6 TNHRYLVC 14  
 :||:|:  
 DB 9 SHHVFLLIC 17

RESULT 89

ADV53056  
 ID ADV53056 standard; peptide; 19 AA.

XX ADV53056;

DT 10-MAR-2005 (first entry)

XX Hedgehog pathway peptide SEQ ID NO 553.

XX diagnosis; cancer; obesity; diabetes; asthma; inflammation; depression;  
 KW food; feedstuff; cosmetics; agriculture; animal breeding;  
 KW hedgehog pathway.

XX Unidentified.

XX WO2004111636-A2.

XX 23-DEC-2004.

XX 17-JUN-2004; 2004WO-EP051158.

XX 17-JUN-2003; 2003BP-00101775.  
 PR 17-JUN-2003; 2003US-0479061P.  
 XX  
 XX (VIBV-) VIB VZW.  
 PA (UYGE-) UNIV GENT.  
 XX  
 PI Kas K, Vandekerckhove J, Krols L;  
 XX WPI; 2005-057893/06.  
 DR  
 XX  
 PT Identifying a peptide combo which corresponds with a family of proteins,  
 PT useful for diagnosing a variety of diseases, drug development or in  
 PT agriculture, comprises generating peptides by applying a digest on the  
 PT family of protein.  
 XX  
 PS Example; SEQ ID NO 553; 265pp; English.  
 XX  
 CC The invention relates to a method of identifying a peptide combo which  
 CC corresponds with a family of proteins where each of the members of the  
 CC peptide combo is derived from a unique protein from the family. The  
 CC peptide combo is useful for quantifying specific known splice variants of  
 CC one or more particular proteins in a sample, for diagnosing complex  
 CC genetic diseases such as cancer, obesity, diabetes, asthma and  
 CC inflammation, neuropsychiatric disorders such as depression, for  
 CC quantifying one to several hundreds of protein disease markers  
 CC simultaneously leading to a more accurate diagnostic sub-classification,  
 CC for determining the extent of protein modification in a particular sample  
 CC of proteins, for tissue-typing analysis, for prenatal testing to detect  
 CC the presence of a congenital disease or for quantitating protein levels  
 CC diagnostic of a chromosomal abnormality, for diagnosing immune diseases  
 CC or neurological diseases, as biomarkers preclinical drug development,  
 CC development of improved animal models, biomarkers related with  
 CC toxicology, clinical drug development, guidance marketed drugs,  
 CC prognostic or diagnostic disease markers, drug target validation and  
 CC selection, monitoring protein splicing, drug lead profiling, pathway  
 CC analysis, answering basic disease biology questions, and in the fields of  
 CC food and feed, cosmetics, agriculture and animal breeding. The present  
 CC sequence represents a peptide from a hedgehog pathway peptide combo.  
 XX  
 SQ Sequence 19 AA;  
 DB  
 QY 2 IPHPTNIHKYLVCE 15  
 |||| : :  
 DB 4 IPHPSGRGPPPTCQ 17  
 Query Match 27.0%; Score 31; DB 9; Length 19;  
 Best Local Similarity 35.7%; Pred. No. 9e+02;  
 Matches 5; Conservative 3; Mismatches 6; Indels 0; Gaps 0;  
 RESULT 90  
 ADV52657  
 ID ADV52657 standard; peptide; 19 AA.  
 XX  
 AC ADV52657;  
 XX  
 DT 10-MAR-2005 (first entry)  
 XX  
 DB Hedgehog pathway peptide SEQ ID NO 154.  
 XX  
 KW diagnosed; cancer; obesity; diabetes; asthma; inflammation; depression;  
 KW food; feedstuff; cosmetics; agriculture; animal breeding;  
 KW hedgehog pathway.  
 XX  
 OS Unidentified.  
 XX  
 PN MO2004111636-A2.  
 XX  
 PD 23-DEC-2004.  
 XX  
 PF 17-JUN-2004; 2004MO-BP051158.  
 XX

PR 17-JUN-2003; 2003BP-00101775.  
 PR 17-JUN-2003; 2003US-0479061P.  
 XX  
 XX (VIBV-) VIB VZW.  
 PA (UYGE-) UNIV GENT.  
 XX  
 PI Kas K, Vandekerckhove J, Krols L;  
 XX WPI; 2005-057893/06.  
 DR  
 XX  
 PT Identifying a peptide combo which corresponds with a family of proteins,  
 PT useful for diagnosing a variety of diseases, drug development or in  
 PT agriculture, comprises generating peptides by applying a digest on the  
 PT family of protein.  
 XX  
 PS Example; SEQ ID NO 154; 265pp; English.  
 XX  
 CC The invention relates to a method of identifying a peptide combo which  
 CC corresponds with a family of proteins where each of the members of the  
 CC peptide combo is derived from a unique protein from the family. The  
 CC peptide combo is useful for quantifying specific known splice variants of  
 CC one or more particular proteins in a sample, for diagnosing complex  
 CC genetic diseases such as cancer, obesity, diabetes, asthma and  
 CC inflammation, neuropsychiatric disorders such as depression, for  
 CC quantifying one to several hundreds of protein disease markers  
 CC simultaneously leading to a more accurate diagnostic sub-classification,  
 CC for determining the extent of protein modification in a particular sample  
 CC of proteins, for tissue-typing analysis, for prenatal testing to detect  
 CC the presence of a congenital disease or for quantitating protein levels  
 CC diagnostic of a chromosomal abnormality, for diagnosing immune diseases  
 CC or neurological diseases, as biomarkers preclinical drug development,  
 CC development of improved animal models, biomarkers related with  
 CC toxicology, clinical drug development, guidance marketed drugs,  
 CC prognostic or diagnostic disease markers, drug target validation and  
 CC selection, monitoring protein splicing, drug lead profiling, pathway  
 CC analysis, answering basic disease biology questions, and in the fields of  
 CC food and feed, cosmetics, agriculture and animal breeding. The present  
 CC sequence represents a peptide from a hedgehog pathway peptide combo.  
 XX  
 SQ Sequence 19 AA;  
 DB  
 QY 2 IPHPTNIHKYLVCE 15  
 |||| : :  
 DB 4 IPHPSGRGPPPTCQ 17  
 Query Match 27.0%; Score 31; DB 9; Length 19;  
 Best Local Similarity 35.7%; Pred. No. 9e+02;  
 Matches 5; Conservative 3; Mismatches 6; Indels 0; Gaps 0;  
 RESULT 91  
 AAM85293  
 ID AAM85293 standard; peptide; 20 AA.  
 XX  
 AC AAM85293;  
 XX  
 DT 16-FEB-1999 (first entry)  
 XX  
 DB Helper T-cell class II peptide derived from core protein.  
 XX  
 KW Helper T-cell peptide; human leucocyte antigen; HLA; DR4w4; DR1; DR7;  
 KW cytotoxic T lymphocyte; CTL; hepatitis; autoimmune disease;  
 KW acquired immune deficiency syndrome; malaria; cancer;  
 KW allograft rejection; allergy; Lyme disease; hepatitis;  
 KW post-streptococcal endocarditis; glomerulonephritis;  
 KW food hypersensitivity.  
 XX  
 OS Synthetic.  
 OS Hepatitis B virus.  
 XX  
 PN MO9832456-A1.  
 XX  
 PD 30-JUL-1998.  
 XX

XX 23-JAN-1998; 98WO-US001373.  
XX  
XX  
PR 23-JAN-1997; 97US-0036713P.  
PR 07-FEB-1997; 97US-0037432P.  
XX  
XX (EPIM-) EPIMMUNE INC.  
XX  
XX  
PI Sette A, Sidney J, Southwood S;  
XX  
XX WPI; 1998-427679/36.  
XX  
XX Composition containing peptide that induces cytotoxic T lymphocyte  
PT response, and helper peptide - can bind to human leucocyte antigen  
PT alleles, used to treat or prevent cancers, parasitic infections and  
PT autoimmune disease.  
XX  
XX  
XX Disclosure; Page 40; 51pp; English.  
XX  
XX AAW85284-451 represent helper T-cell class II peptides, which can bind to  
CC the human leucocyte antigens (HLA) DR4W4, DR1 and DR7. The peptides are  
CC used in the course of the invention. The specification describes peptides  
CC that induce a cytotoxic T lymphocyte (CTL) response, and T-helper  
CC peptides, that are used together to generate a CTL response for the  
CC treatment or prevention of viral, fungal, bacterial or parasitic  
CC infections (e.g. hepatitis, acquired immune deficiency syndrome or  
CC malaria) or cancer (e.g. renal or cervical carcinoma, lymphoma, prostate  
CC cancer or condyloma acuminatum). Helper T-cell peptides may be used alone  
CC to induce a helper T cell response, e.g. in cases of autoimmune disease,  
CC allograft rejection, allergy, Lyme disease, hepatitis, post-streptococcal  
CC endocarditis, glomerulonephritis and food hypersensitivity  
XX  
XX  
SQ Sequence 20 AA;

Query Match 27.0%; Score 31; DB 2; Length 20;  
Best Local Similarity 41.7%; Pred. No. 9.6e+02;  
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 3 PPHPTNHKYLVC 14  
| | | | | | | | | | | | | | | | | |  
Db 1 PPHPTNRQALVC 12

RESULT 92

AA90154  
ID AAY90154 standard; peptide; 20 AA.

XX  
AC AAY90154;

XX  
DT 06-AUG-2003 (revised)  
DT 21-BEP-2000 (first entry)

XX  
DE UPAR targeting sequence with spacers #3.

XX  
XX Ligand epitope; UPAR; urokinase-type plasminogen activator receptor;  
KM adenovirus; hexon HVPS loop; hexon HI loop; peripheral artery disease;  
KM recombinant adenovirus vector; tumour; restenosis; gene therapy; aschma;  
KM smooth muscle cell proliferation inhibitor; coronary artery disease;  
KM obesity; neurodegenerative disease; infection; autoimmune disease; HIV;  
XX thrombosis; diabetes; tropism-modified virus.  
XX  
XX  
OS Synthetic.

XX  
PN WO200012738-A1.

XX  
PD 09-MAR-2000.

XX  
PF 27-AUG-1999; 99WO-IB001524.

XX  
PR 27-AUG-1998; 98US-0098028P.

XX  
PA (AVERT ) AVENTIS PHARMA SA.

XX

PI Vigne B, Dedieu J, Latta M, Yeh P, Perricaudet M;  
XX  
XX WPI; 2000-256653/22.  
XX  
XX  
PT Urokinase-type plasminogen activator receptor (UPAR)-targeted adenovirus  
PT vectors having modified hexon HVPS and HI loops and modified fiber  
XX proteins useful for targeted gene therapy to treat cancer or restenosis.  
XX  
XX  
PS Claim 15; Page 69; 128pp; English.

XX  
XX This sequence represents a targeting sequence for UPAR, and is flanked by  
CC linkers. The invention relates to an adenovirus from which at least a  
CC part of the hexon HVPS or HI loop is replaced with a binding peptide, or  
CC targeting sequence, flanked by connecting amino acid spacers, to  
CC functionally display its binding specificity at the capsid surface. The  
CC invention also relates to a recombinant adenovirus vector where a binding  
CC peptide, or targeting sequence, is connected to the C-terminus of the  
CC fiber by a connecting spacer, or linker, so as to functionally display  
CC its binding specificity at the capsid surface. The adenovirus or  
CC recombinant adenovirus vector can be used to preferentially express a  
CC gene in a target cell, especially a cell that expresses a UPAR. The  
CC targeted adenovirus vector preferably comprises a heterologous gene  
CC encoding a gene for treatment of a tumour or restenosis. The targeted  
CC adenovirus vector is useful for gene therapy treatment of a disease, and  
CC for manufacturing a medicine used in gene therapy treatment of a disease.  
CC The viruses can also be used to inhibit smooth muscle cell proliferation,  
CC to treat peripheral artery diseases, coronary artery diseases, obesity,  
CC neurodegenerative diseases, infections, autoimmune diseases, aschma, HIV,  
CC thrombosis, and diabetes. The viruses are particularly targeted against a  
CC urokinase-type plasminogen activator receptor (UPAR). The adenoviruses  
CC are tropism-modified without adversely impacting productivity of the  
CC vectors. (Updated on 06-AUG-2003 to correct OS field.)  
XX  
XX  
SQ Sequence 20 AA;

Query Match 27.0%; Score 31; DB 3; Length 20;  
Best Local Similarity 45.5%; Pred. No. 9.6e+02;  
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 IPHPTNHKYL 12  
| | | | | | | | | | | | | | | | | |  
Db 6 MPHSLNFSQYL 16

RESULT 93

AA88603  
ID AAW88603 standard; protein; 14 AA.

XX  
AC AAW88603;

XX  
DT 01-MAR-1999 (first entry)

XX  
DE Secreted protein encoded by gene 70 clone HHFR32.

XX  
XX Human; secreted protein; fusion protein; gene therapy; protein therapy;  
KM diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;  
KM developmental abnormality; foetal deficiency; blood; allergy; renal;  
KM immune system; aschma; lymphocytic disease; brain; hepatic; lymphoma;  
KM inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;  
KM cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;  
KM osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;  
XX endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.

XX  
OS Homo sapiens.

XX  
PN WO9854963-A2.

XX  
PD 10-DEC-1998.

XX  
PF 04-JUN-1998; 98WO-US011422.

XX  
PR 06-JUN-1997; 97US-0048875P.  
PR 06-JUN-1997; 97US-0048876P.

XX

[illegible]

Young P, Greene JM, Ferlie AM, Ruben SM, Rosen CA, Hu J, Olsen HS, Ehler R, Brewer LA, Moore PA, Shi Y, Florence C, Plazencia K, Lafleur DW, Ni J, Fan P, Wei Y, Fischer CL, Soppet DR, Li Y, Zeng Z, Kyaw H, Yu G, Feng P, Dillon PJ, Endress GA, Carter KC;  
 WPI, 1999-059865/05.  
 N-PSDB; AAV84480.  
 New isolated human genes and the secreted polypeptides they encode - useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders.  
 Claim 11; Page 520; 772pp; English.  
 The invention relates to nucleic acid sequences (AAV84411 to AAV84633) encoding human secreted proteins (AAV88534 to AAV88756). The secreted protein gene sequences are deposited with the ATCC under deposit numbers ATCC 97979, 97974, 97975, 97976, 97977, 209007, 209008, 209009, 209010, 209011, 209080, 209081, 209082, 209083, 209084, 209085, 209511. Host cells comprising recombinant vectors containing the nucleic acid sequences are used for the recombinant production of the secreted proteins. The polynucleotide and amino acid sequences are useful for are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Pathological conditions can be also diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new polynucleotides. Specific uses are described for each of the polynucleotides, based on which tissues they are most highly expressed in, and include developing products for the diagnosis or treatment of cancer, neurodegenerative disorders, developmental abnormalities and foetal deficiencies, blood disorders, tumours, leukemias, diseases of the immune system, autoimmune diseases, hepatic and renal disease, lymphomas, inflammation, allergies, ischemic shock, Alzheimer's and cognitive disorders, schizophrenia, reestenosis, prostate diseases, obesity, disorders involving osteoclasts such as osteoporosis, arthritis or malignancies, diseases of testes, lung or thymus, digestive/endocrine disorders, infections and AIDS. The polypeptides are also useful for identifying their binding partners. The present sequence represents human secreted protein (see descriptor line for gene number and clone identification)  
 Sequence 14 AA;  
 Query March 26.5%; Score 30.5; DB 2; Length 14;  
 Best Local Similarity 46.2%; Pred. No. 7.6e+02;  
 Matches 6; Conservative 4; Mismatches 2; Indels 1; Gaps 1;  
 QY 6 TNHKY-LVCESV 17  
 ||| : |||  
 Db 1 THTHTHILICSV 13  
 RESULT 94  
 ADE70889  
 ID ADE70889 standard; peptide: 15 AA.  
 AC ADE70889,  
 XX  
 DT 29-JAN-2004 (first entry)  
 XX  
 DE Human 161P2F10B protein-related peptide 4894.  
 XX  
 KM 161P2F10B; cancer; cytostatic; gene therapy; vaccine; human.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2003040340-A2.  
 XX  
 PD 15-MAY-2003.  
 XX  
 PF 07-NOV-2002; 2002WO-US036002.  
 XX

PR 07-NOV-2001; 2001US-00005480.  
PR 31-JAN-2002; 2002US-00062109.  
XX  
XX (AGEN-) AGENSYS INC.  
XX  
XX Jakobovits A, Raitano AB, Faris M, Hubert RS, Ge W, Morrison KM;  
PI Morrison RK, Challita-Bid PM;  
XX  
XX WPI; 2003-441560/41.  
XX  
PT A composition for diagnosing, preventing and treating cancer (e.g.  
PT prostatic, renal or uterine cancer) comprises 161P2F10B polynucleotides  
PS and polypeptides.  
XX  
PS Claim 13; Page 183; 135pp; English.  
XX  
CC This invention relates to a novel composition which comprises a substance  
CC that modulates the status of a novel human protein (161P2F10B) and its  
CC variants having a sequence of 875 amino acids provided in the  
CC specification. The protein of the invention is over-expressed in certain  
CC cancers. The compounds of the invention may have cytostatic activity and  
CC the sequence of the 161P2F10B protein, and the gene which encodes it, may  
CC be useful for gene therapy or the development of a vaccine. The  
CC composition and methods of the invention are useful in diagnosing,  
CC preventing and treating cancer. The present sequence is the amino acid  
CC sequence of a peptide which is derived from the sequence of the human  
CC 161P2F10B protein and which may be used in the development of the  
CC compounds of the invention.  
XX  
SQ Sequence 15 AA;  
XX  
Query Match 26.5%; Score 30.5; DB 7; Length 15;  
Best Local Similarity 47.4%; Pred. No. 8.3e+02;  
Matches 9; Conservative 1; Mismatches 2; Indels 7; Gaps 2;  
XX  
QY 3 PH-PTNIHKYLCESVNGG 20  
||| |  
1 PHRPNTV-----ESCPG 13  
DB  
XX  
RESULT 95  
ADE70286  
ID ADE70286 standard; peptide; 15 AA.  
XX  
AC ADE70286;  
XX  
DT 29-JAN-2004 (first entry)  
XX  
XX Human 161P2F10B protein-related peptide 4291.  
XX  
XX 161P2F10B; cancer; cytostatic; gene therapy; vaccine; human.  
XX  
OS Homo sapiens.  
XX  
XX WO2003040340-A2.  
XX  
XX 15-MAY-2003.  
XX  
PD 07-NOV-2002; 2002WO-US036002.  
XX  
PF 07-NOV-2001; 2001US-00005480.  
XX  
PR 31-JAN-2002; 2002US-00062109.  
XX  
XX (AGEN-) AGENSYS INC.  
XX  
XX Jakobovits A, Raitano AB, Faris M, Hubert RS, Ge W, Morrison KM;  
PI Morrison RK, Challita-Bid PM;  
XX  
XX WPI; 2003-441560/41.  
XX  
PT A composition for diagnosing, preventing and treating cancer (e.g.  
PT prostatic, renal or uterine cancer) comprises 161P2F10B polynucleotides  
PS and polypeptides.

XX  
XX Claim 13; Page 178; 135pp; English.  
XX  
PS  
XX  
CC This invention relates to a novel composition which comprises a substance  
CC that modulates the status of a novel human protein (161P2F10B) and its  
CC variants having a sequence of 875 amino acids provided in the  
CC specification. The protein of the invention is over-expressed in certain  
CC cancers. The compounds of the invention may have cytostatic activity and  
CC the sequence of the 161P2F10B protein, and the gene which encodes it, may  
CC be useful for gene therapy or the development of a vaccine. The  
CC composition and methods of the invention are useful in diagnosing,  
CC preventing and treating cancer. The present sequence is the amino acid  
CC sequence of a peptide which is derived from the sequence of the human  
CC compounds of the invention.  
XX  
SQ Sequence 15 AA;  
XX  
Query Match 26.5%; Score 30.5; DB 7; Length 15;  
Best Local Similarity 47.4%; Pred. No. 8.3e+02;  
Matches 9; Conservative 1; Mismatches 2; Indels 7; Gaps 2;  
XX  
QY 3 PH-PTNIHKYLCESVNGG 20  
||| |  
1 PHRPNTV-----ESCPG 13  
DB  
XX  
RESULT 96  
ADE70871  
ID ADE70871 standard; peptide; 15 AA.  
XX  
AC ADE70871;  
XX  
DT 29-JAN-2004 (first entry)  
XX  
XX Human 161P2F10B protein-related peptide 4876.  
XX  
XX 161P2F10B; cancer; cytostatic; gene therapy; vaccine; human.  
XX  
XX Homo sapiens.  
XX  
OS WO2003040340-A2.  
XX  
XX 15-MAY-2003.  
XX  
PD 07-NOV-2002; 2002WO-US036002.  
XX  
PF 07-NOV-2001; 2001US-00005480.  
XX  
PR 31-JAN-2002; 2002US-00062109.  
XX  
XX (AGEN-) AGENSYS INC.  
XX  
XX Jakobovits A, Raitano AB, Faris M, Hubert RS, Ge W, Morrison KM;  
PI Morrison RK, Challita-Bid PM;  
XX  
XX WPI; 2003-441560/41.  
XX  
PT A composition for diagnosing, preventing and treating cancer (e.g.  
PT prostatic, renal or uterine cancer) comprises 161P2F10B polynucleotides  
PS and polypeptides.  
XX  
PS Claim 13; Page 183; 135pp; English.  
XX  
CC This invention relates to a novel composition which comprises a substance  
CC that modulates the status of a novel human protein (161P2F10B) and its  
CC variants having a sequence of 875 amino acids provided in the  
CC specification. The protein of the invention is over-expressed in certain  
CC cancers. The compounds of the invention may have cytostatic activity and  
CC the sequence of the 161P2F10B protein, and the gene which encodes it, may  
CC be useful for gene therapy or the development of a vaccine. The  
CC composition and methods of the invention are useful in diagnosing,  
CC preventing and treating cancer. The present sequence is the amino acid  
CC sequence of a peptide which is derived from the sequence of the human

CC 161P210B protein and which may be used in the development of the  
CC compounds of the invention.  
XX  
SQ Sequence 15 AA;

Query Match 26.5%; Score 30.5; DB 7; Length 15;  
Best Local Similarity 47.4%; Pred. No. 8.3e+02;  
Matches 9; Conservative 1; Mismatches 2; Indels 7; Gaps 2;

OY 3 PH-PTN1HKYLVCSVNGG 20  
| | | | | | | | | | | | | | | | | | | | | |  
DB 1 PHRPYV-----SSCPGG 13

## RESULT 97

ADT92805  
ID ADT92805 standard; peptide; 8 AA.

XX ADT92805;  
XX

DT 13-JAN-2005 (first entry)

DE Consensus peptide mapped onto actin surface.

KM Epitope mapping; tertiary structure; antibody imprinting; actin.

XX Unidentified.

OS WO2004092741-A2.

XX 28-OCT-2004.

PD 14-APR-2004; 2004WO-US011905.

PR 14-APR-2003; 2003US-0462870P.

PA (UYMO-) UNIV MONTANA STATE.

XX Dratz EA, Mumey BM, Jeeaitis AJ;

PI WPI; 2004-795230/78.

XX Mapping discontinuous/surface antibody epitopes on target protein.  
PT comprises binding antibody that binds to target protein with library of  
PT random peptides, computationally aligning peptide sequences to construct  
PT epitope on target protein.

XX Example 2; Page 22; 40pp; English.

XX The invention relates to mapping (M1) discontinuous epitopes on a target  
CC protein. The method of the invention comprises contacting a solid support  
CC having an antibody capable of binding to the target protein, with a  
CC library of random peptides, where the set of probe peptides bind to  
CC antibody, eluting the set of probe peptides, determining the amino acid  
CC sequence of members of the probe peptides, computationally aligning the  
CC probe peptide sequences to the target protein, and constructing a  
CC discontinuous epitope on the target protein. The solid support comprises  
CC a first protein, and is then contacted with a second protein under  
CC conditions, where the first protein binds to the second protein. The  
CC solid support is then contacted with a library of random peptides under  
CC conditions, where a set of probe peptides compete with the second protein  
CC for binding to the first protein, eluting the set of probe peptides,  
CC determining the amino acid sequence of the members of the set of probe  
CC peptides, computationally aligning the amino acid sequences of the  
CC members of the set of probe peptides to the target protein, constructing  
CC the binding site on the protein. A computing device for carrying out  
CC (M1), is also disclosed. The method of the invention is useful for  
CC mapping discontinuous antibody or aptamer epitopes on a target protein.  
CC It is also useful for elucidating the tertiary structure of proteins, and  
CC for providing structural information in antibody imprinting, to reveal  
CC distant segments of primary sequence that are in close spatial proximity  
CC on the native, folded protein. The current sequence represents a  
CC consensus peptide that is mapped onto the surface actin. This peptide is

CC from an example of the invention in which the method of the invention is  
CC validated using actin as a model protein.  
XX

SQ Sequence 8 AA;

Query Match 26.1%; Score 30; DB 8; Length 8;  
Best Local Similarity 80.0%; Pred. No. 2e+06;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 IPHPT 6  
| | | | | | | | | | | | | | | | | | | | | |  
DB 1 VPHPT 5

## RESULT 98

AAM22945  
ID AAM22945 standard; peptide; 9 AA.

XX AAM22945;  
XX

DT 22-OCT-2001 (first entry)

DE HIV peptide SEQ ID NO 830.

XX Cytotoxic T cell lymphocyte; CTL; anti-HIV; viral disease; HIV;  
KM human immunodeficiency virus; vaccine.

XX Human immunodeficiency virus.

OS Synthetic.

XX WO200155177-A2.

PD 02-AUG-2001.

PF 29-JAN-2001; 2001WO-DK000059.

PR 28-JAN-2000; 2000EP-00610017.

PR 31-JAN-2000; 2000US-0179333P.

PA (STAT-) STATENS SERUM INST.

XX Fomsgaard A, Brunak S, Buus S, Corbet S, Laemmoller SL, Hansen J;

PI WPI; 2001-476184/51.

XX The generation of cytotoxic T cell lymphocytes epitopes for use in anti-  
PT HIV vaccines.  
PT

XX Example 4; Page 69; 383pp; English.

XX The invention relates to identification of cytotoxic T cell lymphocyte  
CC (CTL) epitopes (AAM22116-AAM23484) that generate anti-HIV activity. CTL  
CC are a major protective mechanism against viral diseases. Antibodies may  
CC neutralise extracellular human immunodeficiency virus (HIV) and limit or  
CC prevent infection of cells in the host, but CTL will limit viral  
CC production by killing the cell. The CTL epitopes are useful in medicine,  
CC in the manufacture of vaccines or diagnostic agents  
CC

SQ Sequence 9 AA;

Query Match 26.1%; Score 30; DB 4; Length 9;  
Best Local Similarity 71.4%; Pred. No. 2e+06;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 IPHPTNI 8  
| | | | | | | | | | | | | | | | | | | | | |  
DB 3 IPHPAGI 9

## RESULT 99

AAM22902  
ID AAM22902 standard; peptide; 9 AA.

XX

AC AAM22902;  
 XX  
 DT 22-OCT-2001 (first entry)  
 XX  
 DE HIV peptide SEQ ID NO 787.  
 XX  
 KM Cytotoxic T cell lymphocyte; CTL; anti-HIV; viral disease; HIV;  
 XX human immunodeficiency virus; vaccine.  
 OS  
 OS Human immunodeficiency virus.  
 OS Synthetic.  
 OS  
 PN WO200155177-A2.  
 XX  
 PD 02-AUG-2001.  
 XX  
 PF 29-JAN-2001; 2001WO-DK000059.  
 XX  
 PR 28-JAN-2000; 2000EP-00610017.  
 XX 31-JAN-2000; 2000US-0179333P.  
 XX  
 PA (STAT-) STATENS SERUM INST.  
 XX  
 PI Fomsgaard A, Brunak S, Buus S, Corbet S, Lauemoller SL, Hansen J;  
 XX WPI; 2001-476184/51.  
 XX  
 DR  
 XX  
 PT The generation of cytotoxic T cell lymphocytes epitopes for use in anti-  
 PT HIV vaccines.  
 XX  
 PS Example 4; Page 69; 383pp; English.  
 XX  
 CC The invention relates to identification of cytotoxic T cell lymphocyte  
 CC (CTL) epitopes (AAM22116-AAM23484) that generate anti-HIV activity. CTL  
 CC are a major protective mechanism against viral diseases. Antibodies may  
 CC neutralise extracellular human immunodeficiency virus (HIV) and limit or  
 CC prevent infection of cells in the host, but CTL will limit viral  
 CC production by killing the cell. The CTL epitopes are useful in medicine,  
 CC in the manufacture of vaccines or diagnostic agents  
 CC  
 SQ Sequence 9 AA;  
 Query Match 26.1%; Score 30; DB 4; Length 9;  
 Best Local Similarity 71.4%; Pred. No. 2e+06;  
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 2 IHPHNI 8  
 |||||  
 Db 3 IHPHAGI 9  
 |||||  
 RESULT 100  
 ADY92047  
 ID ADY92047 standard; peptide; 9 AA.  
 XX  
 AC ADY92047;  
 XX  
 DT 02-JUN-2005 (first entry)  
 XX  
 DE Human tumor-associated antigen LDHC MHC I epitope peptide - SEQ ID 367.  
 XX  
 KM tumor-associated antigen; LDHC; lactate dehydrogenase C; gene expression;  
 XX cell death; cell growth; tumor; cancer; neoplasm; cytostatic.  
 OS  
 OS Homo sapiens.  
 OS  
 PN WO2005026205-A2.  
 XX  
 PD 24-MAR-2005.  
 XX  
 PF 10-SEP-2004; 2004WO-EP010164.  
 XX  
 PR 10-SEP-2003; 2003DE-01041812.

XX  
 PA (GANY-) GANYMED PHARM AG.  
 XX  
 PI Tureci O, Sahin U, Koslowski M;  
 XX  
 DR WPI; 2005-242374/25.  
 XX  
 PT Pharmaceutical composition, with an agent to restrict the expression or  
 PT activity of an antigen associated with a tumor, incorporates structured  
 PT nucleic acids.  
 XX  
 XX  
 PS Disclosure; SEQ ID NO 367; 353pp; German.  
 XX  
 CC  
 CC The invention relates to a novel pharmaceutical composition, whereby the  
 CC composition contains an agent which restricts the expression or activity  
 CC of an antigen associated with a tumor and the antigen has a sequence,  
 CC coded by a nucleic acid, where the nucleic acid is selected from SEQ ID  
 CC NOs: 19-21, 54-57, 1-5, 29, 31-33, 37, 39, 40, 62, 63, 70, 74 or 85-88.  
 CC The composition of the invention induces cell death and a reduction of  
 CC cell growth, cell membrane damage or secretion of cytokines. The  
 CC composition may be useful for the identification of differentially  
 CC expressed genes in tumors with combined in silico and wet bench studies.  
 CC The current sequence is that of a human tumor-associated antigen lactate  
 CC dehydrogenase C (LDHC) MHC class I HLA-B\*0702 epitope peptide of the  
 CC invention which stimulates cytotoxic T-lymphocytes in vivo.  
 CC  
 SQ Sequence 9 AA;  
 Query Match 26.1%; Score 30; DB 9; Length 9;  
 Best Local Similarity 44.4%; Pred. No. 2e+06;  
 Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
 QY 4 HPTNHRKL 12  
 |||||  
 Db 1 HPTSCHGI 9  
 |||||  
 Search completed: January 20, 2006, 19:05:14  
 Job time : 79.5769 secs



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OW protein - protein search, using sw model

Run on: January 20, 2006, 18:58:05 / Search time 20.9615 seconds

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Perfect score: 115  
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Gapop 10.0, Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 223517

Minimum DB seq length: 0  
Maximum DB seq length: 20

Post-processing: Minimum Match 0%

Maximum Match 100%  
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4: /cgn2\_6/ptodata/1/1aa/H.COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/PCITUS.COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/backfile1.pep:\*

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and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	115	100.0	20	2	US-09-292-225-3
2	109	94.8	19	2	US-09-292-225-11
3	35	30.4	15	2	US-08-595-945-3
4	35	30.4	19	2	US-08-595-945-15
5	35	30.4	20	2	US-09-026-276-20
6	35	30.4	20	2	US-09-964-201A-20
7	34	29.6	15	1	US-07-829-462-6
8	32	27.8	10	2	US-08-159-339A-551
9	32	27.8	15	2	US-09-009-953-109
10	31	27.0	8	1	US-08-529-190B-73
11	31	27.0	16	2	US-09-791-524A-3
12	31	27.0	17	1	US-08-370-567-1
13	31	27.0	17	1	US-08-438-759-1
14	31	27.0	17	1	US-08-538-911-20
15	31	27.0	17	2	US-09-402-641-10
16	31	27.0	17	2	US-09-411-067C-2
17	31	27.0	17	2	US-09-428-082B-16
18	31	27.0	17	2	US-09-155-260C-16
19	31	27.0	17	2	US-09-402-464-1
20	31	27.0	17	2	US-09-791-524A-4
21	31	27.0	17	4	PCT-US94-05591-20
22	31	27.0	17	4	PCT-US94-05684-1
23	31	27.0	20	2	US-09-791-524A-9
24	30	26.1	10	1	US-07-890-422B-19
25	30	26.1	10	2	US-09-139-802-58
26	30	26.1	10	2	US-09-659-786-58
27	30	26.1	10	2	US-08-926-914-58

28	30	26.1	15	2	US-09-300-410A-2	Sequence 2, Appl
29	30	26.1	16	2	US-09-541-345-7	Sequence 7, Appl
30	30	26.1	16	2	US-09-825-517A-7	Sequence 7, Appl
31	29.5	25.7	20	1	US-08-614-935-75	Sequence 75, Appl
32	29.5	25.7	20	1	US-09-130-287-75	Sequence 75, Appl
33	29	25.2	6	1	US-08-192-243-1	Sequence 1, Appl
34	29	25.2	6	1	US-08-448-059-1	Sequence 1, Appl
35	29	25.2	6	2	US-09-295-996B-15	Sequence 15, Appl
36	29	25.2	6	2	US-09-295-846B-18	Sequence 18, Appl
37	29	25.2	6	2	US-09-551-737C-18	Sequence 18, Appl
38	29	25.2	6	2	US-09-295-924B-10	Sequence 10, Appl
39	29	25.2	6	2	US-09-551-738B-15	Sequence 15, Appl
40	29	25.2	11	1	US-07-942-245-495	Sequence 495, App
41	29	25.2	11	1	US-08-024-253-16	Sequence 16, Appl
42	29	25.2	11	2	US-09-649-063-16	Sequence 16, Appl
43	29	25.2	17	2	US-08-918-428D-15	Sequence 15, Appl
44	29	25.2	20	1	US-08-305-871A-11	Sequence 11, Appl
45	29	25.2	20	1	US-08-614-935-26	Sequence 26, Appl
46	29	25.2	20	1	US-08-797-842-7	Sequence 7, Appl
47	29	25.2	20	2	US-09-100-409A-47	Sequence 47, Appl
48	29	25.2	20	2	US-09-130-287-26	Sequence 26, Appl
49	29	25.2	20	2	US-09-009-953-195	Sequence 195, App
50	29	25.2	20	2	US-08-788-822A-14	Sequence 14, Appl
51	29	25.2	20	2	US-09-311-784B-150	Sequence 150, App
52	29	25.2	20	2	US-09-239-043D-2566	Sequence 2566, Ap
53	29	25.2	20	2	US-09-701-623C-71	Sequence 71, Appl
54	29	25.2	20	2	US-09-674-183-8	Sequence 8, Appl
55	29	25.2	20	2	US-10-666-480-5	Sequence 5, Appl
56	29	25.2	20	2	US-09-618-592-7	Sequence 7, Appl
57	28	24.3	9	2	US-08-159-339A-526	Sequence 526, Appl
58	28	24.3	11	2	US-09-119-507B-51	Sequence 51, Appl
59	28	24.3	11	2	US-08-897-556A-51	Sequence 51, Appl
60	28	24.3	11	2	US-09-647-693-51	Sequence 51, Appl
61	28	24.3	13	1	US-08-147-011-1	Sequence 11, Appl
62	28	24.3	13	1	US-08-480-190-221	Sequence 221, App
63	28	24.3	13	1	US-08-488-379-221	Sequence 221, App
64	28	24.3	13	2	US-08-475-399A-221	Sequence 221, App
65	28	24.3	13	2	US-08-077-255A-221	Sequence 221, App
66	28	24.3	13	4	PCT-US93-07545-221	Sequence 221, App
67	28	24.3	14	1	US-08-480-190-90	Sequence 90, Appl
68	28	24.3	14	1	US-08-480-190-220	Sequence 220, Appl
69	28	24.3	14	1	US-08-488-379-90	Sequence 90, Appl
70	28	24.3	14	1	US-08-488-379-220	Sequence 220, Appl
71	28	24.3	14	1	US-08-475-399A-90	Sequence 90, Appl
72	28	24.3	14	2	US-08-077-255A-220	Sequence 220, Appl
73	28	24.3	14	2	US-08-077-255A-90	Sequence 90, Appl
74	28	24.3	14	2	US-08-077-255A-220	Sequence 220, Appl
75	28	24.3	14	4	PCT-US93-07545-220	Sequence 220, Appl
76	28	24.3	14	4	PCT-US93-07545-220	Sequence 220, Appl
77	28	24.3	15	1	US-08-480-190-88	Sequence 88, Appl
78	28	24.3	15	1	US-08-480-190-89	Sequence 89, Appl
79	28	24.3	15	1	US-08-488-379-88	Sequence 88, Appl
80	28	24.3	15	1	US-08-488-379-88	Sequence 88, Appl
81	28	24.3	15	2	US-09-009-953-110	Sequence 89, Appl
82	28	24.3	15	2	US-08-475-399A-88	Sequence 88, Appl
83	28	24.3	15	2	US-08-475-399A-88	Sequence 88, Appl
84	28	24.3	15	2	US-08-077-255A-88	Sequence 88, Appl
85	28	24.3	15	4	US-08-077-255A-88	Sequence 88, Appl
86	28	24.3	15	4	PCT-US93-07545-88	Sequence 88, Appl
87	28	24.3	15	4	PCT-US93-07545-88	Sequence 88, Appl
88	28	24.3	16	1	US-08-480-190-85	Sequence 85, Appl
89	28	24.3	16	1	US-08-480-190-86	Sequence 86, Appl
90	28	24.3	16	1	US-08-480-190-87	Sequence 87, Appl
91	28	24.3	16	1	US-08-488-379-85	Sequence 85, Appl
92	28	24.3	16	1	US-08-488-379-85	Sequence 85, Appl
93	28	24.3	16	1	US-08-488-379-87	Sequence 87, Appl
94	28	24.3	16	2	US-08-810-009-51	Sequence 51, Appl
95	28	24.3	16	2	US-08-475-399A-85	Sequence 85, Appl
96	28	24.3	16	2	US-08-475-399A-86	Sequence 86, Appl
97	28	24.3	16	2	US-08-475-399A-87	Sequence 87, Appl
98	28	24.3	16	2	US-09-776-490-51	Sequence 51, Appl
99	28	24.3	16	2	US-08-077-255A-85	Sequence 85, Appl
100	28	24.3	16	2	US-08-077-255A-86	Sequence 86, Appl

## ALIGNMENTS

## RESULT 1

US-09-292-225-3  
; Sequence 3, Application US/09292225  
; Patent No. 6455686  
; GENERAL INFORMATION:  
; APPLICANT: McCall, Catherine A.  
; APPLICANT: Hunter, Shirley Wu  
; APPLICANT: Weber, Eric R.  
; TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS  
; TITLE OF INVENTION: AND USES THEREOF  
; FILE REFERENCE: AL-2-C3  
; CURRENT APPLICATION NUMBER: US/09/292,225  
; EARLIER FILING DATE: 1999-04-15  
; EARLIER APPLICATION NUMBER: 60/098,909  
; EARLIER FILING DATE: 1998-09-02  
; EARLIER APPLICATION NUMBER: 60/085,295  
; EARLIER FILING DATE: 1998-05-13  
; EARLIER APPLICATION NUMBER: 60/098,565  
; EARLIER FILING DATE: 1998-04-17  
; EARLIER APPLICATION NUMBER: 09/062,013  
; EARLIER FILING DATE: 1998-04-17  
; NUMBER OF SEQ ID NOS: 49  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 3  
; LENGTH: 20  
; TYPE: PRT  
; ORGANISM: Dermatophagoides farinae  
US-09-292-225-3

Query Match 100.0%; Score 115; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 7.4e-12;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DHPPTNHHKYLVCESVNG 20  
Db 1 DHPPTNHHKYLVCESVNG 20

## RESULT 2

US-09-292-225-11  
; Sequence 11, Application US/09292225  
; Patent No. 6455686  
; GENERAL INFORMATION:  
; APPLICANT: McCall, Catherine A.  
; APPLICANT: Hunter, Shirley Wu  
; APPLICANT: Weber, Eric R.  
; TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS  
; TITLE OF INVENTION: AND USES THEREOF  
; FILE REFERENCE: AL-2-C3  
; CURRENT APPLICATION NUMBER: US/09/292,225  
; EARLIER FILING DATE: 1999-04-15  
; EARLIER APPLICATION NUMBER: 60/098,909  
; EARLIER FILING DATE: 1998-09-02  
; EARLIER APPLICATION NUMBER: 60/085,295  
; EARLIER FILING DATE: 1998-05-13  
; EARLIER APPLICATION NUMBER: 60/098,565  
; EARLIER FILING DATE: 1998-04-17  
; EARLIER APPLICATION NUMBER: 09/062,013  
; EARLIER FILING DATE: 1998-04-17  
; NUMBER OF SEQ ID NOS: 49  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 11  
; LENGTH: 19  
; TYPE: PRT  
; ORGANISM: Dermatophagoides farinae  
US-09-292-225-11

Query Match 94.8%; Score 109; DB 2; Length 19;

Best Local Similarity 100.0%; Pred. No. 6.5e-11;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DHPPTNHHKYLVCESVNG 19  
Db 1 DHPPTNHHKYLVCESVNG 19

## RESULT 3

US-08-595-945-3  
; Sequence 3, Application US/08595945  
; Patent No. 6143509  
; GENERAL INFORMATION:  
; APPLICANT: DOWELL, BARRY L.  
; APPLICANT: BRIDON, DOMINIQUE P.  
; APPLICANT: QIU, XIAOXING  
; APPLICANT: LITUA, HANS  
; APPLICANT: PIIRONEN, TIMO P.  
; APPLICANT: VIHINEN, MAUNO A.  
; APPLICANT: PETERSSON, KIM S. I.  
; TITLE OF INVENTION: PROSTATE SPECIFIC ANTIGEN PEPTIDES  
; TITLE OF INVENTION: AND USES THEREOF  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESSER: ABBOTT LABORATORIES  
; STREET: 100 ABBOTT PARK ROAD  
; CITY: ABBOTT PARK  
; STATE: IL  
; COUNTRY: USA  
; ZIP: 60064-3500  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/595,945  
; FILING DATE: 06-FEB-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BECKER, CHERYL L.  
; REGISTRATION NUMBER: 35,441  
; REFERENCE/DOCKET NUMBER: 5875.US.01  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 847-935-1729  
; TELEFAX: 847-938-2623  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-595-945-3

Query Match 30.4%; Score 35; DB 2; Length 15;

Best Local Similarity 36.4%; Pred. No. 45;  
Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 4 HPTNHHKYLVC 14  
Db 5 HPOKTKFMFLC 15

## RESULT 4

US-08-595-945-15  
; Sequence 15, Application US/08595945  
; Patent No. 6143509  
; GENERAL INFORMATION:  
; APPLICANT: DOWELL, BARRY L.  
; APPLICANT: BRIDON, DOMINIQUE P.  
; APPLICANT: QIU, XIAOXING  
; APPLICANT: LITUA, HANS

APPLICANT: PIIRONEN, TIMO P.  
APPLICANT: VIHINEN, MAURO A.  
APPLICANT: PETERSSON, KIM S.I.  
TITLE OF INVENTION: PROSTATE SPECIFIC ANTIGEN PEPTIDES  
TITLE OF INVENTION: AND USES THEREOF  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: ABBOTT LABORATORIES  
STREET: 100 ABBOTT PARK ROAD  
CITY: ABBOTT PARK  
STATE: IL  
COUNTRY: USA  
ZIP: 60064-3500  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION NUMBER: US/08/595,945  
APPLICATION NUMBER: US/08/595,945  
FILING DATE: 06-FEB-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: BECKER, CHERYL L.  
REGISTRATION NUMBER: 35,441  
REFERENCE/DOCKET NUMBER: 5875.US.01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 847-935-1729  
TELEFAX: 847-938-2623  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-595-945-15

Query Match 30.4%; Score 35; DB 2; Length 19;  
Best Local Similarity 36.4%; Pred. No. 58;  
Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;  
QY 4 HPTNHYKLYVC 14  
DB 9 HPQKVTKFMLC 19  
RESULT 5  
US-09-026-276-20  
Sequence 20, Application US/09026276  
Patent No. 6319503  
GENERAL INFORMATION:  
APPLICANT: Kenten, John H  
APPLICANT: Tramotoano, Alfonso  
APPLICANT: Pilon, Aprille L.  
APPLICANT: Lohmas, Gerald L.  
APPLICANT: Robertes, Steven P  
TITLE OF INVENTION: HEAT-SHOCK FUSION-BASED VACCINE SYSTEM  
FILE REFERENCE: U.S. Patent Application No. 6319503 09\026,276  
CURRENT APPLICATION NUMBER: US/09/026,276  
CURRENT FILING DATE: 1998-02-19  
NUMBER OF SEQ ID NOS: 35  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 20  
LENGTH: 20  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-026-276-20

Query Match 30.4%; Score 35; DB 2; Length 20;  
Best Local Similarity 36.4%; Pred. No. 61;  
Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 4 HPTNHYKLYVC 14  
DB 7 HPQKVTKFMLC 17

RESULT 6  
US-09-964-201A-20  
Sequence 20, Application US/09964201A  
Patent No. 6660271  
GENERAL INFORMATION:  
APPLICANT: Kenten, John H  
APPLICANT: Tramotoano, Alfonso  
APPLICANT: Pilon, Aprille L.  
APPLICANT: Lohmas, Gerald L.  
APPLICANT: Robertes, Steven P  
TITLE OF INVENTION: HEAT-SHOCK FUSION-BASED VACCINE SYSTEM  
FILE REFERENCE: U.S. Patent Application No. 6660271 09\026,276  
CURRENT APPLICATION NUMBER: US/09/964,201A  
CURRENT FILING DATE: 2002-05-21  
NUMBER OF SEQ ID NOS: 35  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 20  
LENGTH: 20  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-964-201A-20

Query Match 30.4%; Score 35; DB 2; Length 20;  
Best Local Similarity 36.4%; Pred. No. 61;  
Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 4 HPTNHYKLYVC 14  
DB 7 HPQKVTKFMLC 17

RESULT 7  
US-07-829-462-6  
Sequence 6, Application US/07829462  
Patent No. 5453489  
GENERAL INFORMATION:  
APPLICANT: Ruoslahti, Erkki I.  
APPLICANT: Morla, Alex  
TITLE OF INVENTION: NOVEL FRAGMENTS OF FIBRONECTIN AND  
METHODS TO MODULATE THE ROLE OF FIBRONECTIN IN  
TITLE OF INVENTION: EXTRACELLULAR MATRIX ASSEMBLY  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CAMPBELL AND FLORES  
STREET: 4370 La Jolla Village Drive, Suite 700  
CITY: San Diego  
STATE: California  
COUNTRY: USA  
ZIP: 92132  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION NUMBER: US/07/829,462  
CURRENT FILING DATE: 19920131  
FILING DATE: 19920131  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: CAMPBELL, CATHERYN A.  
REGISTRATION NUMBER: 31,547  
REFERENCE/DOCKET NUMBER: P-LA 9179  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-535-8949  
TELEFAX: 619-535-8949  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids

TYPE: AMINO ACID  
TOPOLOGY: linear  
US-07-829-462-6

Query Match 29.6%; Score 34; DB 1; Length 15;  
Best Local Similarity 45.5%; Pred. No. 65;  
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 3 IPHPTNIHKLV 13  
Db 3 PPSHSKIL 13

RESULT 8  
US-08-159-339A-551  
Sequence 551, Application US/08159339A  
Patent No. 6037135

GENERAL INFORMATION:  
APPLICANT: Kubo, Ralph T.  
APPLICANT: Grey, Howard M.  
APPLICANT: Sette, Alessandro  
APPLICANT: Celis, Eateban  
TITLE OF INVENTION: HLA Binding peptides and their  
TITLE OF INVENTION: Uses  
NUMBER OF SEQUENCES: 1254  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: CA

COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/159,339A  
FILING DATE: 29-NOV-1993  
CLASSIFICATION: 424

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/926,666  
FILING DATE: 07-AUG-1992  
APPLICATION NUMBER: US 08/027,746  
FILING DATE: 05-MAR-1993  
APPLICATION NUMBER: US 08/103,396  
FILING DATE: 06-AUG-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Weber, Ellen Lauver  
REGISTRATION NUMBER: 32,762  
REFERENCE/DOCKET NUMBER: 016623-005030US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300

TELEX:  
INFORMATION FOR SEQ ID NO: 551:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-159-339A-551

Query Match 27.8%; Score 32; DB 2; Length 10;  
Best Local Similarity 55.6%; Pred. No. 88;  
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 IPHPTNIHK 10  
Db 2 IPHPAGLKK 10

RESULT 9  
US-09-009-953-109  
Sequence 109, Application US/09009953  
Patent No. 6413517

GENERAL INFORMATION:  
APPLICANT: Sette, Alessandro  
TITLE OF INVENTION: Identification of Broadly  
Reactive DR Restricted Epitopes  
NUMBER OF SEQUENCES: 274  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: CA

COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/009,953  
FILING DATE: 21-Jan-1998  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/036,713  
FILING DATE: 23-JAN-1997  
APPLICATION NUMBER: US 60/037,432  
FILING DATE: 07-FEB-1997

ATTORNEY/AGENT INFORMATION:  
NAME: Weber, Ellen Lauver  
REGISTRATION NUMBER: 32,762  
REFERENCE/DOCKET NUMBER: 016623-011520US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-576-0200  
TELEFAX: 415-576-0300  
TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 109:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 109:  
US-09-009-953-109

Query Match 27.8%; Score 32; DB 2; Length 15;  
Best Local Similarity 55.6%; Pred. No. 1,4e+02;  
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 IPHPTNIHK 10  
Db 6 IPHPAGLKK 14

RESULT 10  
US-08-529-190B-73  
Sequence 73, Application US/08529190B  
Patent No. 5833991

GENERAL INFORMATION:  
APPLICANT: Masucci, Maria G.  
TITLE OF INVENTION: GLYCINE-CONTAINING SEQUENCES  
CONFERRING INVISIBILITY TO THE IMMUNE SYSTEM  
NUMBER OF SEQUENCES: 76  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Banner & Witcoff, Ltd.  
STREET: One Financial Center  
CITY: Boston  
STATE: MA

COUNTRY: USA

ZIP: 02111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: Wordperfect 6.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/529,190B  
FILING DATE: 15-SEP-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: SE9501324-9  
FILING DATE: 10-APR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US08/522,595  
FILING DATE: 01-SEP-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Williams, Ph. D., Kathleen A  
REGISTRATION NUMBER: 34,380  
REFERENCE/DOCKET NUMBER: 3255/53015  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-345-9100  
TELEFAX: 617-345-9111  
INFORMATION FOR SEQ ID NO: 73:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-529-190B-73

Query Match 27.0%; Score 31; DB 1; Length 8;  
Best Local Similarity 71.4%; Pred. No. 4.6e+05;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 8 IHKYLVC 14  
DB 1 IHRYLRC 7

RESULT 11  
US-09-791-524A-3  
Sequence 3, Application US/09791524A  
Patent No. 6911199  
GENERAL INFORMATION:  
APPLICANT: Aventis Pharmaceuticals Products Inc.  
TITLE OF INVENTION: Targeted Adenovirus Vectors For Delivery Of Heterologous Genes  
FILE REFERENCE: P26,992-B USA  
CURRENT APPLICATION NUMBER: US/09/791,524A  
PRIOR FILING DATE: 2001-02-22  
PRIOR APPLICATION NUMBER: PCT/IB99/01524  
PRIOR FILING DATE: 1999-08-27  
PRIOR APPLICATION NUMBER: US 60/098,028  
PRIOR FILING DATE: 1998-08-27  
NUMBER OF SEQ ID NOS: 155  
SOFTWARE: Patent version 3.2  
SEQ ID NO 3  
LENGTH: 16  
TYPE: PRT  
ORGANISM: Adenovirus  
US-09-791-524A-3

Query Match 27.0%; Score 31; DB 2; Length 16;  
Best Local Similarity 45.5%; Pred. No. 2.1e+02;  
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 IHPHNIHKL 12  
DB 4 MPHSLNFSQYL 14

RESULT 12

US-08-370-567-1  
Sequence 1, Application US/08370567  
Patent No. 5656726  
GENERAL INFORMATION:  
APPLICANT: Rosenberg, Steven  
APPLICANT: Doyle, Michael  
TITLE OF INVENTION: Peptide Inhibitors of Urokinase Receptor  
NUMBER OF SEQUENCES: 37  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Chiron Corporation  
STREET: 4560 Horton Street  
CITY: Emeryville  
STATE: CA  
COUNTRY: USA  
ZIP: 94608  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/370,567  
FILING DATE:  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/061,514  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Green, Grant D.  
REGISTRATION NUMBER: 31,259  
REFERENCE/DOCKET NUMBER: 0941.001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 510-601-2706  
TELEFAX: 510-655-3542  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHEICAL: NO  
US-08-370-567-1

Query Match 27.0%; Score 31; DB 1; Length 17;  
Best Local Similarity 45.5%; Pred. No. 2.3e+02;  
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 IHPHNIHKL 12  
DB 4 MPHSLNFSQYL 14

RESULT 13  
US-08-438-759-1  
Sequence 1, Application US/08438759  
Patent No. 5679782  
GENERAL INFORMATION:  
APPLICANT: Rosenberg, Steven  
APPLICANT: Doyle, Michael  
TITLE OF INVENTION: Peptide Inhibitors of Urokinase Receptor  
NUMBER OF SEQUENCES: 37  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Chiron Corporation  
STREET: 4560 Horton Street  
CITY: Emeryville  
STATE: CA  
COUNTRY: USA  
ZIP: 94608  
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/438,759  
FILING DATE:  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/370,567  
FILING DATE:  
APPLICATION NUMBER: US/08/061,514  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Green, Grant D.  
REGISTRATION NUMBER: 31,259  
REFERENCE/DOCKET NUMBER: 0941.001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 510-601-2706  
TELEFAX: 510-655-3542  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
US-08-438-759-1

Query Match 27.0%; Score 31; DB 1; Length 17;  
Best Local Similarity 45.5%; Pred. No. 2.3e+02;  
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 IHPPTNIHKYL 12  
:|||:|  
DB 4 MPHSLNFSQYL 14

RESULT 14  
US-08-538-911-20  
Sequence 20, Application US/08538911  
Patent No. 5750344  
GENERAL INFORMATION:  
APPLICANT: Doyle, Michael  
APPLICANT: Winter, Jill  
TITLE OF INVENTION: Method For Selection Of Biologically  
TITLE OF INVENTION: Active Peptide Sequences  
NUMBER OF SEQUENCES: 21  
CORRESPONDENCE ADDRES:  
ADDRESSEE: Chiron Corporation  
STREET: 4560 Horton Street  
CITY: Emeryville  
STATE: CA  
COUNTRY: USA  
ZIP: 94608  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/538,911  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/069,352  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Green, Grant D.  
REGISTRATION NUMBER: 31,259  
REFERENCE/DOCKET NUMBER: 0407.001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 510-601-2706

TELEFAX: 510-655-3542  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
US-08-538-911-20

Query Match 27.0%; Score 31; DB 1; Length 17;  
Best Local Similarity 45.5%; Pred. No. 2.3e+02;  
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 IHPPTNIHKYL 12  
:|||:|  
DB 4 MPHSLNFSQYL 14

RESULT 15  
US-09-402-641-10  
Sequence 10, Application US/09402641  
Patent No. 6528619  
GENERAL INFORMATION:  
APPLICANT: BURGIE, Markus  
APPLICANT: GRAPP, Heinrich  
APPLICANT: KESSLER, Horst  
APPLICANT: MAGDOLEN, Viktor Robert  
APPLICANT: KOENIG, Bernhard  
APPLICANT: KOPITZ, Marcus  
APPLICANT: RIEMER, Christoph  
APPLICANT: SCHMITT, Manfred  
APPLICANT: WEIDLE, Ulrich  
APPLICANT: WILHELM, Olaf  
TITLE OF INVENTION: INHIBITORS FOR UROKINASE RECEPTOR  
FILE REFERENCE: Case 20367US  
CURRENT APPLICATION NUMBER: US/09/402,641  
CURRENT FILING DATE: 2000-01-10  
PRIOR APPLICATION NUMBER: EP97106024.9  
PRIOR FILING DATE: 1997-04-11  
PRIOR APPLICATION NUMBER: PCT/EP98/02178  
PRIOR FILING DATE: 1998-04-14  
NUMBER OF SEQ ID NOS: 10  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 10  
LENGTH: 17  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: clone-20 peptide  
US-09-402-641-10

Query Match 27.0%; Score 31; DB 2; Length 17;  
Best Local Similarity 45.5%; Pred. No. 2.3e+02;  
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 IHPPTNIHKYL 12  
:|||:|  
DB 4 MPHSLNFSQYL 14

RESULT 16  
US-09-411-067C-2  
Sequence 2, Application US/09411067C  
Patent No. 6576610  
GENERAL INFORMATION:  
APPLICANT: NUVAS, LLC  
APPLICANT: HOUSTON, L.L.  
TITLE OF INVENTION: USE OF A CONTEXT-DEPENDENT FUNCTIONAL ENTITY TO ENHANCE THE EFFI  
TITLE OF INVENTION: AN AGENT  
FILE REFERENCE: NUVAS1140  
CURRENT APPLICATION NUMBER: US/09/411,067C

;; CURRENT FILING DATE: 2002-05-07  
;; NUMBER OF SEQ ID NOS: 5  
;; SOFTWARE: PatentIn version 3.0  
;; SEQ ID NO 2  
;; LENGTH: 17  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-09-411-067C-2

Query Match 27.0%; Score 31; DB 2; Length 17;  
Best Local Similarity 45.5%; Pred. No. 2.3e+02;  
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 IPHPTNIHKYL 12  
: || | : ||  
Db 4 MPHSLNFSQYL 14

RESULT 17  
US-09-428-082B-196  
; Sequence 196, Application US/09428082B  
; Patent No. 6660843  
; GENERAL INFORMATION:  
; APPLICANT: FEIGE, ULRICH  
; APPLICANT: LIU, CHUAN-FA  
; APPLICANT: CHEETHAM, JANET C.  
; APPLICANT: BOONE, THOMAS CHARLES  
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS  
; FILE REFERENCE: A-527  
; CURRENT APPLICATION NUMBER: US/09/428,082B  
; CURRENT FILING DATE: 1999-10-22  
; PRIOR APPLICATION NUMBER: 60/105,371  
; PRIOR FILING DATE: 1998-10-23  
; NUMBER OF SEQ ID NOS: 1133  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 196  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: UKR ANTAGONIST PEPTIDE  
US-09-428-082B-196

Query Match 27.0%; Score 31; DB 2; Length 17;  
Best Local Similarity 45.5%; Pred. No. 2.3e+02;  
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 IPHPTNIHKYL 12  
: || | : ||  
Db 4 MPHSLNFSQYL 14

RESULT 18  
US-09-155-260C-16  
; Sequence 16, Application US/09155260C  
; Patent No. 6794358  
; GENERAL INFORMATION:  
; APPLICANT: ROSENBERG, STEVE  
; APPLICANT: DOYLE, MICHAEL  
; APPLICANT: CHAPMAN, HAROLD  
; TITLE OF INVENTION: PEPTIDE LIGANDS OF THE UROKINASE RECEPTOR  
; FILE REFERENCE: 014024-0284102  
; CURRENT APPLICATION NUMBER: US/09/155,260C  
; CURRENT FILING DATE: 1998-09-23  
; PRIOR APPLICATION NUMBER: PCT/US97/05199  
; PRIOR FILING DATE: 1997-03-28  
; PRIOR APPLICATION NUMBER: 08/623,361  
; PRIOR FILING DATE: 1996-03-28  
; NUMBER OF SEQ ID NOS: 76  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 16  
; LENGTH: 17  
; TYPE: PRT

;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
;; OTHER INFORMATION: peptide ligand  
US-09-155-260C-16

Query Match 27.0%; Score 31; DB 2; Length 17;  
Best Local Similarity 45.5%; Pred. No. 2.3e+02;  
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 IPHPTNIHKYL 12  
: || | : ||  
Db 4 MPHSLNFSQYL 14

RESULT 19  
US-09-402-464-1  
; Sequence 1, Application US/09402464  
; Patent No. 6872702  
; GENERAL INFORMATION:  
; APPLICANT: Kessler, Horst  
; APPLICANT: Graeff, Heinrich  
; APPLICANT: Schmitz, Manfred  
; APPLICANT: Magdolen, Viktor  
; APPLICANT: Wilhelm, Olaf G.  
; APPLICANT: Riemer, Christoph  
; APPLICANT: Burgle, Markus  
; TITLE OF INVENTION: Inhibitors for Urokinase Receptor  
; FILE REFERENCE: 100564-09040  
; CURRENT APPLICATION NUMBER: US/09/402,464  
; CURRENT FILING DATE: 2000-01-07  
; PRIOR APPLICATION NUMBER: EP 97 106 024.9  
; PRIOR FILING DATE: 1997-04-11  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-402-464-1

Query Match 27.0%; Score 31; DB 2; Length 17;  
Best Local Similarity 45.5%; Pred. No. 2.3e+02;  
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 IPHPTNIHKYL 12  
: || | : ||  
Db 4 MPHSLNFSQYL 14

RESULT 20  
US-09-791-524A-4  
; Sequence 4, Application US/09791524A  
; Patent No. 6911199  
; GENERAL INFORMATION:  
; APPLICANT: Aventis Pharmaceuticals Products Inc.  
; TITLE OF INVENTION: Targeted Adenovirus Vectors for Delivery of Heterologous Genes  
; FILE REFERENCE: P26,992-B USA  
; CURRENT APPLICATION NUMBER: US/09/791,524A  
; CURRENT FILING DATE: 2001-02-22  
; PRIOR APPLICATION NUMBER: PCT/IB99/01524  
; PRIOR FILING DATE: 1999-08-27  
; PRIOR APPLICATION NUMBER: US 60/098,028  
; PRIOR FILING DATE: 1998-08-27  
; NUMBER OF SEQ ID NOS: 165  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 4  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Adenovirus  
US-09-791-524A-4

Query Match 27.0%; Score 31; DB 2; Length 17;

Best Local Similarity 45.5%; Pred. No. 2.3e+02;  
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 IPHPTNIHKYL 12  
: || | : ||  
Db 4 MPHSLNFSQYL 14

## RESULT 21

PCT-US94-05591-20

/ Sequence 20, Application PC/TUS9405591  
/ GENERAL INFORMATION:  
/ APPLICANT: Doyle, Michael V.  
/ TITLE OF INVENTION: Method For Selection Of Biologically  
/ TITLE OF INVENTION: Active Peptide Sequences  
/ NUMBER OF SEQUENCES: 21  
/ CORRESPONDENCE ADDRESS:  
/ ADDRESSEE: Chiron Corporation  
/ STREET: 4560 Horton Street  
/ CITY: Emeryville  
/ STATE: CA  
/ COUNTRY: USA  
/ ZIP: 94608  
/ COMPUTER READABLE FORM:  
/ MEDIUM TYPE: Floppy disk  
/ COMPUTER: IBM PC compatible  
/ OPERATING SYSTEM: PC-DOS/MS-DOS  
/ SOFTWARE: PatentIn Release #1.0, Version #1.25  
/ CURRENT APPLICATION DATA:  
/ APPLICATION NUMBER: PCT/US94/05591  
/ FILING DATE: 19-MAY-1994  
/ CLASSIFICATION:  
/ ATTORNEY/AGENT INFORMATION:  
/ NAME: Green, Grant D.  
/ REGISTRATION NUMBER: 31,259  
/ REFERENCE/DOCKET NUMBER: 0407.100  
/ TELECOMMUNICATION INFORMATION:  
/ TELEPHONE: 510-601-2706  
/ TELEFAX: 510-655-3542  
/ INFORMATION FOR SEQ ID NO: 20:  
/ SEQUENCE CHARACTERISTICS:  
/ LENGTH: 17 amino acids  
/ TYPE: amino acid  
/ STRANDEDNESS: single  
/ TOPOLOGY: linear  
/ MOLECULE TYPE: peptide  
/ HYPOTHETICAL: NO  
/ PCT-US94-05591-20

## Query Match

Best Local Similarity 27.0%; Score 31; DB 4; Length 17;  
Best Local Similarity 45.5%; Pred. No. 2.3e+02;  
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 IPHPTNIHKYL 12  
: || | : ||  
Db 4 MPHSLNFSQYL 14

## RESULT 22

PCT-US94-05684-1

/ Sequence 1, Application PC/TUS9405684  
/ GENERAL INFORMATION:  
/ APPLICANT: Chiron Corporation  
/ TITLE OF INVENTION: Peptide Inhibitors of Urokinase Receptor  
/ TITLE OF INVENTION: Activity  
/ NUMBER OF SEQUENCES: 37  
/ CORRESPONDENCE ADDRESS:  
/ ADDRESSEE: Chiron Corporation  
/ STREET: 4560 Horton Street  
/ CITY: Emeryville  
/ STATE: CA  
/ COUNTRY: USA  
/ ZIP: 94608

## COMPUTER READABLE FORM:

/ MEDIUM TYPE: Floppy disk  
/ COMPUTER: IBM PC compatible  
/ OPERATING SYSTEM: PC-DOS/MS-DOS  
/ SOFTWARE: PatentIn Release #1.0, Version #1.25  
/ CURRENT APPLICATION DATA:  
/ APPLICATION NUMBER: PCT/US94/05684  
/ FILING DATE: 19 MAY 1994  
/ CLASSIFICATION:  
/ ATTORNEY/AGENT INFORMATION:  
/ NAME: Green, Grant D.  
/ REGISTRATION NUMBER: 31,259  
/ REFERENCE/DOCKET NUMBER: 0941.100  
/ TELECOMMUNICATION INFORMATION:  
/ TELEPHONE: 510-601-2706  
/ TELEFAX: 510-655-3542  
/ INFORMATION FOR SEQ ID NO: 1:  
/ SEQUENCE CHARACTERISTICS:  
/ LENGTH: 17 amino acids  
/ TYPE: amino acid  
/ TOPOLOGY: linear  
/ MOLECULE TYPE: peptide  
/ HYPOTHETICAL: NO  
/ PCT-US94-05684-1

Query Match 27.0%; Score 31; DB 4; Length 17;  
Best Local Similarity 45.5%; Pred. No. 2.3e+02;  
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 IPHPTNIHKYL 12  
: || | : ||  
Db 4 MPHSLNFSQYL 14

## RESULT 23

US-09-791-524A-9

/ Sequence 9, Application US/09791524A  
/ Patent No. 6911199  
/ GENERAL INFORMATION:  
/ APPLICANT: Aventis Pharmaceuticals Products Inc.  
/ TITLE OF INVENTION: Targeted Adenovirus Vectors For Delivery Of Heterologous Genes  
/ FILE REFERENCE: P26,992-B USA  
/ CURRENT APPLICATION NUMBER: US/09/791,524A  
/ CURRENT FILING DATE: 2001-02-22  
/ PRIOR APPLICATION NUMBER: PCT/IB99/01524  
/ PRIOR FILING DATE: 1998-08-27  
/ PRIOR APPLICATION NUMBER: US 60/098,028  
/ PRIOR FILING DATE: 1998-08-27  
/ SOFTWARE: PatentIn version 3.2  
/ NUMBER OF SEQ ID NOS: 165  
/ SEQ ID NO 9  
/ LENGTH: 20  
/ TYPE: PRT  
/ ORGANISM: Adenovirus  
/ US-09-791-524A-9

Query Match 27.0%; Score 31; DB 2; Length 20;  
Best Local Similarity 45.5%; Pred. No. 2.7e+02;  
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 IPHPTNIHKYL 12  
: || | : ||  
Db 6 MPHSLNFSQYL 16

## RESULT 24

US-07-890-422B-19

/ Sequence 19, Application US/07890422B  
/ Patent No. 5602102  
/ GENERAL INFORMATION:  
/ APPLICANT: THIELS, DWAIN L.  
/ APPLICANT: LIPSKY, PETER E.  
/ APPLICANT: MCGUIRE, MICHAEL J.



TITLE OF INVENTION: DIPEPTIDYL PEPTIDASE-I  
TITLE OF INVENTION: INHIBITORS AND USES THEREOF  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: ARNOLD, WHITE & DUNKER  
STREET: P.O. BOX 4433  
CITY: HOUSTON  
STATE: TEXAS  
COUNTRY: USA  
ZIP: 77210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY DISK  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WORDPERFECT 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/890,422B  
FILING DATE: 19920529  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: MAYFIELD, DENISE L.  
REGISTRATION NUMBER: 33,732  
REFERENCE/DOCKET NUMBER: UTSD:296/MAY  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 512-320-7200  
TELEFAX: 512-474-7577  
TELEX: NOT APPLICABLE  
INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acid residues  
TYPE: AMINO ACID  
TOPOLOGY: linear  
US-07-890-422B-19

Query Match 26.1%; Score 30; DB 1; Length 10;  
Best Local Similarity 62.5%; Pred. No. 1.8e+02;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 13 VCESVNGG 20  
DB 3 VCEKRIIG 10

RESULT 25  
US-09-139-802-58  
Sequence 58, Application US/09139802  
Patent No. 6180084  
GENERAL INFORMATION:  
APPLICANT: Ruoslahti, Erkki  
APPLICANT: Pasqualini, Renata  
TITLE OF INVENTION: NGR Receptor and Methods of Identifying Tumor Homing  
TITLE OF INVENTION: Molecules That Home to Angiogenic Vasculature Using  
FILE REFERENCES: P-LJ 3203  
CURRENT APPLICATION NUMBER: US/09/139,802  
EARLIER APPLICATION NUMBER: 08/926,914  
EARLIER FILING DATE: 1997-09-10  
EARLIER APPLICATION NUMBER: 08/710,067  
EARLIER FILING DATE: 1996-09-10  
NUMBER OF SEQ ID NOS: 226  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 58  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-139-802-58

Query Match 26.1%; Score 30; DB 2; Length 10;  
Best Local Similarity 83.3%; Pred. No. 1.8e+02;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 14 CESVNG 19  
DB 1 CEGVNG 6

RESULT 26  
US-09-659-786-58  
Sequence 58, Application US/09659786  
Patent No. 6491894  
GENERAL INFORMATION:  
APPLICANT: Ruoslahti, Erkki  
APPLICANT: Pasqualini, Renata  
TITLE OF INVENTION: NGR Receptor and Methods of Identifying Tumor Homing  
TITLE OF INVENTION: Molecules That Home to Angiogenic Vasculature Using  
FILE REFERENCES: P-LJ 3203  
CURRENT APPLICATION NUMBER: US/09/659,786  
PRIOR FILING DATE: 2000-09-11  
PRIOR APPLICATION NUMBER: 08/926,914  
PRIOR FILING DATE: 1997-09-10  
PRIOR APPLICATION NUMBER: 08/710,067  
PRIOR FILING DATE: 1996-09-10  
NUMBER OF SEQ ID NOS: 226  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 58  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-659-786-58

Query Match 26.1%; Score 30; DB 2; Length 10;  
Best Local Similarity 83.3%; Pred. No. 1.8e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 14 CESVNG 19  
DB 1 CEGVNG 6

RESULT 27  
US-08-926-914-58  
Sequence 58, Application US/08926914  
Patent No. 6576239  
GENERAL INFORMATION:  
APPLICANT: Ruoslahti, Erkki  
APPLICANT: Pasqualini, Renata  
TITLE OF INVENTION: Tumor Homing Molecules, Conjugates  
TITLE OF INVENTION: Derived Therefrom, and Methods of Using Same  
NUMBER OF SEQUENCES: 199  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Campbell & Flores  
STREET: 4370 La Jolla Village Drive, Suite 700  
CITY: San Diego  
STATE: California  
COUNTRY: United States  
ZIP: 92122  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/926,914  
FILING DATE: 10-SEP-1997  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Campbell, Cathryn A.  
REGISTRATION NUMBER: 31,815

REFERENCE/DOCKET NUMBER: P-LJ 2725  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 535-9001  
TELEFAX: (619) 535-8949  
INFORMATION FOR SEQ ID NO: 58:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
TOPOLOGY: both  
MOLECULE TYPE: peptide  
US-08-926-914-58

Query Match 26.1%; Score 30; DB 2; Length 10;  
Best Local Similarity 83.3%; Pred. No. 1.8e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 14 CEEVNG 19  
DB 1 CEEVNG 6

RESULT 28  
US-09-300-410A-2  
Sequence 2, Application US/09300410A  
Patent No. 6414113  
GENERAL INFORMATION:  
APPLICANT: SATO, Atsuehi  
APPLICANT: JINGAMI, HISAO  
TITLE OF INVENTION: PEPTIDES BINDING TO BONE MARROW STROMAL CELL ANTIGEN  
FILE REFERENCE: 99-0449\*/JC/00177  
CURRENT APPLICATION NUMBER: US/09/300,410A  
CURRENT FILING DATE: 1999-04-27  
NUMBER OF SEQ ID NOS: 2  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 2  
LENGTH: 15  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-300-410A-2

Query Match 26.1%; Score 30; DB 2; Length 15;  
Best Local Similarity 83.3%; Pred. No. 2.9e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 TWIKY 11  
DB 6 TWIKY 11

RESULT 29  
US-09-541-345-7  
Sequence 7, Application US/09541345  
Patent No. 6774209  
GENERAL INFORMATION:  
APPLICANT: Rondon, Isaac J  
APPLICANT: Ladner, Robert C  
TITLE OF INVENTION: BINDING PEPTIDES FOR CARCINOEMBRYONIC ANTIGEN (CEA)  
FILE REFERENCE: Sequence Listing DYX-016.0 US  
Patent No. 6774209  
CURRENT APPLICATION NUMBER: US/09/541,345  
CURRENT FILING DATE: 2000-04-03  
NUMBER OF SEQ ID NOS: 107  
SEQ ID NO 7  
LENGTH: 16  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: CEA binding  
US-09-541-345-7

Query Match 26.1%; Score 30; DB 2; Length 16;  
Best Local Similarity 62.5%; Pred. No. 3.1e+02;  
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 13 VCESVNG 20  
DB 3 VCEKTTGG 10

RESULT 30  
US-09-825-517A-7  
Sequence 7, Application US/09825517A  
Patent No. 6919424  
GENERAL INFORMATION:  
APPLICANT: Rondon, Isaac J  
APPLICANT: Ladner, Robert C  
TITLE OF INVENTION: BINDING PEPTIDES FOR CARCINOEMBRYONIC  
TITLE OF INVENTION: ANTIGEN (CEA)  
FILE REFERENCE: DYX-016.1 (3421.1005-001)  
CURRENT APPLICATION NUMBER: US/09/825,517A  
CURRENT FILING DATE: 2003-03-24  
PRIORITY APPLICATION NUMBER: US 09/541,345  
PRIORITY FILING DATE: 2000-04-03  
NUMBER OF SEQ ID NOS: 151  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 7  
LENGTH: 16  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: CEA binding polypeptide  
US-09-825-517A-7

Query Match 26.1%; Score 30; DB 2; Length 16;  
Best Local Similarity 62.5%; Pred. No. 3.1e+02;  
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 13 VCESVNG 20  
DB 3 VCEKTTGG 10

RESULT 31  
US-08-614-935-75  
Sequence 75, Application US/08614935  
Patent No. 5804201  
GENERAL INFORMATION:  
APPLICANT: King, Te P.  
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES OF VESPID  
TITLE OF INVENTION: ANTIGEN 5  
NUMBER OF SEQUENCES: 81  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: David A. Jackson, Esq.  
STREET: 411 Hackensack Ave, Continental Plaza, 4th  
FLOOR  
CITY: Hackensack  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07601  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/614,935  
FILING DATE: 11-MAR-1996  
CLASSIFICATION: 436  
ATTORNEY/AGENT INFORMATION:  
NAME: Jackson Esq., David A.  
REGISTRATION NUMBER: 26,742  
REFERENCE/DOCKET NUMBER: 600-1-156

```
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 75:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULAR TYPE: peptide
HYPOTHEICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: Internal
US-08-614-935-75

Query Match      25.7%; Score 29.5; DB 1; Length 20;
Best Local Similarity 77.8%; Pred. No. 4.7e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
```

```
QY      7 NIHK-YLVC 14
         |||||
Db       4 NWHKHYLVC 12
```

```
RESULT 32
US-09-130-287-75
Sequence 75, Application US/0910287
Patent No. 6106844
GENERAL INFORMATION:
APPLICANT: King, Te P.
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES OF VESPID
TITLE OF INVENTION: ANTIGEN 5
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESSES:
ADDRESS: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
STREET: Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/130,287
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/614,935
FILING DATE: 11-MAR-1996
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-156 DIV
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 75:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULAR TYPE: peptide
HYPOTHEICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: Internal
US-09-130-287-75
```

```
Query Match      25.7%; Score 29.5; DB 2; Length 20;
Best Local Similarity 77.8%; Pred. No. 4.7e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
```

```
QY      7 NIHK-YLVC 14
         |||||
Db       4 NWHKHYLVC 12
```

```
RESULT 33
US-08-192-243-1
Sequence 1, Application US/08192243
Patent No. 5459130
GENERAL INFORMATION:
APPLICANT: Borovsky, Dov
APPLICANT: De loof, Arnold
APPLICANT: Byllemans, Dany
TITLE OF INVENTION: No. 5459130el Methode and Compositions for
TITLE OF INVENTION: the Control of the Flesh Fly
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESSES:
ADDRESS: Ted W. Whitlock
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/192,243
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Whitlock, Ted W.
REGISTRATION NUMBER: 36,965
REFERENCE/DOCKET NUMBER: UF137
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULAR TYPE: peptide
HYPOTHEICAL: NO
ANTI-SENSE: NO
US-08-192-243-1

Query Match      25.2%; Score 29; DB 1; Length 6;
Best Local Similarity 66.7%; Pred. No. 4.6e+05;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      4 HPTNTH 9
         |||||
Db       1 NPTNTH 6
```

```
RESULT 34
US-08-448-059-1
Sequence 1, Application US/08448059
Patent No. 5501976
GENERAL INFORMATION:
APPLICANT: Borovsky, Dov
APPLICANT: De loof, Arnold
APPLICANT: Byllemans, Dany
TITLE OF INVENTION: No. 5501976el Methods and Compositions for
TITLE OF INVENTION: the Control of the Flesh Fly
```

NUMBER OF SEQUENCES: 1  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Ted W. Whitlock  
 STREET: 2421 N.W. 41st Street, Suite A-1  
 CITY: Gainesville  
 STATE: FL  
 COUNTRY: USA  
 ZIP: 32606  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/448,059  
 FILING DATE:  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Whitlock, Ted W.  
 REGISTRATION NUMBER: 36,965  
 REFERENCE/DOCKET NUMBER: UF137  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 904-375-8100  
 TELEFAX: 904-372-5800  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 6 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 US-08-448-059-1

Query Match 25.2% Score 29; DB 1; Length 6;  
 Best Local Similarity 66.7%; Pred. No. 4.6e+05;  
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 HPTNTH 9  
 :|||:  
 1 NPTNTH 6

RESULT 35  
 US-09-295-996B-15  
 ; Sequence 15, Application US/09295996B  
 ; Patent No. 6413530  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Borovsky, Dov  
 ; TITLE OF INVENTION: PESTICIDAL PEPTIDES  
 ; FILE REFERENCE: UF-230  
 ; CURRENT APPLICATION NUMBER: US/09/295,996B  
 ; CURRENT FILING DATE: 1999-04-21  
 ; NUMBER OF SEQ ID NOS: 60  
 ; SOFTWARE: Patentin version 3.1  
 ; SEQ ID NO 15  
 ; LENGTH: 6  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: TMOP peptide  
 US-09-295-996B-15

Query Match 25.2% Score 29; DB 2; Length 6;  
 Best Local Similarity 66.7%; Pred. No. 4.6e+05;  
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 HPTNTH 9  
 :|||:  
 1 NPTNTH 6

RESULT 36  
 US-09-295-846B-18  
 ; Sequence 18, Application US/09295846B  
 ; Patent No. 6562590  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Borovsky, Dov  
 ; TITLE OF INVENTION: Transformed Cells Useful for the Control of Pests  
 ; FILE REFERENCE: UF-223  
 ; CURRENT APPLICATION NUMBER: US/09/295,846B  
 ; CURRENT FILING DATE: 1999-04-21  
 ; NUMBER OF SEQ ID NOS: 59  
 ; SOFTWARE: Patentin Ver. 2.0  
 ; SEQ ID NO 18  
 ; LENGTH: 6  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: TMOP peptide  
 US-09-295-846B-18

Query Match 25.2% Score 29; DB 2; Length 6;  
 Best Local Similarity 66.7%; Pred. No. 4.6e+05;  
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 HPTNTH 9  
 :|||:  
 1 NPTNTH 6

RESULT 37  
 US-09-551-737C-18  
 ; Sequence 18, Application US/09551737C  
 ; Patent No. 6566129  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Borovsky, Dov  
 ; APPLICANT: Schlesinger, Yaagov  
 ; APPLICANT: Nauwelaers, Sabine M. I.  
 ; TITLE OF INVENTION: Transformed Cells Useful for the Control of Pests  
 ; FILE REFERENCE: UF-223C1  
 ; CURRENT APPLICATION NUMBER: US/09/551,737C  
 ; CURRENT FILING DATE: 2000-04-18  
 ; PRIOR APPLICATION NUMBER: US 09/295,846  
 ; PRIOR FILING DATE: 1999-04-21  
 ; NUMBER OF SEQ ID NOS: 71  
 ; SOFTWARE: Patentin version 3.1  
 ; SEQ ID NO 18  
 ; LENGTH: 6  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: TMOP peptide  
 US-09-551-737C-18

Query Match 25.2% Score 29; DB 2; Length 6;  
 Best Local Similarity 66.7%; Pred. No. 4.6e+05;  
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 HPTNTH 9  
 :|||:  
 1 NPTNTH 6

RESULT 38  
 US-09-295-924B-10  
 ; Sequence 10, Application US/09295924B  
 ; Patent No. 6593299  
 ; GENERAL INFORMATION:  
 ; APPLICANT: John, Bennett  
 ; APPLICANT: Alan, Brandt  
 ; APPLICANT: Dov, Borovski  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR CONTROLLING PESTS  
 ; FILE REFERENCE: 4137-120  
 ; CURRENT APPLICATION NUMBER: US/09/295,924B

/ CURRENT FILING DATE: 1999-04-21  
/ NUMBER OF SEQ ID NOS: 54  
/ SOFTWARE: PatentIn version 3.0  
/ SEQ ID NO 10  
/ LENGTH: 6  
/ TYPE: PRT  
/ ORGANISM: Artificial Sequence  
/ FEATURE:  
/ OTHER INFORMATION: Truncated TMOP  
US-09-295-924B-10

Query Match 25.2%; Score 29; DB 2; Length 6;  
Best Local Similarity 66.7%; Pred. No. 4.6e+05;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 HPTNIIH 9  
: |||: |  
Db 1 NPTNLIH 6

RESULT 39  
US-09-551-738B-15  
/ Sequence 15, Application US/09551738B  
/ Patent No. 6635265  
/ GENERAL INFORMATION:  
/ APPLICANT: Borovsky, Dov  
/ TITLE OF INVENTION: Materials and Methods Useful for the Control of Insect Larvae  
/ FILE REFERENCE: UF-224C1  
/ CURRENT APPLICATION NUMBER: US/09/551,738B  
/ CURRENT FILING DATE: 2000-04-18  
/ PRIOR APPLICATION NUMBER: US 09/296,113  
/ PRIOR FILING DATE: 1999-04-21  
/ NUMBER OF SEQ ID NOS: 63  
/ SOFTWARE: PatentIn version 3.1  
/ SEQ ID NO 15  
/ LENGTH: 6  
/ TYPE: PRT  
/ ORGANISM: Artificial Sequence  
/ FEATURE:  
/ OTHER INFORMATION: TMOP peptide  
US-09-551-738B-15

Query Match 25.2%; Score 29; DB 2; Length 6;  
Best Local Similarity 66.7%; Pred. No. 4.6e+05;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 HPTNIIH 9  
: |||: |  
Db 1 NPTNLIH 6

RESULT 40  
US-07-942-245-495  
/ Sequence 495, Application US/07942245  
/ Patent No. 5639641  
/ GENERAL INFORMATION:  
/ APPLICANT: PEDERSEN, Jan T.  
/ APPLICANT: SEARLE, Stephen M. J.  
/ APPLICANT: REES, Anthony R.  
/ APPLICANT: ROGUSKA, Michael A.  
/ APPLICANT: GUILD, Braydon C.  
/ TITLE OF INVENTION: SURFACE RESIDUE VENERING OF RODENT  
/ TITLE OF INVENTION: ANTIBODIES  
/ NUMBER OF SEQUENCES: 522  
/ CORRESPONDENCE ADDRESS:  
/ ADDRESSEE: Sughrie, Mlon, Zlun, Macpeak & Seas  
/ STREET: 2100 Pennsylvania Avenue, N.W.  
/ CITY: Washington  
/ STATE: D.C.  
/ COUNTRY: United States  
/ ZIP: 20037-3202  
/ COMPUTER READABLE FORM:  
/ MEDIUM TYPE: Floppy disk

/ COMPUTER: HP 9000/700 Workstation  
/ OPERATING SYSTEM: UNIX  
/ SOFTWARE: In house  
/ CURRENT APPLICATION DATA:  
/ APPLICATION NUMBER: US/07/942,245  
/ FILING DATE: 09-SEP-1992  
/ CLASSIFICATION: 530  
/ TELECOMMUNICATION INFORMATION:  
/ TELEPHONE: (202) 293-7060  
/ TELEFAX: (202) 293-7860  
/ TELEX: 6491103  
/ INFORMATION FOR SEQ ID NO: 495:  
/ SEQUENCE CHARACTERISTICS:  
/ LENGTH: 11 amino acids  
/ TYPE: amino acid  
/ TOPOLOGY: linear  
/ MOLECULE TYPE: peptide  
US-07-942-245-495

Query Match 25.2%; Score 29; DB 1; Length 11;  
Best Local Similarity 83.3%; Pred. No. 3e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 NIKKYL 12  
: |||: |  
Db 5 NIKKYL 10

RESULT 41  
US-08-024-253-16  
/ Sequence 16, Application US/08024253  
/ Patent No. 5785968  
/ GENERAL INFORMATION:  
/ APPLICANT: KIMACHI, Kazuhiko  
/ APPLICANT: MAEDA, Hiroaki  
/ APPLICANT: NISHIYAMA, Kiyoko  
/ APPLICANT: TOKIYOSHI, Sachio  
/ APPLICANT: TOHYA, Yukinobu  
/ APPLICANT: MIRAMI, Takeshi  
/ TITLE OF INVENTION: ANTI-FELINE CALICIVIRUS RECOMBINANT  
/ TITLE OF INVENTION: ANTIBODY AND GENE FRAGMENT ENCODING THE SAME  
/ NUMBER OF SEQUENCES: 23  
/ CORRESPONDENCE ADDRESS:  
/ ADDRESSEE: WEGNER, CANTOR, MUELLER & PLAYER  
/ STREET: 1233 20th Street, N.W., Suite 300  
/ CITY: Washington  
/ STATE: D.C.  
/ COUNTRY: U.S.A.  
/ ZIP: 20036-8218  
/ COMPUTER READABLE FORM:  
/ MEDIUM TYPE: Floppy disk  
/ COMPUTER: IBM PC compatible  
/ OPERATING SYSTEM: PC-DOS/MS-DOS  
/ SOFTWARE: PatentIn Release #1.0, Version #1.25  
/ CURRENT APPLICATION DATA:  
/ APPLICATION NUMBER: US/08/024,253  
/ FILING DATE: 19930301  
/ CLASSIFICATION: 424  
/ PRIOR APPLICATION DATA:  
/ APPLICATION NUMBER: JP 79189/1992  
/ FILING DATE: 28-FEB-1992  
/ ATTORNEY/AGENT INFORMATION:  
/ NAME: CANTOR, Herbert I.  
/ REGISTRATION NUMBER: 24,192  
/ REFERENCE/DOCKET NUMBER: P-500-23744  
/ TELECOMMUNICATION INFORMATION:  
/ TELEPHONE: (202) 887-0400  
/ TELEFAX: (202) 835-0605  
/ TELEX: 440706 WEGHR  
/ INFORMATION FOR SEQ ID NO: 16:  
/ SEQUENCE CHARACTERISTICS:  
/ LENGTH: 11 amino acids  
/ TYPE: amino acid

TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-024-253-16

Query Match 25.2%; Score 29; DB 1; Length 11;  
Best Local Similarity 83.3%; Pred. No. 3e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 NHHKYL 12  
|||  
Db 5 NHHNYL 10

RESULT 42  
US-09-649-063-16  
Sequence 16, Application US/09649063  
Patent No. 6600022  
GENERAL INFORMATION:  
APPLICANT: TORIGOE, Kakuji  
USHIO, Shimpel  
KUNIKATA, Toashio  
KURIMOTO, Masashi  
TITLE OF INVENTION: INTERLEUKIN-18 RECEPTOR PROTEINS  
NUMBER OF SEQUENCES: 31  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: BROWDY AND NEIMARK  
STREET: 419 Seventh Street, N.W., Suite 300  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/649,063  
FILING DATE: 29-Aug-2000  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/996,140  
FILING DATE: <Unknown>  
APPLICATION NUMBER: JP 52,526/1997  
FILING DATE: 21-FEB-1997  
APPLICATION NUMBER: JP 163,490/1997  
FILING DATE: 6-JUN-1997  
APPLICATION NUMBER: JP 215,490/1997  
FILING DATE: 28-JUL-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: BROWDY, Roger L.  
REGISTRATION NUMBER: 25,618  
REFERENCE/DOCKET NUMBER: TORIGOE=2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: internal fragment  
SEQUENCE DESCRIPTION: SEQ ID NO: 16:  
US-09-649-063-16

Query Match 25.2%; Score 29; DB 2; Length 11;  
Best Local Similarity 83.3%; Pred. No. 3e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 NHHKYL 12  
|||  
Db 5 NHHNYL 10

RESULT 43  
US-08-918-428D-15  
Sequence 15, Application US/08918428D  
Patent No. 6432636  
GENERAL INFORMATION:  
APPLICANT: Grace Mareah and Alan Snow  
TITLE OF INVENTION: Therapeutic and Diagnostic Applications  
of Perlecan Domain I Splice Variants  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Patrick M. Dwyer  
STREET: 1818 Westlake Avenue N, Suite 114  
CITY: Seattle  
STATE: WA (Washington)  
COUNTRY: United States of America  
ZIP: 98109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette - 3.50 Inch, 1.44 Mb storage  
COMPUTER: IBM PC  
OPERATING SYSTEM: PC-DOS (Windows NT '95)  
SOFTWARE: WordPerfect 9  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/918,428D  
FILING DATE: 26-August-1997  
CLASSIFICATION:  
PRIOR APPLICATION DATA: n/a  
ATTORNEY/AGENT INFORMATION:  
NAME: Dwyer, Patrick M.  
REGISTRATION NUMBER: 32,411  
REFERENCE/DOCKET NUMBER: PROTEO.P02  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 343-7074  
TELEFAX: (206) 343-7085  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 AMINO ACIDS  
TYPE: AMINO ACID  
STRANDEDNESS: SINGLE  
TOPOLOGY: LINEAR  
MOLECULE TYPE: PROTEIN  
US-08-918-428D-15

Query Match 25.2%; Score 29; DB 2; Length 17;  
Best Local Similarity 43.8%; Pred. No. 4.8e+02;  
Matches 7; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 5 PTNHHKYLVCESVNG 20  
|||  
Db 1 PTPGHSAPVPSLHGG 16

RESULT 44  
US-08-305-871A-11  
Sequence 11, Application US/08305871A  
Patent No. 5736142  
GENERAL INFORMATION:  
APPLICANT: Sette, Alessandro  
APPLICANT: Gaeta, Federico  
APPLICANT: Grey, Howard M.  
APPLICANT: Sidney, John  
APPLICANT: Alexander, Jeffrey L.  
TITLE OF INVENTION: Alteration of Immune Response Using Pan  
DR-Binding Peptides  
NUMBER OF SEQUENCES: 29  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/305,871A  
 FILING DATE: 14-SEP-1994  
 CLASSIFICATION: 424  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/121,101  
 FILING DATE: 14-SEP-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Baslian, Kevin L.  
 REGISTRATION NUMBER: 34,774  
 REFERENCE/DOCKET NUMBER: 14137-0062-10  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 576-0200  
 TELEFAX: (415) 576-0300  
 INFORMATION FOR SEQ ID NO: 11:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 20 amino acids  
 TYPE: amino acid  
 STRANDEDNESS:  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 US-08-305-871A-11

Query Match 25.2%; Score 29; DB 1; Length 20;  
 Best Local Similarity 33.3%; Pred. No. 5.7e+02;  
 Matches 4; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 3 PPHTHIKYLC 14  
 Db 1 PPHTHLRQALYC 12

RESULT 45  
 US-08-614-935-26  
 Sequence 26, Application US/08614935  
 Patent No. 5804201  
 GENERAL INFORMATION:  
 APPLICANT: King, Te P.  
 TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES OF VESPID  
 TITLE OF INVENTION: ANTIGEN 5  
 NUMBER OF SEQUENCES: 81  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: David A. Jackson, Esq.  
 STREET: 411 Hackensack Ave, Continental Plaza, 4th  
 STREET: Floor  
 CITY: Hackensack  
 STATE: New Jersey  
 COUNTRY: USA  
 ZIP: 07601  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/614,935  
 FILING DATE: 11-MAR-1996  
 CLASSIFICATION: 436  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Jackson Esq., David A.  
 REGISTRATION NUMBER: 26,742  
 REFERENCE/DOCKET NUMBER: 600-1-156  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 201-487-5800  
 TELEFAX: 201-343-1684  
 INFORMATION FOR SEQ ID NO: 26:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 20 amino acids  
 TYPE: amino acid

STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 FRAGMENT TYPE: internal  
 US-08-614-935-26

Query Match 25.2%; Score 29; DB 1; Length 20;  
 Best Local Similarity 60.0%; Pred. No. 5.7e+02;  
 Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 11 YLVCSVNGG 20  
 Db 9 YLVCSVNGPG 18

RESULT 46  
 US-08-797-842-7  
 Sequence 7, Application US/08797842  
 Patent No. 5932706  
 GENERAL INFORMATION:  
 APPLICANT: Mertens, Koenraad et al  
 TITLE OF INVENTION: Antibodies specific for a haemostatic protein,  
 TITLE OF INVENTION: their use for isolating intact protein, haemostatic compo  
 TITLE OF INVENTION: of proteolytic cleavage products of the protein  
 NUMBER OF SEQUENCES: 16  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Michaelson and Wallace  
 STREET: Parkway 109 Office Center, 328 Newman Springs  
 STREET: Road, P. O. Box 8489  
 CITY: Red Bank  
 STATE: New Jersey  
 COUNTRY: USA  
 ZIP: 07701

COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3 1/2" 1.44 MByte IBM compatible diskette  
 COMPUTER: IBM PC  
 OPERATING SYSTEM: MS-DOS, Windows for Workgroups 3.11  
 SOFTWARE: Microsoft Word for Windows 6  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/797,842  
 FILING DATE: 10-Feb-1997  
 CLASSIFICATION: 530  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/381,891  
 FILING DATE: February 8, 1995  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Michaelson, Peter L.  
 REGISTRATION NUMBER: 30090  
 REFERENCE/DOCKET NUMBER: Stichling-5  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (908) 530-6671  
 TELEFAX: (908) 530-6584  
 INFORMATION FOR SEQ ID NO: 7:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 20 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: unknown  
 TOPOLOGY: unknown  
 MOLECULE TYPE: peptide  
 HYPOTHETICAL: NO  
 US-08-797-842-7

Query Match 25.2%; Score 29; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 5.7e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 KYLYC 14  
 Db 4 KYLYC 8

RESULT 47  
US-09-100-409A-47  
; Sequence 47, Application US/09100409A  
; Patent No. 6090388  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Chang Y1  
; TITLE OF INVENTION: PEPTIDE COMPOSITION FOR  
; TITLE OF INVENTION: PREVENTION AND TREATMENT OF HIV INFECTION AND  
; TITLE OF INVENTION: IMMUNE DISORDERS  
; NUMBER OF SEQUENCES: 64  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORGAN & FINNEGAN  
; STREET: 345 Park Avenue  
; CITY: New York  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10154-0054  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/100,409A  
; FILING DATE:  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME:  
; REGISTRATION NUMBER:  
; REFERENCE/DOCKET NUMBER: 1151-4154  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-758-4800  
; TELEFAX: 212-751-6849  
; INFORMATION FOR SEQ ID NO: 47:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 20 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-09-100-409A-47

Query Match 25.2%; Score 29; DB 2; Length 20;  
Best Local Similarity 33.3%; Pred. No. 5.7e+02;  
Matches 4; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 3 PPHNTHKYLVC 14  
||| : : :  
Db 1 PPHNTHLRQAILC 12

RESULT 48  
US-09-130-287-26  
; Sequence 26, Application US/09130287  
; Patent No. 6106844  
; GENERAL INFORMATION:  
; APPLICANT: King, Te P.  
; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES OF VESPID  
; TITLE OF INVENTION: ANTIGEN 5  
; NUMBER OF SEQUENCES: 81  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: David A. Jackson, Esq.  
; STREET: 411 Hackensack Ave, Continental Plaza, 4th  
; STREET: Floor  
; CITY: Hackensack  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 07601  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/130,287  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/614,935  
FILING DATE: 11-MAR-1996  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Jackson Esq., David A.  
REGISTRATION NUMBER: 26,742  
REFERENCE/DOCKET NUMBER: 600-1-156 DIV  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201-487-5800  
TELEFAX: 201-343-1684  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: Internal  
US-09-130-287-26

Query Match 25.2%; Score 29; DB 2; Length 20;  
Best Local Similarity 60.0%; Pred. No. 5.7e+02;  
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 11 YLVCSVNGG 20  
||||| : : :  
Db 9 YLVCSVNGG 18

RESULT 49  
US-09-009-953-195  
; Sequence 195, Application US/09009953  
; Patent No. 6413517  
; GENERAL INFORMATION:  
; APPLICANT: Sette, Alessandro  
; TITLE OF INVENTION: Identification of Broadly  
; TITLE OF INVENTION: Reactive DR Restricted Epitopes  
; NUMBER OF SEQUENCES: 274  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; OPERATING SYSTEM: DOS  
; SOFTWARE: PASCSEQ for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/009,953  
; FILING DATE: 21-Jan-1998  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/036,713  
; FILING DATE: 23-JAN-1997  
; APPLICATION NUMBER: US 60/037,432  
; FILING DATE: 07-FEB-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Weber, Ellen Lauver  
; REGISTRATION NUMBER: 32,762  
; REFERENCE/DOCKET NUMBER: 018623-011520US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-576-0200  
; TELEFAX: 415-576-0300



```
/
/      TELEX: <Unknown>
/      INFORMATION FOR SEQ ID NO: 195:
/      SEQUENCE CHARACTERISTICS:
/          LENGTH: 20 amino acids
/          TYPE: amino acid
/          STRANDEDNESS: single
/          TOPOLOGY: linear
/      MOLECULE TYPE: peptide
/      SEQUENCE DESCRIPTION: SEQ ID NO: 195:
US-09-009-953-195

Query Match      25.2%; Score 29; DB 2; Length 20;
Best Local Similarity 33.3%; Pred. No. 5.7e+02;
Matches 4; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY      3 PHPTNKHLYVC 14
DB      1 PHHTALRQAILC 12

RESULT 50
US-08-788-822A-14
/ Sequence 14, Application US/08788822A
/ Patent No. 6413935
/ GENERAL INFORMATION:
/   APPLICANT: Alexander, Jeffrey L.
/   APPLICANT: Defrees, Shawn
/   APPLICANT: Sette, Alessandro
/   TITLE OF INVENTION: Induction of Immune Response Against
/   TITLE OF INVENTION: Desired Determinants
/   NUMBER OF SEQUENCES: 30
/   CORRESPONDENCE ADDRESSES:
/   ADDRESSES: Townsend and Townsend and Crew LLP
/   STREET: Two Embarcadero Center, Eighth Floor
/   CITY: San Francisco
/   STATE: California
/   COUNTRY: USA
/   ZIP: 94111-3834
/   COMPUTER READABLE FORM:
/   MEDIUM TYPE: floppy disk
/   COMPUTER: IBM PC compatible
/   OPERATING SYSTEM: PC-DOS/MS-DOS
/   SOFTWARE: Patent Release #1.0, Version #1.30
/   CURRENT APPLICATION DATA:
/   APPLICATION NUMBER: US/08/788,822A
/   FILING DATE: 23-JAN-1997
/   CLASSIFICATION: 424
/   PRIOR APPLICATION DATA:
/   APPLICATION NUMBER: US 60/010,510
/   FILING DATE: 24-JAN-1996
/   ATTORNEY/AGENT INFORMATION:
/   NAME: Baelian, Kevin L.
/   REGISTRATION NUMBER: 34,774
/   REFERENCE/DOCKET NUMBER: 014137-009210US
/   TELECOMMUNICATION INFORMATION:
/   TELEPHONE: (415) 576-0200
/   TELEFAX: (415) 576-0300
/   INFORMATION FOR SEQ ID NO: 14:
/   SEQUENCE CHARACTERISTICS:
/       LENGTH: 20 amino acids
/       TYPE: amino acid
/       STRANDEDNESS:
/       TOPOLOGY: linear
/   MOLECULE TYPE: peptide
US-08-788-822A-14

Query Match      25.2%; Score 29; DB 2; Length 20;
Best Local Similarity 33.3%; Pred. No. 5.7e+02;
Matches 4; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY      3 PHPTNKHLYVC 14
DB      1 PHHTALRQAILC 12
```

```
RESULT 51
US-09-311-784A-150
/ Sequence 150, Application US/09311784A
/ Patent No. 6534482
/ GENERAL INFORMATION:
/   APPLICANT: Pike, John D.
/   APPLICANT: Hermanson, Gary G.
/   APPLICANT: Sette, Alessandro
/   APPLICANT: Iehloka, Glenn Y.
/   APPLICANT: Livingston, Brian
/   APPLICANT: Chesnut, Robert W.
/   APPLICANT: SpImmune Inc.
/   TITLE OF INVENTION: Expression Vectors for Stimulating an
/   TITLE OF INVENTION: Immune Response and Methods of Using the Same
/   FILE REFERENCE: 39963-20022.01
/   CURRENT APPLICATION NUMBER: US/09/311,784A
/   CURRENT FILING DATE: 1999-05-13
/   PRIOR APPLICATION NUMBER: US 60/085,751
/   PRIOR FILING DATE: 1998-05-15
/   NUMBER OF SEQ ID NOS: 463
/   SOFTWARE: FastSeq for Windows Version 3.0
/   SEQ ID NO 150
/   LENGTH: 20
/   TYPE: PRT
/   ORGANISM: Artificial Sequence
/   FEATURE:
/   OTHER INFORMATION: HBV CORE 50 (peptide 857.02)
US-09-311-784A-150

Query Match      25.2%; Score 29; DB 2; Length 20;
Best Local Similarity 33.3%; Pred. No. 5.7e+02;
Matches 4; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY      3 PHPTNKHLYVC 14
DB      1 PHHTALRQAILC 12

RESULT 52
US-09-239-043D-2566
/ Sequence 2566, Application US/09239043D
/ Patent No. 6689363
/ GENERAL INFORMATION:
/   APPLICANT: Sette, Alessandro
/   APPLICANT: Sidney, John
/   APPLICANT: Southwood, Scott
/   APPLICANT: Vitello, Maria A.
/   APPLICANT: Livingston, Brian D.
/   APPLICANT: Celis, Bastejan
/   APPLICANT: Kubo, Ralph T.
/   APPLICANT: Grey, Howard M.
/   APPLICANT: Chesnut, Robert
/   APPLICANT: SpImmune Inc.
/   TITLE OF INVENTION: Inducing Cellular Immune Responses to Hepatitis B Virus
/   TITLE OF INVENTION: Using Peptide and Nucleic Acid Compositions
/   FILE REFERENCE: 2060.0060007
/   CURRENT APPLICATION NUMBER: US/09/239,043D
/   CURRENT FILING DATE: 1999-01-27
/   PRIOR APPLICATION NUMBER: US 09/189,702
/   PRIOR FILING DATE: 1998-11-10
/   PRIOR APPLICATION NUMBER: US 08/978,291
/   PRIOR FILING DATE: 1997-11-25
/   PRIOR APPLICATION NUMBER: US 08/820,360
/   PRIOR FILING DATE: 1997-03-12
/   PRIOR APPLICATION NUMBER: US 60/013,363
/   PRIOR FILING DATE: 1996-03-13
/   PRIOR APPLICATION NUMBER: US 08/461,603
/   PRIOR FILING DATE: 1995-06-05
/   PRIOR APPLICATION NUMBER: US 08/347,610
/   PRIOR FILING DATE: 1994-12-01
/   PRIOR APPLICATION NUMBER: US 08/344,824
```

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/ PRIOR FILING DATE: 1994-11-23
/ PRIOR APPLICATION NUMBER: US 08/278,634
/ PRIOR FILING DATE: 1994-07-21
/ PRIOR APPLICATION NUMBER: US 08/205,713
/ PRIOR FILING DATE: 1994-03-04
/ PRIOR APPLICATION NUMBER: US 08/197,484
/ PRIOR FILING DATE: 1994-02-16
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 2579
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 2566
/ LENGTH: 20
/ TYPE: PRT
/ ORGANISM: Orthohepadnaviridae hepatitis B virus
US-09-239-043D-2566

Query Match          25.2%; Score 29; DB 2; Length 20;
Best Local Similarity 33.3%; Pred. No. 5.7e+02;
Matches 4; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY      3 PPHNIHKYLV 14
      ||| : : : ||
Db      1 PPHITLRQAILC 12

RESULT 53
US-09-701-623C-71
/ Sequence 71, Application US/09701623C
/ Patent No. 6811782
/ GENERAL INFORMATION:
/ APPLICANT: Wang Ph.D., Chang Y1
/ TITLE OF INVENTION: PEPTIDE COMPOSITION AS IMMUNOGEN FOR THE TREATMENT OF
/ FILE REFERENCE: 11514151US1
/ CURRENT APPLICATION NUMBER: US/09/701,623C
/ CURRENT FILING DATE: 2000-12-01
/ PRIOR APPLICATION NUMBER: PCT/US99/13959
/ PRIOR FILING DATE: 1999-06-21
/ PRIOR APPLICATION NUMBER: 09/100,287
/ PRIOR FILING DATE: 1998-06-20
/ NUMBER OF SEQ ID NOS: 91
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 71
/ LENGTH: 20
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-701-623C-71

Query Match          25.2%; Score 29; DB 2; Length 20;
Best Local Similarity 33.3%; Pred. No. 5.7e+02;
Matches 4; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY      3 PPHNIHKYLV 14
      ||| : : : ||
Db      1 PPHITLRQAILC 12

RESULT 54
US-09-674-183-8
/ Sequence 8, Application US/09674183
/ Patent No. 6855321
/ GENERAL INFORMATION:
/ APPLICANT: RAPPUOLI, Rino
/ APPLICANT: GRANDI, Guido
/ TITLE OF INVENTION: POLYPEPTIDE CARRIER PROTEIN
/ FILE REFERENCE: PP00362.102 / 2302-0362
/ CURRENT APPLICATION NUMBER: US/09/674,183
/ CURRENT FILING DATE: 2000-11-14
/ PRIOR APPLICATION NUMBER: PCT/IB99/00844
/ PRIOR FILING DATE: 1999-04-27
/ PRIOR APPLICATION NUMBER: GB9808932.9
```

```
/ PRIOR FILING DATE: 1998-04-27
/ NUMBER OF SEQ ID NOS: 20
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 8
/ LENGTH: 20
/ TYPE: PRT
/ ORGANISM: T-cell epitope HBVnc
US-09-674-183-8

Query Match          25.2%; Score 29; DB 2; Length 20;
Best Local Similarity 33.3%; Pred. No. 5.7e+02;
Matches 4; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY      3 PPHNIHKYLV 14
      ||| : : : ||
Db      1 PPHITLRQAILC 12

RESULT 55
US-10-666-480-5
/ Sequence 5, Application US/10666480
/ Patent No. 6919426
/ GENERAL INFORMATION:
/ APPLICANT: Boone, Thomas C
/ APPLICANT: Wild, Kenneth D
/ APPLICANT: Stiney, Karen C
/ APPLICANT: Min, Hosing
/ APPLICANT: Kimmel, Bruce
/ TITLE OF INVENTION: Peptides and Related Molecules That Modulate Nerve Growth Factor
/ FILE REFERENCE: A-8270S
/ CURRENT APPLICATION NUMBER: US/10/666,480
/ CURRENT FILING DATE: 2003-09-18
/ PRIOR APPLICATION NUMBER: 60/412,524
/ PRIOR FILING DATE: 2002-09-19
/ NUMBER OF SEQ ID NOS: 286
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 5
/ LENGTH: 20
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Therapeutically active peptide of randomly generated, non-natural
US-10-666-480-5

Query Match          25.2%; Score 29; DB 2; Length 20;
Best Local Similarity 44.4%; Pred. No. 5.7e+02;
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY      5 PTNIHKYLV 13
      ||| : : : ||
Db      10 PSNIDRYWL 18

RESULT 56
US-09-618-592-7
/ Sequence 7, Application US/09618592
/ Patent No. R838202
/ GENERAL INFORMATION:
/ APPLICANT: Mertens, Koenraad et al
/ TITLE OF INVENTION: Antibodies specific for a haemostatic protein,
/ their use for isolating intact protein, haemostatic composi
/ of proteolytic cleavage products of the protein
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESSES:
ADDRESSER: Michaelson and Wallace
STREET: Parkway 109 Office Center, 328 Newman Springs
Road, P. O. Box 8489
CITY: Red Bank
STATE: New Jersey
COUNTRY: USA
ZIP: 07701
COMPUTER READABLE FORM:
```

```

MEDIUM TYPE: 3 1/2" 1.44 MByte IBM compatible diskette
COMPUTER: IBM PC
OPERATING SYSTEM: MS-DOS, Windows for Workgroups 3.11
SOFTWARE: Microsoft Word for Windows 6
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/618,592
FILING DATE: 17-Jul-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/797,842
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Michaelson, Peter L.
REGISTRATION NUMBER: 30090
REFERENCE/DOCKET NUMBER: Stitching-5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908)530-6671
TELEFAX: (908)530-6584
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-618-592-7

Query Match      25.2%; Score 29; DB 5; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      10 KYLYC 14
      |||||
      4 KYLYC 8

RESULT 57
US-08-159-339A-526
Sequence 526, Application US/08159339A
Patent No. 6037135
GENERAL INFORMATION:
APPLICANT: Kubo, Ralph T.
APPLICANT: Grey, Howard M.
APPLICANT: Sette, Alessandro
APPLICANT: Celis, Balleben
TITLE OF INVENTION: HLA Binding peptides and Their
TITLE OF INVENTION: Uses
NUMBER OF SEQUENCES: 1254
CORRESPONDENCE ADDRESSES:
ADDRESSER: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Paradox for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/159,339A
FILING DATE: 29-NOV-1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/926,666
FILING DATE: 07-AUG-1992
APPLICATION NUMBER: US 08/027,746
FILING DATE: 05-MAR-1993
APPLICATION NUMBER: US 08/103,396
FILING DATE: 06-AUG-1993

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ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 018623-0050300S
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
TELEX:
INFORMATION FOR SEQ ID NO: 526:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-159-339A-526

Query Match      24.3%; Score 28; DB 2; Length 9;
Best Local Similarity 57.1%; Pred. No. 4.6e+05;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      2 IPHPTNI 8
      |||||
      2 IPHPAGL 8

RESULT 58
US-09-119-507B-51
Sequence 51, Application US/09119507B
Patent No. 6548642
GENERAL INFORMATION:
APPLICANT: Kieliszewski, Marcia J.
TITLE OF INVENTION: No. 6548642el Synthetic Genes for Plant Gums
FILE REFERENCE: OHU-03417
CURRENT APPLICATION NUMBER: US/09/119,507B
CURRENT FILING DATE: 1998-07-20
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 51
LENGTH: 11
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURES:
NAME/KEY: SITE
LOCATION: (8)
OTHER INFORMATION: The Proline at this position is a hydroxyproline.
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-119-507B-51

Query Match      24.3%; Score 28; DB 2; Length 11;
Best Local Similarity 57.1%; Pred. No. 4.3e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      4 HPTPIHK 10
      |||||
      5 HPTPYVK 11

RESULT 59
US-08-897-556A-51
Sequence 51, Application US/08897556A
Patent No. 6570062
GENERAL INFORMATION:
APPLICANT: KIELISZEWSKI, MARCIA J.
TITLE OF INVENTION: SYNTHETIC GENES FOR PLANT GUMS AND OTHER
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESSES:
ADDRESSER: MEDLEN & CARROLL, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California

```

```
/ COUNTRY: United States of America
/ ZIP: 94104
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/897,556A
/ FILING DATE: 21-JUL-1997
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: CARROLL, PETER G.
/ REGISTRATION NUMBER: 32,837
/ REFERENCE/DOCKET NUMBER: OHU-02908
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 397-8338
/ TELEFAX: (415) 705-8410
/ INFORMATION FOR SEQ ID NO: 51:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 11 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: not relevant
/ TOPOLOGY: unknown
/ MOLECULE TYPE: protein
/ FEATURE:
/ NAME/KEY: Modified-site
/ LOCATION: 8
/ OTHER INFORMATION: /note= "The Proline at this
/ OTHER INFORMATION: position is a hydroxyproline."
US-08-897-556A-51
```

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Query Match 24.3%; Score 28; DB 2; Length 11;
Best Local Similarity 57.1%; Pred. No. 4.3e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 HPTNHR 10
DB 5 HPTPVYK 11

RESULT 60
US-09-547-693-51
/ Sequence 51, Application US/09547693
/ Patent No. 6639050
/ GENERAL INFORMATION:
/ APPLICANT: Kieliszewski, Marcia
/ TITLE OF INVENTION: Synthetic Genes for Plant Gums and Other Hydroxyproline-Rich
/ TITLE OF INVENTION: Glycoproteins
/ FILE REFERENCE: OHU-04089
/ CURRENT APPLICATION NUMBER: US/09/547,693
/ CURRENT FILING DATE: 2000-04-12
/ NUMBER OF SEQ ID NOS: 236
/ SOFTWARE: Patentin version 3.0
/ SEQ ID NO 51
/ LENGTH: 11
/ TYPE: PRT
/ ORGANISM: Artificial/Unknown
/ FEATURE:
/ NAME/KEY: misc.feature
/ OTHER INFORMATION: Synthetic
/ NAME/KEY: SITE
/ LOCATION: (6)..(8)
/ OTHER INFORMATION: The Proline at this position is a hydroxyproline.
US-09-547-693-51
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Query Match 24.3%; Score 28; DB 2; Length 11;
Best Local Similarity 57.1%; Pred. No. 4.3e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 HPTNHR 10
DB 5 HPTPVYK 11
```

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RESULT 61
US-08-147-011-1
/ Sequence 1, Application US/08147011
/ Patent No. 5478724
/ GENERAL INFORMATION:
/ APPLICANT: Morse, Stephen S.
/ APPLICANT: Gelman, Irwin H.
/ APPLICANT: Hanafusa, Hideaburo
/ TITLE OF INVENTION: Lentivirus-Specific Nucleotide Probes
/ TITLE OF INVENTION: and Methods of Use
/ NUMBER OF SEQUENCES: 8
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Kilpatrick & Cody
/ STREET: 100 Peachtree Street
/ CITY: Atlanta
/ STATE: Georgia
/ COUNTRY: US
/ ZIP: 30303
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/147,011
/ FILING DATE:
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/07/746,706
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Pabst, Patricia L.
/ REGISTRATION NUMBER: 31,284
/ REFERENCE/DOCKET NUMBER: RU100
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 404-572-6508
/ TELEFAX: 404-572-6555
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 13 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ HYPOTHETICAL: NO
/ ANTI-SENSE: NO
/ FRAGMENT TYPE: Internal
/ ORIGINAL SOURCE:
/ ORGANISM: lentivirus
/ FEATURE:
/ NAME/KEY: Modified-site
/ LOCATION: 4
/ OTHER INFORMATION: /note= "X" at position 4 is A, P,
/ OTHER INFORMATION: or G."
/ FEATURE:
/ NAME/KEY: Modified-site
/ LOCATION: 7
/ OTHER INFORMATION: /note= "X" at position 7 is K or
/ OTHER INFORMATION: A."
/ FEATURE:
/ NAME/KEY: Modified-site
/ LOCATION: 9
/ OTHER INFORMATION: /note= "X" at position 9 is K or
/ OTHER INFORMATION: R."
/ FEATURE:
/ NAME/KEY: Modified-site
/ LOCATION: 10
/ OTHER INFORMATION: /note= "X" at position 10 is K or
/ OTHER INFORMATION: R."
/ FEATURE:
/ NAME/KEY: Modified-site
```

LOCATION: 11  
OTHER INFORMATION: /note= "X" at position 11 is S or  
OTHER INFORMATION: R."  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 12  
OTHER INFORMATION: /note= "X" at position 12 is V or  
OTHER INFORMATION: I."  
US-08-147-011-1

Query Match 24.3%; Score 28; DB 1; Length 13;  
Best Local Similarity 50.0%; Pred. No. 5.2e+02;  
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 PHEPNIHK 10  
DB 1 PHEPGLMK 8

## RESULT 62

US-08-480-190-221  
Sequence 221, Application US/08480190  
Patent No. 5827516  
GENERAL INFORMATION:  
APPLICANT: Robert G. Urban  
APPLICANT: Roman M. Chicz  
APPLICANT: Dario A. A. Vignali  
APPLICANT: Mary L. Hedley  
APPLICANT: Lawrence J. Stern  
APPLICANT: Jack L. Strominger  
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES  
NUMBER OF SEQUENCES: 274  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Fish & Richardson  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: U.S.A.  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 MB  
COMPUTER: IBM PS/2 Model 502 or 55SX  
OPERATING SYSTEM: MS-DOS (Version 5.0)  
SOFTWARE: Wordperfect (Version 5.1)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/480,190  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/077,255  
FILING DATE: June 15, 1993  
APPLICATION NUMBER: 07/925,460  
FILING DATE: August 11, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Clark, Paul T.  
REGISTRATION NUMBER: 30,162  
REFERENCE/DOCKET NUMBER: 00246/168001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 542-5070  
TELEFAX: (617) 542-8906  
TELEX: 200154  
INFORMATION FOR SEQ. ID NO: 221:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 13  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
US-08-480-190-221

Query Match 24.3%; Score 28; DB 1; Length 13;  
Best Local Similarity 41.7%; Pred. No. 5.2e+02;  
Matches 5; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 9 HKYLVGESVNGG 20  
DB 2 HKYVACEVTHQG 13

## RESULT 63

US-08-488-379-221  
Sequence 221, Application US/08488379  
Patent No. 5880103  
GENERAL INFORMATION:  
APPLICANT: Robert G. Urban  
APPLICANT: Roman M. Chicz  
APPLICANT: Dario A. A. Vignali  
APPLICANT: Mary L. Hedley  
APPLICANT: Lawrence J. Stern  
APPLICANT: Jack L. Strominger  
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES  
NUMBER OF SEQUENCES: 274  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Fish & Richardson  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: U.S.A.  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 MB  
COMPUTER: IBM PS/2 Model 502 or 55SX  
OPERATING SYSTEM: MS-DOS (Version 5.0)  
SOFTWARE: Wordperfect (Version 5.1)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/488,379  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/077,255  
FILING DATE: June 15, 1993  
APPLICATION NUMBER: 07/925,460  
FILING DATE: August 11, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Clark, Paul T.  
REGISTRATION NUMBER: 30,162  
REFERENCE/DOCKET NUMBER: 00246/168001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 542-5070  
TELEFAX: (617) 542-8906  
TELEX: 200154  
INFORMATION FOR SEQ. ID NO: 221:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 13  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
US-08-488-379-221

Query Match 24.3%; Score 28; DB 1; Length 13;  
Best Local Similarity 41.7%; Pred. No. 5.2e+02;  
Matches 5; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 9 HKYLVGESVNGG 20  
DB 2 HKYVACEVTHQG 13

## RESULT 64

US-08-475-399A-221  
Sequence 221, Application US/08475399A  
Patent No. 6509033  
GENERAL INFORMATION:  
APPLICANT: Urban, Robert G.  
APPLICANT: Chicz, Roman M.  
APPLICANT: Vignali, Dario A.A.  
APPLICANT: Hedley, Mary L.

```

APPLICANT: Stern, Lawrence J.
APPLICANT: Strominger, Jack L.
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
NUMBER OF SEQUENCES: 276
CORRESPONDENCE ADDRESS:
ADDRESSER: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,399A
FILING DATE: 07-JUN-1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/077,255
FILING DATE: 15-JUN-1993
APPLICATION NUMBER: 07/925,460
FILING DATE: 11-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 00246/168003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-507
TELEFAX: 617/542-890
TELEX: 200154
INFORMATION FOR SEQ ID NO: 221:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-475-399A-221

Query Match      24.3% Score 28; DB 2; Length 13;
Best Local Similarity 41.7%; Pred. No. 5.2e+02;
Matches 5; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY      9 HKYLVCSYVNGG 20
DB      2 HKVYACEVTHQG 13

RESULT 65
US-08-077-255A-221
Sequence 221, Application US/08077255A
Patent No. 6696061
GENERAL INFORMATION:
APPLICANT: Robert G. Urban
APPLICANT: Roman M. Chicz
APPLICANT: Darío A. A. Vignali
APPLICANT: Mary L. Hedley
APPLICANT: Lawrence J. Stern
APPLICANT: Jack L. Strominger
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
NUMBER OF SEQUENCES: 274
CORRESPONDENCE ADDRESS:
ADDRESSER: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MB
COMPUTER: IBM PS/2 Model 502 or 555X
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
APPLICATION NUMBER: PCT/US93/07545
FILING DATE: 19930811
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/925,460
FILING DATE: August 11, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00246/168001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 221:
SEQUENCE CHARACTERISTICS:
LENGTH: 13
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-077-255A-221

Query Match      24.3% Score 28; DB 2; Length 13;
Best Local Similarity 41.7%; Pred. No. 5.2e+02;
Matches 5; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY      9 HKYLVCSYVNGG 20
DB      2 HKVYACEVTHQG 13

RESULT 66
PCT-US93-07545-221
Sequence 221, Application PC/TUS9307545
GENERAL INFORMATION:
APPLICANT: Robert G. Urban
APPLICANT: Roman M. Chicz
APPLICANT: Darío A. A. Vignali
APPLICANT: Mary L. Hedley
APPLICANT: Lawrence J. Stern
APPLICANT: Jack L. Strominger
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
NUMBER OF SEQUENCES: 273
CORRESPONDENCE ADDRESS:
ADDRESSER: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MB
COMPUTER: IBM PS/2 Model 502 or 555X
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/07545
FILING DATE: 19930811
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/925,460
FILING DATE: August 11, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00246/168001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 221:
SEQUENCE CHARACTERISTICS:

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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/077,255A
FILING DATE: June 15, 1993
CLASSIFICATION: 424
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/925,460
FILING DATE: August 11, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00246/168001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 221:
SEQUENCE CHARACTERISTICS:
LENGTH: 13
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-077-255A-221

Query Match      24.3% Score 28; DB 2; Length 13;
Best Local Similarity 41.7%; Pred. No. 5.2e+02;
Matches 5; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY      9 HKYLVCSYVNGG 20
DB      2 HKVYACEVTHQG 13

RESULT 66
PCT-US93-07545-221
Sequence 221, Application PC/TUS9307545
GENERAL INFORMATION:
APPLICANT: Robert G. Urban
APPLICANT: Roman M. Chicz
APPLICANT: Darío A. A. Vignali
APPLICANT: Mary L. Hedley
APPLICANT: Lawrence J. Stern
APPLICANT: Jack L. Strominger
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
NUMBER OF SEQUENCES: 273
CORRESPONDENCE ADDRESS:
ADDRESSER: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MB
COMPUTER: IBM PS/2 Model 502 or 555X
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/07545
FILING DATE: 19930811
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/925,460
FILING DATE: August 11, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00246/168001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 221:
SEQUENCE CHARACTERISTICS:

```

LENGTH: 13  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
PCT-US93-07545-221

Query Match 24.3%; Score 28; DB 4; Length 13;  
Best Local Similarity 41.7%; Pred. No. 5.2e+02;  
Matches 5; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 9 HKYLVCEVNG 20  
DB 2 HKYVACEVTHOG 13

RESULT 67  
US-08-480-190-90  
Sequence 90, Application US/08480190  
Patent No. 5827516  
GENERAL INFORMATION:  
APPLICANT: Robert G. Urban  
APPLICANT: Roman M. Chicz  
APPLICANT: Dario A. A. Vignali  
APPLICANT: Mary L. Hedley  
APPLICANT: Lawrence J. Stern  
APPLICANT: Jack L. Strominger  
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES  
NUMBER OF SEQUENCES: 274  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: U.S.A.  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
COMPUTER: IBM PS/2 Model 50z or 55SX  
OPERATING SYSTEM: MS-DOS (Version 5.0)  
SOFTWARE: WordPerfect (Version 5.1)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/480,190  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/077,255  
FILING DATE: June 15, 1993  
APPLICATION NUMBER: 07/925,460  
FILING DATE: August 11, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Clark, Paul T.  
REGISTRATION NUMBER: 30,162  
REFERENCE/DOCKET NUMBER: 00246/168001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 542-5070  
TELEFAX: (617) 542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 90:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
US-08-480-190-90

Query Match 24.3%; Score 28; DB 1; Length 14;  
Best Local Similarity 41.7%; Pred. No. 5.6e+02;  
Matches 5; Conservative 1; Mismatches 6; Indels 0; Gaps 0;  
QY 9 HKYLVCEVNG 20  
DB 3 HKYVACEVTHOG 14

RESULT 68  
US-08-480-190-220

Sequence 220, Application US/08480190  
Patent No. 5827516  
GENERAL INFORMATION:

APPLICANT: Robert G. Urban  
APPLICANT: Roman M. Chicz  
APPLICANT: Dario A. A. Vignali  
APPLICANT: Mary L. Hedley  
APPLICANT: Lawrence J. Stern  
APPLICANT: Jack L. Strominger  
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES  
NUMBER OF SEQUENCES: 274  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: U.S.A.  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
COMPUTER: IBM PS/2 Model 50z or 55SX  
OPERATING SYSTEM: MS-DOS (Version 5.0)  
SOFTWARE: WordPerfect (Version 5.1)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/480,190  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/077,255  
FILING DATE: June 15, 1993  
APPLICATION NUMBER: 07/925,460  
FILING DATE: August 11, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Clark, Paul T.  
REGISTRATION NUMBER: 30,162  
REFERENCE/DOCKET NUMBER: 00246/168001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 542-5070  
TELEFAX: (617) 542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 220:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
US-08-480-190-220

Query Match 24.3%; Score 28; DB 1; Length 14;  
Best Local Similarity 41.7%; Pred. No. 5.6e+02;  
Matches 5; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 9 HKYLVCEVNG 20  
DB 2 HKYVACEVTHOG 13

RESULT 69  
US-08-488-379-90  
Sequence 90, Application US/08488379  
Patent No. 5880103  
GENERAL INFORMATION:  
APPLICANT: Robert G. Urban  
APPLICANT: Roman M. Chicz  
APPLICANT: Dario A. A. Vignali  
APPLICANT: Mary L. Hedley  
APPLICANT: Lawrence J. Stern  
APPLICANT: Jack L. Strominger  
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES  
NUMBER OF SEQUENCES: 274

;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Fish & Richardson  
;; STREET: 225 Franklin Street  
;; CITY: Boston  
;; STATE: Massachusetts  
;; COUNTRY: U.S.A.  
;; ZIP: 02110-2804  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
;; OPERATING SYSTEM: MS-DOS (Version 5.0)  
;; SOFTWARE: WordPerfect (Version 5.1)  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/488,379  
;; FILING DATE:  
;; CLASSIFICATION: 514  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 08/077,255  
;; FILING DATE: June 15, 1993  
;; APPLICATION NUMBER: 07/925,460  
;; FILING DATE: August 11, 1992  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Clark, Paul T.  
;; REGISTRATION NUMBER: 30,162  
;; REFERENCE/DOCKET NUMBER: 00246/168001  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (617) 542-5070  
;; TELEFAX: (617) 542-8906  
;; TELEX: 200154  
;; INFORMATION FOR SEQ ID NO: 90:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 14  
;; TYPE: amino acid  
;; STRANDEDNESS:  
;; TOPOLOGY: linear  
;;  
US-08-488-379-90  
;;  
Query Match 24.3%; Score 28; DB 1; Length 14;  
Best Local Similarity 41.7%; Pred. No. 5.6e+02;  
Matches 5; Conservative 1; Mismatches 6; Indels 0; Gaps 0;  
Qy 9 HKVYCVSVNG 20  
Db 3 HKVYACEVTHQG 14  
;;  
RESULT 70  
US-08-488-379-220  
;; Sequence 220, Application US/08488379  
;; Patent No. 5880103  
;; GENERAL INFORMATION:  
;; APPLICANT: Robert G. Urban  
;; APPLICANT: Roman M. Chiciz  
;; APPLICANT: Dario A. A. Vignali  
;; APPLICANT: Mary L. Hedley  
;; APPLICANT: Lawrence J. Stern  
;; APPLICANT: Jack L. Strominger  
;; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES  
;; NUMBER OF SEQUENCES: 274  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Fish & Richardson  
;; STREET: 225 Franklin Street  
;; CITY: Boston  
;; STATE: Massachusetts  
;; COUNTRY: U.S.A.  
;; ZIP: 02110-2804  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
;; OPERATING SYSTEM: MS-DOS (Version 5.0)  
;; SOFTWARE: WordPerfect (Version 5.1)  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/488,379

;; FILING DATE:  
;; CLASSIFICATION: 514  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 08/077,255  
;; FILING DATE: June 15, 1993  
;; APPLICATION NUMBER: 07/925,460  
;; FILING DATE: August 11, 1992  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Clark, Paul T.  
;; REGISTRATION NUMBER: 30,162  
;; REFERENCE/DOCKET NUMBER: 00246/168001  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (617) 542-5070  
;; TELEFAX: (617) 542-8906  
;; TELEX: 200154  
;; INFORMATION FOR SEQ ID NO: 220:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 14  
;; TYPE: amino acid  
;; STRANDEDNESS:  
;; TOPOLOGY: linear  
;;  
US-08-488-379-220  
;;  
Query Match 24.3%; Score 28; DB 1; Length 14;  
Best Local Similarity 41.7%; Pred. No. 5.6e+02;  
Matches 5; Conservative 1; Mismatches 6; Indels 0; Gaps 0;  
Qy 9 HKVYCVSVNG 20  
Db 2 HKVYACEVTHQG 13  
;;  
RESULT 71  
US-08-475-399A-90  
;; Sequence 90, Application US/08475399A  
;; Patent No. 6509033  
;; GENERAL INFORMATION:  
;; APPLICANT: Urban, Robert G.  
;; APPLICANT: Chiciz, Roman M.  
;; APPLICANT: Vignali, Dario A.A.  
;; APPLICANT: Hedley, Mary L.  
;; APPLICANT: Stern, Lawrence J.  
;; APPLICANT: Strominger, Jack L.  
;; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES  
;; NUMBER OF SEQUENCES: 276  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Fish & Richardson, P.C.  
;; STREET: 225 Franklin Street  
;; CITY: Boston  
;; STATE: MA  
;; COUNTRY: US  
;; ZIP: 02110-2804  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Diskette  
;; OPERATING SYSTEM: IBM Compatible  
;; SOFTWARE: Pastsq for Windows Version 2.0  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/475,399A  
;; FILING DATE: 07-JUN-1995  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 08/077,255  
;; FILING DATE: 15-JUN-1993  
;; APPLICATION NUMBER: 07/925,460  
;; FILING DATE: 11-AUG-1992  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Frazer, Janis K.  
;; REGISTRATION NUMBER: 34,819  
;; REFERENCE/DOCKET NUMBER: 00246/168003  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 617/542-507  
;; TELEFAX: 617/542-890  
;; TELEX: 200154



INFORMATION FOR SEQ ID NO: 90:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-475-399A-90

Query Match 24.3%; Score 28; DB 2; Length 14;  
Best Local Similarity 41.7%; Pred. No. 5.6e+02;  
Matches 5; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 9 HKYLVCEVNG 20  
DB 3 HKYLVCEVTHG 14

RESULT 72  
US-08-475-399A-220

Sequence 220, Application US/08475399A  
Patent No. 6509033

GENERAL INFORMATION:  
APPLICANT: Urban, Robert G.  
APPLICANT: Chiciz, Roman M.  
APPLICANT: Vignali, Dario A.A.  
APPLICANT: Hedley, Mary L.  
APPLICANT: Stern, Lawrence J.  
APPLICANT: Strominger, Jack L.  
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES  
NUMBER OF SEQUENCES: 276  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson, P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: US  
ZIP: 02110-2804

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette

COMPUTER: IBM compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: PASTESQ for Windows Version 2.0

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/475,399A  
FILING DATE: 07-JUN-1995

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/077,255  
FILING DATE: 15-JUN-1993

APPLICATION NUMBER: 07/925,460  
FILING DATE: 11-AUG-1992

ATTORNEY/AGENT INFORMATION:  
NAME: Frazer, Janis K.  
REGISTRATION NUMBER: 34,819

REFERENCE/DOCKET NUMBER: 00246/168003  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/542-507  
TELEFAX: 617/542-890

TELEX: 200154  
INFORMATION FOR SEQ ID NO: 220:

SEQUENCE CHARACTERISTICS:  
LENGTH: 14 amino acids  
TYPE: amino acid  
TOPOLOGY: linear

US-08-475-399A-220

Query Match 24.3%; Score 28; DB 2; Length 14;  
Best Local Similarity 41.7%; Pred. No. 5.6e+02;  
Matches 5; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 9 HKYLVCEVNG 20  
DB 2 HKYLVCEVTHG 13

RESULT 73

US-08-077-255A-90

Sequence 90, Application US/08077255A  
Patent No. 6696061

GENERAL INFORMATION:  
APPLICANT: Robert G. Urban  
APPLICANT: Roman M. Chiciz  
APPLICANT: Dario A. A. Vignali  
APPLICANT: Mary L. Hedley  
APPLICANT: Lawrence J. Stern  
APPLICANT: Jack L. Strominger  
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES  
NUMBER OF SEQUENCES: 274  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: U.S.A.  
ZIP: 02110-2804

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 MB  
COMPUTER: IBM PS/2 Model 502 or 555X  
OPERATING SYSTEM: MS-DOS (Version 5.0)

SOFTWARE: WordPerfect (Version 5.1)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/077,255A  
FILING DATE: June 15, 1993

CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/925,460  
FILING DATE: August 11, 1992

ATTORNEY/AGENT INFORMATION:  
NAME: Clark, Paul T.  
REGISTRATION NUMBER: 30,162

REFERENCE/DOCKET NUMBER: 00246/168001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 542-5070  
TELEFAX: (617) 542-8906

TELEX: 200154

INFORMATION FOR SEQ ID NO: 90:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear

US-08-077-255A-90

Query Match 24.3%; Score 28; DB 2; Length 14;  
Best Local Similarity 41.7%; Pred. No. 5.6e+02;  
Matches 5; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 9 HKYLVCEVNG 20  
DB 3 HKYLVCEVTHG 14

RESULT 74  
US-08-077-255A-220

Sequence 220, Application US/08077255A  
Patent No. 6696061

GENERAL INFORMATION:  
APPLICANT: Robert G. Urban  
APPLICANT: Roman M. Chiciz  
APPLICANT: Dario A. A. Vignali  
APPLICANT: Mary L. Hedley  
APPLICANT: Lawrence J. Stern  
APPLICANT: Jack L. Strominger  
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES  
NUMBER OF SEQUENCES: 274  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson  
STREET: 225 Franklin Street

```

/ CITY: Boston
/ STATE: Massachusetts
/ COUNTRY: U.S.A.
/ ZIP: 02110-2804
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 3.5" Diskette, 1.44 MB
/ COMPUTER: IBM PS/2 Model 502 or 558X
/ OPERATING SYSTEM: MS-DOS (Version 5.0)
/ SOFTWARE: Wordperfect (Version 5.1)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/077,255A
/ FILING DATE: June 15, 1993
/ CLASSIFICATION: 424
/ PRIORITY APPLICATION NUMBER: 07/925,460
/ FILING DATE: August 11, 1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Clark, Paul T.
/ REGISTRATION NUMBER: 30,162
/ REFERENCE/DOCKET NUMBER: 00246/168001
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (617) 542-5070
/ TELEFAX: (617) 542-8906
/ TELEX: 200154
/ INFORMATION FOR SEQ ID NO: 220:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 14
/ TYPE: amino acid
/ STRANDEDNESS:
/ TOPOLOGY: linear
/ US-08-077-255A-220

```

```

Query Match      24.3% Score 28; DB 2; Length 14;
Best Local Similarity 41.7%; Pred. No. 5.6e+02;
Matches 5; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
Qy      9 HKVLCESVNGG 20
Db      2 HKVACEVTHQG 13

```

```

RESULT 75
PCT-US93-07545-90
/ Sequence 90, Application PC/TUS9307545
/ GENERAL INFORMATION:
/ APPLICANT: Robert G. Urban
/ APPLICANT: Roman M. Chicz
/ APPLICANT: Dario A. A. Vignali
/ APPLICANT: Mary L. Hedley
/ APPLICANT: Lawrence J. Stern
/ APPLICANT: Jack L. Strominger
/ TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
/ NUMBER OF SEQUENCES: 273
/ CORRESPONDENCE ADDRESS:
/ ADDRESSER: Fish & Richardson
/ STREET: 225 Franklin Street
/ CITY: Boston
/ STATE: Massachusetts
/ COUNTRY: U.S.A.
/ ZIP: 02110-2804
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 3.5" Diskette, 1.44 MB
/ COMPUTER: IBM PS/2 Model 502 or 558X
/ OPERATING SYSTEM: MS-DOS (Version 5.0)
/ SOFTWARE: Wordperfect (Version 5.1)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: PCT/US93/07545
/ FILING DATE: 19930811
/ CLASSIFICATION:
/ PRIORITY APPLICATION DATA:
/ APPLICATION NUMBER: 07/925,460
/ FILING DATE: August 11, 1992
/ ATTORNEY/AGENT INFORMATION:

```

```

/ NAME: Clark, Paul T.
/ REGISTRATION NUMBER: 30,162
/ REFERENCE/DOCKET NUMBER: 00246/168001
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (617) 542-5070
/ TELEFAX: (617) 542-8906
/ TELEX: 200154
/ INFORMATION FOR SEQ ID NO: 90:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 14
/ TYPE: amino acid
/ STRANDEDNESS:
/ TOPOLOGY: linear
/ PCT-US93-07545-90

```

```

Query Match      24.3% Score 28; DB 4; Length 14;
Best Local Similarity 41.7%; Pred. No. 5.6e+02;
Matches 5; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
Qy      9 HKVLCESVNGG 20
Db      3 HKVACEVTHQG 14

```

```

RESULT 76
PCT-US93-07545-220
/ Sequence 220, Application PC/TUS9307545
/ GENERAL INFORMATION:
/ APPLICANT: Robert G. Urban
/ APPLICANT: Roman M. Chicz
/ APPLICANT: Dario A. A. Vignali
/ APPLICANT: Mary L. Hedley
/ APPLICANT: Lawrence J. Stern
/ APPLICANT: Jack L. Strominger
/ TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
/ NUMBER OF SEQUENCES: 273
/ CORRESPONDENCE ADDRESS:
/ ADDRESSER: Fish & Richardson
/ STREET: 225 Franklin Street
/ CITY: Boston
/ STATE: Massachusetts
/ COUNTRY: U.S.A.
/ ZIP: 02110-2804
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 3.5" Diskette, 1.44 MB
/ COMPUTER: IBM PS/2 Model 502 or 558X
/ OPERATING SYSTEM: MS-DOS (Version 5.0)
/ SOFTWARE: Wordperfect (Version 5.1)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: PCT/US93/07545
/ FILING DATE: 19930811
/ CLASSIFICATION:
/ PRIORITY APPLICATION DATA:
/ APPLICATION NUMBER: 07/925,460
/ FILING DATE: August 11, 1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Clark, Paul T.
/ REGISTRATION NUMBER: 30,162
/ REFERENCE/DOCKET NUMBER: 00246/168001
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (617) 542-5070
/ TELEFAX: (617) 542-8906
/ TELEX: 200154
/ INFORMATION FOR SEQ ID NO: 220:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 14
/ TYPE: amino acid
/ STRANDEDNESS:
/ TOPOLOGY: linear
/ PCT-US93-07545-220

```

Matches 5; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 9 HKYLVCSVNG 20  
DB 2 HKYVACEVTHQG 13

RESULT 77  
US-08-480-190-88  
Sequence 88, Application US/08480190  
Patent No. 5827516  
GENERAL INFORMATION:  
APPLICANT: Robert G. Urban  
APPLICANT: Roman M. Chicz  
APPLICANT: Dario A. A. Vignali  
APPLICANT: Mary L. Hedley  
APPLICANT: Lawrence J. Stern  
APPLICANT: Jack L. Strominger  
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES  
NUMBER OF SEQUENCES: 274  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: U.S.A.  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 MB  
COMPUTER: IBM PS/2 Model 502 or 55SX  
OPERATING SYSTEM: MS-DOS (Version 5.0)  
SOFTWARE: Wordperfect (Version 5.1)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/480,190  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/077,255  
FILING DATE: June 15, 1993  
APPLICATION NUMBER: 07/925,460  
FILING DATE: August 11, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Clark, Paul T.  
REGISTRATION NUMBER: 30,162  
REFERENCE/DOCKET NUMBER: 00246/168001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 542-5070  
TELEFAX: (617) 542-8906  
TELEX: 200154  
INFORMATION FOR SEQ. ID NO: 88:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
US-08-480-190-88

Query Match 24.3%; Score 28; DB 1; Length 15;  
Best Local Similarity 41.7%; Pred. No. 66+02;  
Matches 5; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 9 HKYLVCSVNG 20  
DB 2 HKYVACEVTHQG 13

RESULT 78  
US-08-480-190-89  
Sequence 89, Application US/08480190  
Patent No. 5827516  
GENERAL INFORMATION:  
APPLICANT: Robert G. Urban  
APPLICANT: Roman M. Chicz  
APPLICANT: Dario A. A. Vignali  
APPLICANT: Mary L. Hedley  
APPLICANT: Lawrence J. Stern  
APPLICANT: Jack L. Strominger  
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES  
NUMBER OF SEQUENCES: 274  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: U.S.A.  
ZIP: 02110-2804  
COMPUTER READABLE FORM:

APPLICANT: Dario A. A. Vignali  
APPLICANT: Mary L. Hedley  
APPLICANT: Lawrence J. Stern  
APPLICANT: Jack L. Strominger  
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES  
NUMBER OF SEQUENCES: 274  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: U.S.A.  
ZIP: 02110-2804  
COMPUTER READABLE FORM:

RESULT 79  
US-08-488-379-88  
Sequence 88, Application US/08488379  
Patent No. 5880103  
GENERAL INFORMATION:  
APPLICANT: Robert G. Urban  
APPLICANT: Roman M. Chicz  
APPLICANT: Dario A. A. Vignali  
APPLICANT: Mary L. Hedley  
APPLICANT: Lawrence J. Stern  
APPLICANT: Jack L. Strominger  
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES  
NUMBER OF SEQUENCES: 274  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: U.S.A.  
ZIP: 02110-2804  
COMPUTER READABLE FORM:

QY 9 HKYLVCSVNG 20  
DB 1 HKYVACEVTHQG 12

Query Match 24.3%; Score 28; DB 1; Length 15;  
Best Local Similarity 41.7%; Pred. No. 66+02;  
Matches 5; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 9 HKYLVCSVNG 20  
DB 1 HKYVACEVTHQG 12

RESULT 79  
US-08-488-379-88  
Sequence 88, Application US/08488379  
Patent No. 5880103  
GENERAL INFORMATION:  
APPLICANT: Robert G. Urban  
APPLICANT: Roman M. Chicz  
APPLICANT: Dario A. A. Vignali  
APPLICANT: Mary L. Hedley  
APPLICANT: Lawrence J. Stern  
APPLICANT: Jack L. Strominger  
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES  
NUMBER OF SEQUENCES: 274  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: U.S.A.  
ZIP: 02110-2804  
COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 MB  
COMPUTER: IBM PS/2 Model 502 or 55SX  
OPERATING SYSTEM: MS-DOS (Version 5.0)  
SOFTWARE: WordPerfect (Version 5.1)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/488,379  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/077,255  
FILING DATE: June 15, 1993  
APPLICATION NUMBER: 07/925,460  
FILING DATE: August 11, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Clark, Paul T.  
REGISTRATION NUMBER: 30,162  
REFERENCE/DOCKET NUMBER: 00246/168001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 542-5070  
TELEFAX: (617) 542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 88:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
US-08-488-379-88

Query Match 24.3% Score 28; DB 1; Length 15;  
Best Local Similarity 41.7% Pred. No. 6e+02;  
Matches 5; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 9 HKVYVCSVNGG 20  
DB 2 HKVYVCEVTHQG 13

RESULT 80  
US-08-488-379-89  
Sequence 89, Application US/08488379  
Patent No. 5880103  
GENERAL INFORMATION:  
APPLICANT: Robert G. Urban  
APPLICANT: Roman M. Chicz  
APPLICANT: Dario A. A. Vignali  
APPLICANT: Mary L. Hedley  
APPLICANT: Lawrence J. Stern  
APPLICANT: Jack L. Strominger  
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES  
NUMBER OF SEQUENCES: 274  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: U.S.A.  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 MB  
COMPUTER: IBM PS/2 Model 502 or 55SX  
OPERATING SYSTEM: MS-DOS (Version 5.0)  
SOFTWARE: WordPerfect (Version 5.1)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/488,379  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/077,255  
FILING DATE: June 15, 1993  
APPLICATION NUMBER: 07/925,460  
FILING DATE: August 11, 1992  
ATTORNEY/AGENT INFORMATION:

NAME: Clark, Paul T.  
REGISTRATION NUMBER: 30,162  
REFERENCE/DOCKET NUMBER: 00246/168001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 542-5070  
TELEFAX: (617) 542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 89:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
US-08-488-379-89

Query Match 24.3% Score 28; DB 1; Length 15;  
Best Local Similarity 41.7% Pred. No. 6e+02;  
Matches 5; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 9 HKVYVCSVNGG 20  
DB 1 HKVYVCEVTHQG 12

RESULT 81  
US-09-009-953-110  
Sequence 110, Application US/09009953  
Patent No. 6413517  
GENERAL INFORMATION:  
APPLICANT: Sette, Alessandro  
TITLE OF INVENTION: Identification of Broadly  
Reactive DR Restricted Epitopes  
NUMBER OF SEQUENCES: 274  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: Fast-Seq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/009,953  
FILING DATE: 21-Jan-1998  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/036,713  
FILING DATE: 23-JAN-1997  
APPLICATION NUMBER: US 60/037,432  
FILING DATE: 07-FEB-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Weber, Ellen Lauver  
REGISTRATION NUMBER: 32,762  
REFERENCE/DOCKET NUMBER: 018623-011520US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-576-0200  
TELEFAX: 415-576-0300  
TELEX: <Unknown>  
INFORMATION FOR SEQ ID NO: 110:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 110:  
US-09-009-953-110  
Query Match 24.3% Score 28; DB 2; Length 15;

Best Local Similarity 57.1%; Pred. No. 6e+02;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 IPHPTNI 8  
DB 8 IPHAGL 14

## RESULT 82

US-08-475-399A-88  
Sequence 88, Application US/08475399A  
Patent No. 6509033  
GENERAL INFORMATION:  
APPLICANT: Urban, Robert G.  
APPLICANT: Chicz, Roman M.  
APPLICANT: Vignall, Dario A.A.  
APPLICANT: Hedley, Mary L.  
APPLICANT: Stern, Lawrence J.  
APPLICANT: Strominger, Jack L.  
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES  
NUMBER OF SEQUENCES: 276  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Fish & Richardson, P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: US  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/475,399A  
FILING DATE: 07-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/077,255  
FILING DATE: 15-JUN-1993  
APPLICATION NUMBER: 07/925,460  
FILING DATE: 11-AUG-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Fraser, Janis K.  
REGISTRATION NUMBER: 34,819  
REFERENCE/DOCKET NUMBER: 00246/168003  
TELEPHONE: 617/542-507  
TELEFAX: 617/542-890  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 88:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-475-399A-88

Query Match 24.3%; Score 28; DB 2; Length 15;  
Best Local Similarity 41.7%; Pred. No. 6e+02;  
Matches 5; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 9 HKYLVCSYVNG 20  
DB 2 HKYVACEVTHQG 13

## RESULT 83

US-08-475-399A-89  
Sequence 89, Application US/08475399A  
Patent No. 6509033  
GENERAL INFORMATION:  
APPLICANT: Urban, Robert G.  
APPLICANT: Chicz, Roman M.  
APPLICANT: Vignall, Dario A.A.

APPLICANT: Hedley, Mary L.  
APPLICANT: Stern, Lawrence J.  
APPLICANT: Strominger, Jack L.  
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES  
NUMBER OF SEQUENCES: 276  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Fish & Richardson, P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: US  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/475,399A  
FILING DATE: 07-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/077,255  
FILING DATE: 15-JUN-1993  
APPLICATION NUMBER: 07/925,460  
FILING DATE: 11-AUG-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Fraser, Janis K.  
REGISTRATION NUMBER: 34,819  
REFERENCE/DOCKET NUMBER: 00246/168003  
TELEPHONE: 617/542-507  
TELEFAX: 617/542-890  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 89:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-475-399A-89

Query Match 24.3%; Score 28; DB 2; Length 15;  
Best Local Similarity 41.7%; Pred. No. 6e+02;  
Matches 5; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 9 HKYLVCSYVNG 20  
DB 1 HKYVACEVTHQG 12

## RESULT 84

US-08-077-255A-88  
Sequence 88, Application US/08077255A  
Patent No. 6696061  
GENERAL INFORMATION:  
APPLICANT: Robert G. Urban  
APPLICANT: Roman M. Chicz  
APPLICANT: Dario A. A. Vignall  
APPLICANT: Mary L. Hedley  
APPLICANT: Lawrence J. Stern  
APPLICANT: Jack L. Strominger  
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES  
NUMBER OF SEQUENCES: 274  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Fish & Richardson  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: U.S.A.  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 MB  
COMPUTER: IBM PS/2 Model 502 or 558X  
OPERATING SYSTEM: MS-DOS (Version 5.0)

SOFTWARE: WordPerfect (Version 5.1)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/077,255A  
FILING DATE: June 15, 1993  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/925,460  
FILING DATE: August 11, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Clark, Paul T.  
REGISTRATION NUMBER: 30,162  
REFERENCE/DOCKET NUMBER: 00246/168001  
TELEPHONE: (617) 542-5070  
TELEFAX: (617) 542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 88:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
US-08-077-255A-88

Query Match 24.3%; Score 28; DB 2; Length 15;  
Best Local Similarity 41.7%; Pred. No. 6e+02;  
Matches 5; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 9 HKVYCESVNGG 20  
DB 2 HKVYACEVTHQG 13

RESULT 85  
US-08-077-255A-89  
Sequence 89, Application US/08077255A  
Patent No. 6696061  
GENERAL INFORMATION:  
APPLICANT: Robert G. Urban  
APPLICANT: Roman M. Chicz  
APPLICANT: Dario A. A. Vignali  
APPLICANT: Mary L. Hedley  
APPLICANT: Lawrence J. Stern  
APPLICANT: Jack L. Strominger  
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES  
NUMBER OF SEQUENCES: 274  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: U.S.A.  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
COMPUTER: IBM PS/2 Model 502 or 55SX  
OPERATING SYSTEM: MS-DOS (Version 5.0)  
SOFTWARE: WordPerfect (Version 5.1)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/077,255A  
FILING DATE: June 15, 1993  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/925,460  
FILING DATE: August 11, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Clark, Paul T.  
REGISTRATION NUMBER: 30,162  
REFERENCE/DOCKET NUMBER: 00246/168001  
TELEPHONE: (617) 542-5070  
TELEFAX: (617) 542-8906  
TELEX: 200154

INFORMATION FOR SEQ ID NO: 89:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
US-08-077-255A-89

Query Match 24.3%; Score 28; DB 2; Length 15;  
Best Local Similarity 41.7%; Pred. No. 6e+02;  
Matches 5; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 9 HKVYCESVNGG 20  
DB 1 HKVYACEVTHQG 12

RESULT 86  
PCT-US93-07545-88  
Sequence 88, Application PC/TUS9307545  
GENERAL INFORMATION:  
APPLICANT: Robert G. Urban  
APPLICANT: Roman M. Chicz  
APPLICANT: Dario A. A. Vignali  
APPLICANT: Mary L. Hedley  
APPLICANT: Lawrence J. Stern  
APPLICANT: Jack L. Strominger  
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES  
NUMBER OF SEQUENCES: 273  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: U.S.A.  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
COMPUTER: IBM PS/2 Model 502 or 55SX  
OPERATING SYSTEM: MS-DOS (Version 5.0)  
SOFTWARE: WordPerfect (Version 5.1)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/07545  
FILING DATE: 19930811  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/925,460  
FILING DATE: August 11, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Clark, Paul T.  
REGISTRATION NUMBER: 30,162  
REFERENCE/DOCKET NUMBER: 00246/168001  
TELEPHONE: (617) 542-5070  
TELEFAX: (617) 542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 88:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
PCT-US93-07545-88

Query Match 24.3%; Score 28; DB 4; Length 15;  
Best Local Similarity 41.7%; Pred. No. 6e+02;  
Matches 5; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 9 HKVYCESVNGG 20  
DB 2 HKVYACEVTHQG 13

RESULT 87  
PCT-US93-07545-89  
Sequence 89, Application PC/TUS9307545  
GENERAL INFORMATION:  
APPLICANT: Robert G. Urban  
APPLICANT: Roman M. Chicz  
APPLICANT: Dario A. A. Vignali  
APPLICANT: Mary L. Hedley  
APPLICANT: Lawrence J. Stern  
APPLICANT: Jack L. Strominger  
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES  
NUMBER OF SEQUENCES: 273  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: U.S.A.  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 MB  
COMPUTER: IBM PS/2 Model 502 or 55SX  
OPERATING SYSTEM: MS-DOS (Version 5.0)  
SOFTWARE: WordPerfect (Version 5.1)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/07545  
FILING DATE: 19930811  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/925,460  
FILING DATE: August 11, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Clark, Paul T.  
REGISTRATION NUMBER: 30,162  
REFERENCE/DOCKET NUMBER: 00246/168001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 542-5070  
TELEFAX: (617) 542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 89:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
PCT-US93-07545-89

Query Match 24.3%; Score 28; DB 4; Length 15;  
Best Local Similarity 41.7%; Pred. No. 6e+02;  
Matches 5; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 9 HKYLVCSVNGG 20  
DB 1 HKYVACEVTHQG 12

RESULT 88  
US-08-480-190-85  
Sequence 85, Application US/08480190  
Patent No. 5827516  
GENERAL INFORMATION:  
APPLICANT: Robert G. Urban  
APPLICANT: Roman M. Chicz  
APPLICANT: Dario A. A. Vignali  
APPLICANT: Mary L. Hedley  
APPLICANT: Lawrence J. Stern  
APPLICANT: Jack L. Strominger  
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES  
NUMBER OF SEQUENCES: 274  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson  
STREET: 225 Franklin Street  
CITY: Boston

STATE: Massachusetts  
COUNTRY: U.S.A.  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 MB  
COMPUTER: IBM PS/2 Model 502 or 55SX  
OPERATING SYSTEM: MS-DOS (Version 5.0)  
SOFTWARE: WordPerfect (Version 5.1)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/480,190  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/077,255  
FILING DATE: June 15, 1993  
APPLICATION NUMBER: 07/925,460  
FILING DATE: August 11, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Clark, Paul T.  
REGISTRATION NUMBER: 30,162  
REFERENCE/DOCKET NUMBER: 00246/168001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 542-5070  
TELEFAX: (617) 542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 85:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
US-08-480-190-85

Query Match 24.3%; Score 28; DB 1; Length 16;  
Best Local Similarity 41.7%; Pred. No. 6.5e+02;  
Matches 5; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 9 HKYLVCSVNGG 20  
DB 2 HKYVACEVTHQG 13

RESULT 89  
US-08-480-190-86  
Sequence 86, Application US/08480190  
Patent No. 5827516  
GENERAL INFORMATION:  
APPLICANT: Robert G. Urban  
APPLICANT: Roman M. Chicz  
APPLICANT: Dario A. A. Vignali  
APPLICANT: Mary L. Hedley  
APPLICANT: Lawrence J. Stern  
APPLICANT: Jack L. Strominger  
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES  
NUMBER OF SEQUENCES: 274  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: U.S.A.  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 MB  
COMPUTER: IBM PS/2 Model 502 or 55SX  
OPERATING SYSTEM: MS-DOS (Version 5.0)  
SOFTWARE: WordPerfect (Version 5.1)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/480,190  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/077,255

FILING DATE: June 15, 1993  
 APPLICATION NUMBER: 07/925,460  
 FILING DATE: August 11, 1992  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Clark, Paul T.  
 REGISTRATION NUMBER: 30,162  
 REFERENCE/DOCKET NUMBER: 00246/168001  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (617) 542-5070  
 TELEFAX: (617) 542-8906  
 TELEX: 200154  
 INFORMATION FOR SEQ ID NO: 86:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 16  
 TYPE: amino acid  
 STRANDEDNESS:  
 TOPOLOGY: linear  
 US-08-480-190-86

Query Match 24.3% Score 28; DB 1; Length 16;  
 Best Local Similarity 41.7%; Pred. No. 6.5e+02;  
 Matches 5; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 9 HKYVCESYNG 20  
 DB 1 HKYVCEVTHQG 12

RESULT 90  
 US-08-480-190-87  
 Sequence 87, Application US/08480190  
 Patent No. 5827516  
 GENERAL INFORMATION:  
 APPLICANT: Robert G. Urban  
 APPLICANT: Roman M. Chicz  
 APPLICANT: Dario A. A. Vignali  
 APPLICANT: Mary L. Hedley  
 APPLICANT: Lawrence J. Stern  
 APPLICANT: Jack L. Strominger  
 TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES  
 NUMBER OF SEQUENCES: 274  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Fish & Richardson  
 STREET: 225 Franklin Street  
 CITY: Boston  
 STATE: Massachusetts  
 COUNTRY: U.S.A.  
 ZIP: 02110-2804  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5" Diskette, 1.44 MB  
 COMPUTER: IBM PS/2 Model 502 or 55SX  
 OPERATING SYSTEM: MS-DOS (Version 5.0)  
 SOFTWARE: WordPerfect (Version 5.1)  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/480,190  
 FILING DATE:  
 CLASSIFICATION: 424  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/077,255  
 FILING DATE: June 15, 1993  
 APPLICATION NUMBER: 07/925,460  
 FILING DATE: August 11, 1992  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Clark, Paul T.  
 REGISTRATION NUMBER: 30,162  
 REFERENCE/DOCKET NUMBER: 00246/168001  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (617) 542-5070  
 TELEFAX: (617) 542-8906  
 TELEX: 200154  
 INFORMATION FOR SEQ ID NO: 87:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 16

TYPE: amino acid  
 STRANDEDNESS:  
 TOPOLOGY: linear  
 US-08-480-190-87

Query Match 24.3% Score 28; DB 1; Length 16;  
 Best Local Similarity 41.7%; Pred. No. 6.5e+02;  
 Matches 5; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 9 HKYVCESYNG 20  
 DB 3 HKYVCEVTHQG 14

RESULT 91  
 US-08-488-379-85  
 Sequence 85, Application US/08488379  
 Patent No. 5880103  
 GENERAL INFORMATION:  
 APPLICANT: Robert G. Urban  
 APPLICANT: Roman M. Chicz  
 APPLICANT: Dario A. A. Vignali  
 APPLICANT: Mary L. Hedley  
 APPLICANT: Lawrence J. Stern  
 APPLICANT: Jack L. Strominger  
 TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES  
 NUMBER OF SEQUENCES: 274  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Fish & Richardson  
 STREET: 225 Franklin Street  
 CITY: Boston  
 STATE: Massachusetts  
 COUNTRY: U.S.A.  
 ZIP: 02110-2804  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5" Diskette, 1.44 MB  
 COMPUTER: IBM PS/2 Model 502 or 55SX  
 OPERATING SYSTEM: MS-DOS (Version 5.0)  
 SOFTWARE: WordPerfect (Version 5.1)  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/488,379  
 FILING DATE:  
 CLASSIFICATION: 514  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/077,255  
 FILING DATE: June 15, 1993  
 APPLICATION NUMBER: 07/925,460  
 FILING DATE: August 11, 1992  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Clark, Paul T.  
 REGISTRATION NUMBER: 30,162  
 REFERENCE/DOCKET NUMBER: 00246/168001  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (617) 542-5070  
 TELEFAX: (617) 542-8906  
 TELEX: 200154  
 INFORMATION FOR SEQ ID NO: 85:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 16  
 TYPE: amino acid  
 STRANDEDNESS:  
 TOPOLOGY: linear  
 US-08-488-379-85

Query Match 24.3% Score 28; DB 1; Length 16;  
 Best Local Similarity 41.7%; Pred. No. 6.5e+02;  
 Matches 5; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 9 HKYVCESYNG 20  
 DB 2 HKYVCEVTHQG 13



RESULT 92  
US-08-488-379-86  
Sequence 86, Application US/08488379  
Patent No. 5880103  
GENERAL INFORMATION:  
APPLICANT: Robert G. Urban  
APPLICANT: Roman M. Chicz  
APPLICANT: Darlo A. A. Vignali  
APPLICANT: Mary L. Hedley  
APPLICANT: Lawrence J. Stern  
APPLICANT: Jack L. Strominger  
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES  
NUMBER OF SEQUENCES: 274  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Fish & Richardson  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: U.S.A.  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
COMPUTER: IBM PS/2 Model 502 or 55SX  
OPERATING SYSTEM: MS-DOS (Version 5.0)  
SOFTWARE: WordPerfect (Version 5.1)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/488,379  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/077,255  
FILING DATE: June 15, 1993  
APPLICATION NUMBER: 07/925,460  
FILING DATE: August 11, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Clark, Paul T.  
REGISTRATION NUMBER: 30,162  
REFERENCE/DOCKET NUMBER: 00246/168001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 542-5070  
TELEFAX: (617) 542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 86:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
US-08-488-379-86  
Query Match 24.3%; Score 28; DB 1; Length 16;  
Best Local Similarity 41.7%; Pred. No. 6.5e+02;  
Matches 5; Conservative 1; Mismatches 6; Indels 0; Gaps 0;  
QY 9 HXYLVCSVNG 20  
DB 1 HXYVACEVTHQG 12  
RESULT 93  
US-08-488-379-87  
Sequence 87, Application US/08488379  
Patent No. 5880103  
GENERAL INFORMATION:  
APPLICANT: Robert G. Urban  
APPLICANT: Roman M. Chicz  
APPLICANT: Darlo A. A. Vignali  
APPLICANT: Mary L. Hedley  
APPLICANT: Lawrence J. Stern  
APPLICANT: Jack L. Strominger  
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES  
NUMBER OF SEQUENCES: 274  
CORRESPONDENCE ADDRESSES:

ADDRESSEE: Fish & Richardson  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: U.S.A.  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
COMPUTER: IBM PS/2 Model 502 or 55SX  
OPERATING SYSTEM: MS-DOS (Version 5.0)  
SOFTWARE: WordPerfect (Version 5.1)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/488,379  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/077,255  
FILING DATE: June 15, 1993  
APPLICATION NUMBER: 07/925,460  
FILING DATE: August 11, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Clark, Paul T.  
REGISTRATION NUMBER: 30,162  
REFERENCE/DOCKET NUMBER: 00246/168001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 542-5070  
TELEFAX: (617) 542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 87:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
US-08-488-379-87  
Query Match 24.3%; Score 28; DB 1; Length 16;  
Best Local Similarity 41.7%; Pred. No. 6.5e+02;  
Matches 5; Conservative 1; Mismatches 6; Indels 0; Gaps 0;  
QY 9 HXYLVCSVNG 20  
DB 3 HXYVACEVTHQG 14  
RESULT 94  
US-08-810-009-51  
Sequence 51, Application US/08810009  
Patent No. 6211437  
GENERAL INFORMATION:  
APPLICANT: Briggs, Steven P.  
APPLICANT: Jhal, Gurmukh S.  
APPLICANT: Gray, John  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROLLING  
CELL DEATH AND DISEASE RESISTANCE IN PLANTS  
NUMBER OF SEQUENCES: 65  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: BELL, SELTZER, PARK & GIBSON  
STREET: P.O. Drawer 34009  
CITY: Charlotte  
STATE: No. 6211437ch Carolina  
COUNTRY: USA  
ZIP: 28234  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/810,009  
FILING DATE: 04-MAR-1997  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:

NAME: Sprull, W. Murray  
REGISTRATION NUMBER: 32,943  
REFERENCE/DOCKET NUMBER: 5718-4  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 919-881-3140  
TELEFAX: 919-881-3175  
TELEX: 575102  
INFORMATION FOR SEQ ID NO: 51:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-010-009-51

Query Match 24.3%; Score 28; DB 2; Length 16;  
Best Local Similarity 44.4%; Pred. No. 6.5e+02;  
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 DHPPTNIH 9  
DB 7 DLTHETVH 15

RESULT 95  
US-08-475-399A-85  
Sequence 85, Application US/08475399A  
Patent No. 6509033  
GENERAL INFORMATION:  
APPLICANT: Urban, Robert G.  
APPLICANT: Chicz, Roman M.  
APPLICANT: Vignali, Dario A.A.  
APPLICANT: Hedley, Mary L.  
APPLICANT: Stern, Lawrence J.  
APPLICANT: Strominger, Jack L.  
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES  
NUMBER OF SEQUENCES: 276  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Fish & Richardson, P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: US  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: PastsEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/475,399A  
FILING DATE: 07-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/077,255  
FILING DATE: 15-JUN-1993  
APPLICATION NUMBER: 07/925,460  
FILING DATE: 11-AUG-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Frazer, Janis K.  
REGISTRATION NUMBER: 34,819  
REFERENCE/DOCKET NUMBER: 00246/168003  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/542-507  
TELEFAX: 617/542-890  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 85:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-475-399A-85

Query Match 24.3%; Score 28; DB 2; Length 16;  
Best Local Similarity 41.7%; Pred. No. 6.5e+02;  
Matches 5; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 9 HKYVCESYNG 20  
DB 2 HKYVCEVTTHQG 13

RESULT 96  
US-08-475-399A-86  
Sequence 86, Application US/08475399A  
Patent No. 6509033  
GENERAL INFORMATION:  
APPLICANT: Urban, Robert G.  
APPLICANT: Chicz, Roman M.  
APPLICANT: Vignali, Dario A.A.  
APPLICANT: Hedley, Mary L.  
APPLICANT: Stern, Lawrence J.  
APPLICANT: Strominger, Jack L.  
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES  
NUMBER OF SEQUENCES: 276  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Fish & Richardson, P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: US  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: PastsEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/475,399A  
FILING DATE: 07-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/077,255  
FILING DATE: 15-JUN-1993  
APPLICATION NUMBER: 07/925,460  
FILING DATE: 11-AUG-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Frazer, Janis K.  
REGISTRATION NUMBER: 34,819  
REFERENCE/DOCKET NUMBER: 00246/168003  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/542-507  
TELEFAX: 617/542-890  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 86:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-475-399A-86

Query Match 24.3%; Score 28; DB 2; Length 16;  
Best Local Similarity 41.7%; Pred. No. 6.5e+02;  
Matches 5; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 9 HKYVCESYNG 20  
DB 1 HKYVCEVTTHQG 12

RESULT 97  
US-08-475-399A-87  
Sequence 87, Application US/08475399A  
Patent No. 6509033  
GENERAL INFORMATION:  
APPLICANT: Urban, Robert G.  
APPLICANT: Chicz, Roman M.

APPLICANT: Vignali, Dario A.A.  
APPLICANT: Hedley, Mary L.  
APPLICANT: Stern, Lawrence J.  
APPLICANT: Strominger, Jack L.  
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES  
NUMBER OF SEQUENCES: 276  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson, P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: US  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/475,399A  
FILING DATE: 07-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/077,255  
FILING DATE: 15-JUN-1993  
APPLICATION NUMBER: 07/925,460  
FILING DATE: 11-AUG-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Fraser, Janis K.  
REGISTRATION NUMBER: 34,819  
REFERENCE/DOCKET NUMBER: 00246/168003  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/542-507  
TELEFAX: 617/542-890  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 87:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-475-399A-87

Query Match 24.3%; Score 28; DB 2; Length 16;  
Best Local Similarity 41.7%; Pred. No. 6.5e+02;  
Matches 5; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 9 HKYVACEVTHQG 20  
DB 3 HKYVACEVTHQG 14

RESULT 98  
US-09-776-490-51  
Sequence 51, Application US/09776490  
Patent No. 6599725  
GENERAL INFORMATION:  
APPLICANT: Briggs, Steven P.  
Johal, Gurmukh S.  
Gray, John  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROLLING  
CELL DEATH AND DISEASE RESISTANCE IN PLANTS  
NUMBER OF SEQUENCES: 65  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BELL, SELTZER, PARK & GIBSON  
STREET: P.O. Drawer 34009  
CITY: Charlotte  
STATE: No. 6599725th Carolina  
COUNTRY: USA  
ZIP: 28234  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/776,490  
FILING DATE: 02-Feb-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/810,009  
FILING DATE: 04-MAR-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Sprull, W. Murray  
REGISTRATION NUMBER: 32,943  
REFERENCE/DOCKET NUMBER: 5718-4  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 919-881-3140  
TELEFAX: 919-881-3175  
TELEX: 575102  
INFORMATION FOR SEQ ID NO: 51:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 51:  
US-09-776-490-51

Query Match 24.3%; Score 28; DB 2; Length 16;  
Best Local Similarity 44.4%; Pred. No. 6.5e+02;  
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 DIHPPTNIIH 9  
DB 7 DLTHETVTH 15

RESULT 99  
US-08-077-255A-85  
Sequence 85, Application US/08077255A  
Patent No. 6696061  
GENERAL INFORMATION:  
APPLICANT: Robert G. Urban  
APPLICANT: Roman M. Chicz  
APPLICANT: Dario A. A. Vignali  
APPLICANT: Mary L. Hedley  
APPLICANT: Lawrence J. Stern  
APPLICANT: Jack L. Strominger  
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES  
NUMBER OF SEQUENCES: 274  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: U.S.A.  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 MB  
COMPUTER: IBM PS/2 Model 502 or 55SX  
OPERATING SYSTEM: MS-DOS (Version 5.0)  
SOFTWARE: WordPerfect (Version 5.1)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/077,255A  
FILING DATE: June 15, 1993  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/925,460  
FILING DATE: August 11, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Clark, Paul T.  
REGISTRATION NUMBER: 30,162  
REFERENCE/DOCKET NUMBER: 00246/168001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 542-5070  
TELEFAX: (617) 542-8906

Search completed: January 20, 2006, 19:14:12  
 Job time : 21.9615 secs

TELEX: 200154  
 INFORMATION FOR SEQ ID NO: 85:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 16  
 TYPE: amino acid  
 STRANDEDNESS:  
 TOPOLOGY: linear  
 US-08-077-255A-85

Query Match 24.3%; Score 28; DB 2; Length 16;  
 Best Local Similarity 41.7%; Pred. No. 6.5e+02;  
 Matches 5; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 9 HKYLVCEVYNGG 20  
 DB 2 HKYVACEVTHOG 13

RESULT 100  
 US-08-077-255A-86  
 Sequence 86, Application US/0807255A  
 Patent No. 6696061  
 GENERAL INFORMATION:  
 APPLICANT: Robert G. Urban  
 APPLICANT: Roman M. Chicz  
 APPLICANT: Dario A. A. Vignali  
 APPLICANT: Mary L. Hedley  
 APPLICANT: Lawrence J. Stern  
 APPLICANT: Jack L. Strominger  
 TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES  
 NUMBER OF SEQUENCES: 274  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Fish & Richardson  
 STREET: 225 Franklin Street  
 CITY: Boston  
 STATE: Massachusetts  
 COUNTRY: U.S.A.  
 ZIP: 02110-2804  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
 COMPUTER: IBM PS/2 Model 50Z or 55SX  
 OPERATING SYSTEM: MS-DOS (Version 5.0)  
 SOFTWARE: WordPerfect (Version 5.1)  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/077,255A  
 FILING DATE: June 15, 1993  
 CLASSIFICATION: 424  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 07/925,460  
 FILING DATE: August 11, 1992  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Clark, Paul T.  
 REGISTRATION NUMBER: 30,162  
 REFERENCE/DOCKET NUMBER: 00246/168001  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (617) 542-5070  
 TELEFAX: (617) 542-8906  
 TELEX: 200154  
 INFORMATION FOR SEQ ID NO: 86:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 16  
 TYPE: amino acid  
 STRANDEDNESS:  
 TOPOLOGY: linear  
 US-08-077-255A-86

Query Match 24.3%; Score 28; DB 2; Length 16;  
 Best Local Similarity 41.7%; Pred. No. 6.5e+02;  
 Matches 5; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 9 HKYLVCEVYNGG 20  
 DB 1 HKYVACEVTHOG 12

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OM protein - protein search, using sw model

Run on: January 20, 2006, 19:11:21 ; Search time 72.1154 Seconds  
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Title: US-09-662-293-3

Perfect score: 115  
Sequence: 1 DHPPTNHRKYLVCESVNGG 20

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Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 380452

Minimum DB seq length: 0  
Maximum DB seq length: 20

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 100 summaries

Database : Published Applications AA Main:\*

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- 3: /cgn2\_6/prodata/1/pubppa/US09\_PUBCOMB.pep:\*
- 4: /cgn2\_6/prodata/1/pubppa/US10A\_PUBCOMB.pep:\*
- 5: /cgn2\_6/prodata/1/pubppa/US10B\_PUBCOMB.pep:\*
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

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2	109	94.8	19	4	US-10-218-743-11
3	37.5	32.6	20	3	US-09-664-761-38552
4	35	30.4	7	3	US-09-554-385-54
5	35	30.4	7	5	US-10-912-512-54
6	35	30.4	7	5	US-10-235-043-54
7	35	30.4	20	3	US-09-564-201A-20
8	35	30.4	20	4	US-10-681-389-20
9	35	30.4	20	4	US-10-681-388-20
10	32	27.8	10	4	US-10-200-708-47
11	32	27.8	10	4	US-10-200-708-95
12	32	27.8	10	4	US-10-200-708-117
13	32	27.8	10	4	US-10-200-708-119
14	32	27.8	10	4	US-10-200-708-671
15	32	27.8	14	4	US-10-417-895A-36
16	32	27.8	14	5	US-10-808-187-2265
17	32	27.8	14	5	US-10-807-807-2265
18	32	27.8	15	4	US-10-103-395-109
19	32	27.8	16	4	US-10-062-710-19
20	32	27.8	17	4	US-10-442-909-32
21	32	27.8	20	4	US-10-385-649A-9
22	32	27.8	20	6	US-11-008-653-128
23	31.5	27.4	17	4	US-10-430-685-95
24	31	27.0	12	4	US-10-706-391-29
25	31	27.0	15	3	US-09-966-782A-58
26	31	27.0	15	4	US-10-254-905-58
27	31	27.0	16	3	US-09-791-524-3

28	31	27.0	17	3	US-09-791-524-4	Sequence 4, Appl1
29	31	27.0	17	4	US-10-609-217-196	Sequence 196, App
30	31	27.0	17	4	US-10-632-388-196	Sequence 196, App
31	31	27.0	17	4	US-10-651-723-196	Sequence 196, App
32	31	27.0	17	4	US-10-645-761-196	Sequence 196, App
33	31	27.0	17	4	US-10-666-696-196	Sequence 196, App
34	31	27.0	17	4	US-10-653-048-196	Sequence 196, App
35	31	27.0	17	4	US-10-756-289-1	Sequence 1, Appl1
36	31	27.0	17	5	US-10-821-544-16	Sequence 196, App
37	31	27.0	17	5	US-10-645-784-146	Sequence 196, App
38	31	27.0	18	3	US-09-664-761-44227	Sequence 9, Appl1
39	31	27.0	20	3	US-09-791-524-9	Sequence 787, App
40	30	26.1	9	4	US-10-182-252A-787	Sequence 830, App
41	30	26.1	9	4	US-10-182-252A-830	Sequence 58, Appl1
42	30	26.1	10	3	US-09-765-086-58	Sequence 160, App
43	30	26.1	10	3	US-09-573-822C-160	Sequence 58, Appl1
44	30	26.1	10	4	US-10-264-374-58	Sequence 58, Appl1
45	30	26.1	10	4	US-10-375-992-58	Sequence 58, Appl1
46	30	26.1	10	4	US-10-264-374-58	Sequence 58, Appl1
47	30	26.1	10	4	US-10-375-992-58	Sequence 58, Appl1
48	30	26.1	10	5	US-10-838-289-549	Sequence 549, App
49	30	26.1	11	5	US-10-490-911-4	Sequence 4, Appl1
50	30	26.1	15	5	US-10-946-647-769	Sequence 769, App
51	30	26.1	16	3	US-09-825-517A-7	Sequence 7, Appl1
52	30	26.1	16	4	US-10-148-671-10	Sequence 10, Appl1
53	30	26.1	16	6	US-11-045-477-7	Sequence 7, Appl1
54	30	26.1	20	4	US-10-280-066-34	Sequence 34, Appl1
55	30	26.1	20	5	US-10-776-013-463	Sequence 463, App
56	29.5	25.7	9	4	US-10-062-109A-123	Sequence 123, App
57	29.5	25.7	9	4	US-10-005-480A-123	Sequence 123, App
58	29.5	25.7	10	4	US-10-062-109A-164	Sequence 164, App
59	29.5	25.7	10	4	US-10-005-480A-164	Sequence 164, App
60	29.5	25.7	17	5	US-10-485-758-89	Sequence 89, Appl1
61	29	25.2	8	4	US-10-285-390-408	Sequence 408, App
62	29	25.2	9	3	US-09-826-294-41	Sequence 41, Appl1
63	29	25.2	9	3	US-09-791-393-7	Sequence 7, Appl1
64	29	25.2	9	3	US-09-791-389-7	Sequence 7, Appl1
65	29	25.2	9	4	US-10-264-309-239	Sequence 239, App
66	29	25.2	9	4	US-10-182-252A-232	Sequence 232, App
67	29	25.2	9	4	US-10-182-252A-759	Sequence 759, App
68	29	25.2	9	4	US-10-182-252A-832	Sequence 832, App
69	29	25.2	9	4	US-10-182-252A-866	Sequence 866, App
70	29	25.2	9	5	US-10-264-309-239	Sequence 239, App
71	29	25.2	11	2	US-08-596-140-16	Sequence 16, Appl1
72	29	25.2	11	4	US-10-169-351-80	Sequence 80, Appl1
73	29	25.2	11	4	US-10-239-656-9	Sequence 9, Appl1
74	29	25.2	11	5	US-10-879-994-59	Sequence 59, Appl1
75	29	25.2	12	4	US-10-411-869A-36	Sequence 36, Appl1
76	29	25.2	15	4	US-10-283-940-59	Sequence 59, Appl1
77	29	25.2	15	6	US-11-022-454-59	Sequence 59, Appl1
78	29	25.2	16	4	US-10-219-834-123	Sequence 123, App
79	29	25.2	17	4	US-10-244-151-15	Sequence 15, Appl1
80	29	25.2	18	3	US-09-988-493-136	Sequence 136, App
81	29	25.2	19	4	US-10-681-180-280	Sequence 280, App
82	29	25.2	20	3	US-09-466-035-84	Sequence 84, Appl1
83	29	25.2	20	4	US-10-103-395-195	Sequence 195, App
84	29	25.2	20	4	US-10-225-567A-2221	Sequence 2221, App
85	29	25.2	20	4	US-10-029-386-33390	Sequence 33390, A
86	29	25.2	20	4	US-10-371-525-150	Sequence 150, App
87	29	25.2	20	4	US-10-371-645-150	Sequence 150, App
88	29	25.2	20	4	US-10-371-645-150	Sequence 150, App
89	29	25.2	20	4	US-10-371-645-150	Sequence 150, App
90	29	25.2	20	4	US-10-371-260-150	Sequence 150, App
91	29	25.2	20	4	US-10-666-480-5	Sequence 5, Appl1
92	29	25.2	20	4	US-10-732-862A-232	Sequence 232, App
93	29	25.2	20	4	US-10-481-180-283	Sequence 283, App
94	29	25.2	20	5	US-10-474-960A-403	Sequence 403, App
95	29	25.2	20	6	US-10-654-601-2566	Sequence 2566, App
96	28.5	24.8	13	4	US-11-127-702-5	Sequence 106, App
97	28.5	24.8	13	4	US-10-469-304-106	Sequence 107, App
98	28	24.3	9	4	US-10-469-304-107	Sequence 83, Appl1
99	28	24.3	9	4	US-10-133-210-83	Sequence 4, Appl1
100	28	24.3	9	4	US-10-442-909-4	Sequence 758, App

## ALIGNMENTS

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RESULT 1
US-10-218-743-3
; Sequence 3, Application US/10218743
; Publication No. US20030096779A1
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine A.
; APPLICANT: Hunter, Shirley Wu
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
; FILE REFERENCE: AL-2-C3
; CURRENT APPLICATION NUMBER: US/10/218,743
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: US/09/292,225
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: 60/098,909
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/085,295
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/098,565
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: 09/062,013
; PRIOR FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Dermatophagoides farinae
US-10-218-743-3

Query Match      100.0%; Score 115; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 1,6e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DIPHPTNHHKYLVCESVNG 20
DB      1 DIPHPTNHHKYLVCESVNG 20

RESULT 2
US-10-218-743-11
; Sequence 11, Application US/10218743
; Publication No. US20030096779A1
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine A.
; APPLICANT: Hunter, Shirley Wu
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
; FILE REFERENCE: AL-2-C3
; CURRENT APPLICATION NUMBER: US/10/218,743
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: US/09/292,225
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: 60/098,909
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/085,295
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/098,565
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: 09/062,013
; PRIOR FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 19
; TYPE: PRT
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; ORGANISM: Dermatophagoides farinae
US-10-218-743-11

Query Match      94.8%; Score 109; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 1,3e-09;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DIPHPTNHHKYLVCESVNG 19
DB      1 DIPHPTNHHKYLVCESVNG 19

RESULT 3
US-09-864-761-38552
; Sequence 38552, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wenheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aecmca-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
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; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 38552
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC005099.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.6
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.9
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.7
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/ OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.6
/ OTHER INFORMATION: EXPRESSED IN HEIA, SIGNAL = 1.8
/ OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.9
/ OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.9
/ OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.8
/ OTHER INFORMATION: SWISSPROT HIT: P53820, EVALU8.80e+00
US-09-864-761-38552
```

Query Match 32.6%; Score 37.5; DB 3; Length 20;

Best Local Similarity 42.9%; Pred. No. 1.4e+02; Matches 6; Conservative 5; Mismatches 2; Indels 1; Gaps 1;

Qy 2 IPHPTNIHKYLCV 15  
Db 8 LPHR-HSHHTLLCQ 20

## RESULT 4

```
US-09-954-385-54
/ Sequence 54, Application US/09954385
/ Publication No. US20030100467A1
/ GENERAL INFORMATION:
```

```
APPLICANT: Aehle, Wolfgang
APPLICANT: Baldwin, Toby L.
APPLICANT: Van Gastel, Franciscus J.C.
APPLICANT: Janssen, Giselle G.
APPLICANT: Murray, Christopher J.
APPLICANT: Wang, Huaming
APPLICANT: Winetzk, Deborah S.
TITLE OF INVENTION: Binding Phenol Oxidizing Enzyme-peptide
FILE REFERENCE: GC690
```

```
CURRENT APPLICATION NUMBER: US/09/954,385
CURRENT FILING DATE: 2001-09-12
NUMBER OF SEQ ID NOS: 433
```

```
SOFTWARE: FastSeq for Windows Version 4.0
```

```
SEQ ID NO 54
```

```
LENGTH: 7
```

```
TYPE: PRT
```

```
ORGANISM: Artificial Sequence
```

```
FEATURE:
```

```
OTHER INFORMATION: binding peptide
```

```
US-09-954-385-54
```

Query Match 30.4%; Score 35; DB 3; Length 7;

Best Local Similarity 83.3%; Pred. No. 1.7e+06; Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PHPTNI 8  
Db 1 PHPTNL 6

## RESULT 5

```
US-10-912-512-54
/ Sequence 54, Application US/10912512
/ Publication No. US20050042684A1
/ GENERAL INFORMATION:
```

```
APPLICANT: Aehle, Wolfgang
APPLICANT: Baldwin, Toby L.
APPLICANT: Van Gastel, Franciscus J.C.
APPLICANT: Janssen, Giselle G.
APPLICANT: Murray, Christopher J.
APPLICANT: Wang, Huaming
APPLICANT: Winetzk, Deborah S.
TITLE OF INVENTION: Binding Phenol Oxidizing Enzyme-peptide
FILE REFERENCE: GC690
```

```
CURRENT APPLICATION NUMBER: US/10/912,512
```

```
CURRENT FILING DATE: 2004-08-05
```

```
PRIOR APPLICATION NUMBER: US/09/954,385
```

```
PRIOR FILING DATE: 2001-09-12
```

```
NUMBER OF SEQ ID NOS: 433
```

```
/ SOFTWARE: FastSeq for Windows Version 4.0
```

```
SEQ ID NO 54
```

```
LENGTH: 7
```

```
TYPE: PRT
```

```
ORGANISM: Artificial Sequence
```

```
FEATURE:
```

```
OTHER INFORMATION: binding peptide
```

```
US-10-912-512-54
```

Query Match 30.4%; Score 35; DB 5; Length 7;

Best Local Similarity 83.3%; Pred. No. 1.7e+06; Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PHPTNI 8  
Db 1 PHPTNL 6

## RESULT 6

```
US-10-235-043-54
/ Sequence 54, Application US/10235043
/ Publication No. US20050058996A1
/ GENERAL INFORMATION:
```

```
APPLICANT: Aehle, Wolfgang
APPLICANT: Baldwin, Toby M.
APPLICANT: Van Gastel, Franciscus J.C.
APPLICANT: Janssen, Giselle G.
APPLICANT: Murray, Christopher J.
APPLICANT: Wang, Huaming
APPLICANT: Winetzk, Deborah S.
TITLE OF INVENTION: Binding Phenol Oxidizing Enzyme-Peptide
FILE REFERENCE: GC690-2
```

```
CURRENT APPLICATION NUMBER: US/10/235,043
```

```
CURRENT FILING DATE: 2002-09-03
```

```
NUMBER OF SEQ ID NOS: 446
```

```
SOFTWARE: FastSeq for Windows Version 4.0
```

```
SEQ ID NO 54
```

```
LENGTH: 7
```

```
TYPE: PRT
```

```
ORGANISM: Artificial Sequence
```

```
FEATURE:
```

```
OTHER INFORMATION: binding peptide
```

```
US-10-235-043-54
```

Query Match 30.4%; Score 35; DB 5; Length 7;

Best Local Similarity 83.3%; Pred. No. 1.7e+06; Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PHPTNI 8  
Db 1 PHPTNL 6

## RESULT 7

```
US-09-964-201A-20
/ Sequence 20, Application US/09964201A
/ Publication No. US20030091575A1
/ GENERAL INFORMATION:
```

```
APPLICANT: Tramontano, John H.
APPLICANT: Pilon, April L.
APPLICANT: Lohmas, Gerald L.
APPLICANT: Roberts, Steven F.
TITLE OF INVENTION: HEAT-SHOCK FUSION-BASED VACCINE SYSTEM
FILE REFERENCE: U.S. Patent Application No. US20030091575A1 09/026,276
```

```
CURRENT APPLICATION NUMBER: US/09/964,201A
```

```
CURRENT FILING DATE: 2002-05-21
```

```
NUMBER OF SEQ ID NOS: 35
```

```
SOFTWARE: Patentin Ver. 2.0
```

```
SEQ ID NO 20
```

```
LENGTH: 20
```

```
TYPE: PRT
```

ORGANISM: Homo sapiens  
US-09-964-201A-20

Query Match 30.4%; Score 35; DB 3; Length 20;  
Best Local Similarity 36.4%; Pred. No. 3.3e+02;  
Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 4 HPTNIHKYIVC 14  
||| : ||| :  
DB 7 HPQKTKFMLC 17

RESULT 8  
US-10-681-389-20  
Sequence 20, Application US/10681389  
Publication No. US20040115218A1

GENERAL INFORMATION:  
APPLICANT: Kenten, John H  
APPLICANT: Tramonano, Alfonso  
APPLICANT: Pilon, Aprille L  
APPLICANT: Lohmas, Gerald L  
APPLICANT: Roberts, Steven F  
TITLE OF INVENTION: HEAT-SHOCK FUSION-BASED VACCINE SYSTEM  
FILE REFERENCE: U.S. Patent Application No. 09/026,276  
CURRENT FILING DATE: 2003-10-07  
PRIOR APPLICATION NUMBER: US/10/681,389  
PRIOR FILING DATE: 2002-05-21  
NUMBER OF SEQ ID NOS: 35  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 20  
LENGTH: 20  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-681-389-20

Query Match 30.4%; Score 35; DB 4; Length 20;  
Best Local Similarity 36.4%; Pred. No. 3.3e+02;  
Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 4 HPTNIHKYIVC 14  
||| : ||| :  
DB 7 HPQKTKFMLC 17

RESULT 9  
US-10-681-388-20  
Sequence 20, Application US/10681388  
Publication No. US20040170643A1  
GENERAL INFORMATION:  
APPLICANT: Kenten, John H  
APPLICANT: Tramonano, Alfonso  
APPLICANT: Pilon, Aprille L  
APPLICANT: Lohmas, Gerald L  
APPLICANT: Roberts, Steven F  
TITLE OF INVENTION: HEAT-SHOCK FUSION-BASED VACCINE SYSTEM  
FILE REFERENCE: U.S. Patent Application No. 09/026,276  
CURRENT APPLICATION NUMBER: US/10/681,388  
CURRENT FILING DATE: 2003-10-07  
PRIOR APPLICATION NUMBER: US/09/964,201  
PRIOR FILING DATE: 2002-05-21  
NUMBER OF SEQ ID NOS: 35  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 20  
LENGTH: 20  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-681-388-20

Query Match 30.4%; Score 35; DB 4; Length 20;  
Best Local Similarity 36.4%; Pred. No. 3.3e+02;  
Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 4 HPTNIHKYIVC 14  
||| : ||| :  
DB 7 HPQKTKFMLC 17

RESULT 10  
US-10-200-708-47  
Sequence 47, Application US/10200708  
Publication No. US20030180314A1  
GENERAL INFORMATION:  
APPLICANT: Degroot, Anne S.  
TITLE OF INVENTION: HIV VACCINE CANDIDATE PEPTIDES  
FILE REFERENCE: 17999-001  
CURRENT APPLICATION NUMBER: US/10/200,708  
CURRENT FILING DATE: 2002-07-22  
PRIOR APPLICATION NUMBER: US/09/351,036  
PRIOR FILING DATE: 1999-07-09  
PRIOR APPLICATION NUMBER: 60/092,346  
PRIOR FILING DATE: 1998-07-10  
PRIOR APPLICATION NUMBER: 60/115,145  
PRIOR FILING DATE: 1999-01-08  
PRIOR APPLICATION NUMBER: 60/130,677  
PRIOR FILING DATE: 1999-04-23  
NUMBER OF SEQ ID NOS: 672  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 47  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Human immunodeficiency virus  
US-10-200-708-47

Query Match 27.8%; Score 32; DB 4; Length 10;  
Best Local Similarity 55.6%; Pred. No. 4.6e+02;  
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 IPHPTNIHK 10  
||| : ||| :  
DB 1 IPHPAGLKK 9

RESULT 11  
US-10-200-708-95  
Sequence 95, Application US/10200708  
Publication No. US20030180314A1  
GENERAL INFORMATION:  
APPLICANT: Degroot, Anne S.  
TITLE OF INVENTION: HIV VACCINE CANDIDATE PEPTIDES  
FILE REFERENCE: 17999-001  
CURRENT APPLICATION NUMBER: US/10/200,708  
CURRENT FILING DATE: 2002-07-22  
PRIOR APPLICATION NUMBER: US/09/351,036  
PRIOR FILING DATE: 1999-07-09  
PRIOR APPLICATION NUMBER: 60/092,346  
PRIOR FILING DATE: 1998-07-10  
PRIOR APPLICATION NUMBER: 60/115,145  
PRIOR FILING DATE: 1999-01-08  
PRIOR APPLICATION NUMBER: 60/130,677  
PRIOR FILING DATE: 1999-04-23  
NUMBER OF SEQ ID NOS: 672  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 95  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Human immunodeficiency virus  
US-10-200-708-95

Query Match 27.8%; Score 32; DB 4; Length 10;  
Best Local Similarity 55.6%; Pred. No. 4.6e+02;  
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 IPHPTNIHK 10  
||| : ||| :  
DB 2 IPHPAGLKK 10



## RESULT 12

US-10-200-708-117  
 ; Sequence 117, Application US/10200708  
 ; Publication No. US20030180314A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Degroot, Anne S.  
 ; TITLE OF INVENTION: HIV VACCINE CANDIDATE PEPTIDES  
 ; FILE REFERENCE: 17999-001  
 ; CURRENT APPLICATION NUMBER: US/10/200,708  
 ; CURRENT FILING DATE: 2002-07-22  
 ; PRIOR APPLICATION NUMBER: US/09/351,036  
 ; PRIOR FILING DATE: 1999-07-09  
 ; PRIOR APPLICATION NUMBER: 60/092,346  
 ; PRIOR FILING DATE: 1998-07-10  
 ; PRIOR APPLICATION NUMBER: 60/115,145  
 ; PRIOR FILING DATE: 1999-01-08  
 ; PRIOR APPLICATION NUMBER: 60/130,677  
 ; PRIOR FILING DATE: 1999-04-23  
 ; NUMBER OF SEQ ID NOS: 672  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 117  
 ; LENGTH: 10  
 ; TYPE: PRT  
 ; ORGANISM: Human immunodeficiency virus  
 US-10-200-708-117

Query Match 27.8%; Score 32; DB 4; Length 10;  
 Best Local Similarity 55.6%; Pred. No. 4.6e+02;  
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 IHPPTNHHK 10  
 |||||  
 DB 2 IHPAGLKK 10

## RESULT 13

US-10-200-708-119  
 ; Sequence 119, Application US/10200708  
 ; Publication No. US20030180314A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Degroot, Anne S.  
 ; TITLE OF INVENTION: HIV VACCINE CANDIDATE PEPTIDES  
 ; FILE REFERENCE: 17999-001  
 ; CURRENT APPLICATION NUMBER: US/10/200,708  
 ; CURRENT FILING DATE: 2002-07-22  
 ; PRIOR APPLICATION NUMBER: US/09/351,036  
 ; PRIOR FILING DATE: 1999-07-09  
 ; PRIOR APPLICATION NUMBER: 60/092,346  
 ; PRIOR FILING DATE: 1998-07-10  
 ; PRIOR APPLICATION NUMBER: 60/115,145  
 ; PRIOR FILING DATE: 1999-01-08  
 ; PRIOR APPLICATION NUMBER: 60/130,677  
 ; PRIOR FILING DATE: 1999-04-23  
 ; NUMBER OF SEQ ID NOS: 672  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 119  
 ; LENGTH: 10  
 ; TYPE: PRT  
 ; ORGANISM: Human immunodeficiency virus  
 US-10-200-708-119

Query Match 27.8%; Score 32; DB 4; Length 10;  
 Best Local Similarity 55.6%; Pred. No. 4.6e+02;  
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 IHPPTNHHK 10  
 |||||  
 DB 1 IHPAGLKK 9

## RESULT 14

## US-10-200-708-671

; Sequence 671, Application US/10200708  
 ; Publication No. US20030180314A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Degroot, Anne S.  
 ; TITLE OF INVENTION: HIV VACCINE CANDIDATE PEPTIDES  
 ; FILE REFERENCE: 17999-001  
 ; CURRENT APPLICATION NUMBER: US/10/200,708  
 ; CURRENT FILING DATE: 2002-07-22  
 ; PRIOR APPLICATION NUMBER: US/09/351,036  
 ; PRIOR FILING DATE: 1999-07-09  
 ; PRIOR APPLICATION NUMBER: 60/092,346  
 ; PRIOR FILING DATE: 1998-07-10  
 ; PRIOR APPLICATION NUMBER: 60/115,145  
 ; PRIOR FILING DATE: 1999-01-08  
 ; PRIOR APPLICATION NUMBER: 60/130,677  
 ; PRIOR FILING DATE: 1999-04-23  
 ; NUMBER OF SEQ ID NOS: 672  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 671  
 ; LENGTH: 10  
 ; TYPE: PRT  
 ; ORGANISM: Human immunodeficiency virus  
 US-10-200-708-671

Query Match 27.8%; Score 32; DB 4; Length 10;  
 Best Local Similarity 55.6%; Pred. No. 4.6e+02;  
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 IHPPTNHHK 10  
 |||||  
 DB 2 IHPAGLKK 10

## RESULT 15

US-10-417-895A-36  
 ; Sequence 36, Application US/10417895A  
 ; Publication No. US20040033569A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Crea, Roberto  
 ; TITLE OF INVENTION: "DOPING" IN WALK-THROUGH MUTAGENESIS  
 ; FILE REFERENCE: 1551.2002-001  
 ; CURRENT APPLICATION NUMBER: US/10/417,895A  
 ; CURRENT FILING DATE: 2003-04-16  
 ; PRIOR APPLICATION NUMBER: 60/373,686  
 ; PRIOR FILING DATE: 2002-04-17  
 ; NUMBER OF SEQ ID NOS: 86  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 36  
 ; LENGTH: 14  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURES:  
 ; OTHER INFORMATION: variant peptide for second complementarity  
 ; OTHER INFORMATION: determining region of Fv region of an  
 ; OTHER INFORMATION: immunoglobulin  
 US-10-417-895A-36

Query Match 27.8%; Score 32; DB 4; Length 14;  
 Best Local Similarity 55.6%; Pred. No. 6.6e+02;  
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 HPTNHHKL 12  
 |||||  
 DB 4 HPTQHHDIV 12

## RESULT 16

US-10-808-187-2265  
 ; Sequence 2265, Application US/10808187  
 ; Publication No. US20050009009A1  
 ; GENERAL INFORMATION:

```

; APPLICANT: PEIRIS, JOSEPH S. M.
; APPLICANT: YUEN, KWOK YUNG
; APPLICANT: POON, LIT MAN
; APPLICANT: GUAN, YI
; APPLICANT: CHAN, KWOK HUNG
; APPLICANT: NICHOLLS, JOHN
; TITLE OF INVENTION: A DIAGNOSTIC ASSAY FOR THE HUMAN VIRUS CAUSING SEVERE ACUTE
; FILE REFERENCE: V9661.0078
; CURRENT APPLICATION NUMBER: US/10/807,187
; CURRENT FILING DATE: 2004-03-24
; PRIOR APPLICATION NUMBER: 60/457,031
; PRIOR FILING DATE: 2003-03-24
; PRIOR APPLICATION NUMBER: 60/457,730
; PRIOR FILING DATE: 2003-03-26
; PRIOR APPLICATION NUMBER: 60/459,931
; PRIOR FILING DATE: 2003-04-02
; PRIOR APPLICATION NUMBER: 60/460,357
; PRIOR FILING DATE: 2003-04-03
; PRIOR APPLICATION NUMBER: 60/461,265
; PRIOR FILING DATE: 2003-04-08
; PRIOR APPLICATION NUMBER: 60/462,805
; PRIOR FILING DATE: 2003-04-14
; PRIOR APPLICATION NUMBER: 60/468,139
; PRIOR FILING DATE: 2003-05-05
; PRIOR APPLICATION NUMBER: 60/464,886
; PRIOR FILING DATE: 2003-04-23
; PRIOR APPLICATION NUMBER: 60/471,200
; PRIOR FILING DATE: 2003-05-16
; NUMBER OF SEQ ID NOS: 2476
; SOFTWARE: Patentin ver. 3.2
; SEQ ID NO 2265
; LENGTH: 14
; TYPE: prt
; ORGANISM: Human severe acute respiratory system virus
US-10-808-187-2265

Query Match      27.8%; Score 32; DB 5; Length 14;
Best Local Similarity 83.3%; Pred. No. 6.6e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      4 HPTNTH 9
      |||||
      9 HPTTTH 14

Db

RESULT 17
US-10-807-807-2265
; Sequence 2265, Application US/10807807
; Publication No. US20050181357A1
; GENERAL INFORMATION:
; APPLICANT: LEUNG, FREDERICK C.
; APPLICANT: PEIRIS, JOSEPH S. M.
; APPLICANT: YUEN, KWOK YUNG
; APPLICANT: POON, LIT MAN
; APPLICANT: GUAN, YI
; APPLICANT: CHAN, KWOK HUNG
; APPLICANT: NICHOLLS, JOHN M.
; TITLE OF INVENTION: A HIGH-THROUGHPUT DIAGNOSTIC ASSAY FOR THE HUMAN VIRUS
; FILE REFERENCE: V9661.0077
; CURRENT APPLICATION NUMBER: US/10/807,807
; CURRENT FILING DATE: 2004-03-24
; PRIOR APPLICATION NUMBER: 60/457,031
; PRIOR FILING DATE: 2003-03-24
; PRIOR APPLICATION NUMBER: 60/457,730
; PRIOR FILING DATE: 2003-03-26
; PRIOR APPLICATION NUMBER: 60/459,931
; PRIOR FILING DATE: 2003-04-02
; PRIOR APPLICATION NUMBER: 60/460,357
; PRIOR FILING DATE: 2003-04-03
; PRIOR APPLICATION NUMBER: 60/461,265
; PRIOR FILING DATE: 2003-04-08

```

```

; PRIOR APPLICATION NUMBER: 60/462,805
; PRIOR FILING DATE: 2003-04-14
; PRIOR APPLICATION NUMBER: 60/464,886
; PRIOR FILING DATE: 2003-04-23
; PRIOR APPLICATION NUMBER: 60/465,738
; PRIOR FILING DATE: 2003-04-25
; PRIOR APPLICATION NUMBER: 60/470,935
; PRIOR FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 2487
; SOFTWARE: Patentin ver. 3.2
; SEQ ID NO 2265
; LENGTH: 14
; TYPE: prt
; ORGANISM: Human severe acute respiratory system virus
US-10-807-807-2265

Query Match      27.8%; Score 32; DB 5; Length 14;
Best Local Similarity 83.3%; Pred. No. 6.6e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      4 HPTNTH 9
      |||||
      9 HPTTTH 14

Db

RESULT 18
US-10-103-395-109
; Sequence 109, Application US/10103395
; Publication No. US20020160019A1
; GENERAL INFORMATION:
; APPLICANT: BEIMMUNE, Inc.
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; TITLE OF INVENTION: IDENTIFICATION OF BROADLY REACTIVE DR
; FILE REFERENCE: 39963-20016.01
; CURRENT APPLICATION NUMBER: US/10/103,395
; CURRENT FILING DATE: 2003-01-03
; PRIOR APPLICATION NUMBER: US 09/009,953
; PRIOR FILING DATE: 1998-01-21
; PRIOR APPLICATION NUMBER: PCT/US98/01373
; PRIOR FILING DATE: 1998-01-23
; PRIOR APPLICATION NUMBER: US 60/036,713
; PRIOR FILING DATE: 1997-01-23
; PRIOR APPLICATION NUMBER: US 60/037,432
; PRIOR FILING DATE: 1997-02-07
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 109
; LENGTH: 15
; TYPE: prt
; ORGANISM: Homo sapiens
US-10-103-395-109

Query Match      27.8%; Score 32; DB 4; Length 15;
Best Local Similarity 55.6%; Pred. No. 7.1e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      2 IPHPTNTHK 10
      |||||
      6 IPHPAGLKK 14

Db

RESULT 19
US-10-062-710-19
; Sequence 19, Application US/10062710
; Publication No. US20030049253A1
; GENERAL INFORMATION:
; APPLICANT: Li, Frank Q.
; APPLICANT: Chu, Yong-Diang
; APPLICANT: Qiu, Jian-Tai
; TITLE OF INVENTION: Polymeric Conjugates for Delivery of

```

```

/ TITLE OF INVENTION: MHC-Recognized Epitopes
/ FILE REFERENCE: 3781-001-27
/ CURRENT APPLICATION NUMBER: US/10/062,710
/ PRIOR FILING DATE: 2002-02-05
/ PRIOR APPLICATION NUMBER: US 60/310,498
/ NUMBER OF SEQ ID NOS: 232
/ SOFTWARE: FASTSEQ for Windows Version 4.0
/ SEQ ID NO 19
/ LENGTH: 16
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: HIV Helper-T Cell Epitopes
US-10-062-710-19

```

```

Query Match      27.8%; Score 32; DB 4; Length 16;
Best Local Similarity 55.6%; Pred. No. 7.6e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

```

```

QY      2 IHPPTNIHK 10
      ||||| : |
      8 IHPHAGLKK 16

```

```

RESULT 20
US-10-442-909-32
/ Sequence 32, Application US/10442909
/ Publication No. US20040001845A1
/ GENERAL INFORMATION:
/ APPLICANT: Alfeld, Marcus
/ APPLICANT: Yu, Xu
/ APPLICANT: Walker, Bruce
/ APPLICANT: Addo, Marylyn
/ TITLE OF INVENTION: Cytotoxic T-Cell Epitopes of HIV-1 Virus
/ FILE REFERENCE: 24028-010
/ CURRENT APPLICATION NUMBER: US/10/442,909
/ PRIOR FILING DATE: 2003-05-20
/ PRIOR APPLICATION NUMBER: 60/382,120
/ PRIOR FILING DATE: 2002-05-20
/ NUMBER OF SEQ ID NOS: 77
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 32
/ LENGTH: 17
/ TYPE: PRT
/ ORGANISM: Human Immunodeficiency virus type 1
US-10-442-909-32

```

```

Query Match      27.8%; Score 32; DB 4; Length 17;
Best Local Similarity 55.6%; Pred. No. 8.1e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

```

```

QY      2 IHPPTNIHK 10
      ||||| : |
      8 IHPHAGLKK 16

```

```

RESULT 21
US-10-285-649A-9
/ Sequence 9, Application US/10285649A
/ Publication No. US20030106089A1
/ GENERAL INFORMATION:
/ APPLICANT: McBride, Kevin
/ APPLICANT: Stealder, David M.
/ APPLICANT: Bear, Julie
/ APPLICANT: Perez-Grau, Luis
/ TITLE OF INVENTION: COTTON FIBER TRANSCRIPTIONAL FACTORS
/ FILE REFERENCE: 15615/03/US
/ CURRENT APPLICATION NUMBER: US/10/285,649A
/ PRIOR FILING DATE: 2003-02-07
/ PRIOR APPLICATION NUMBER: US 08/984,099
/ PRIOR FILING DATE: 1997-12-03

```

```

/ PRIOR APPLICATION NUMBER: PCT/US96/09897
/ PRIOR FILING DATE: 1996-06-07
/ PRIOR APPLICATION NUMBER: US 08/480,178
/ PRIOR FILING DATE: 1995-06-07
/ NUMBER OF SEQ ID NOS: 18
/ SOFTWARE: IBM PC; Windows 2000; Microsoft Word 2000
/ SEQ ID NO 9
/ LENGTH: 20
/ TYPE: PRT
/ ORGANISM: Gossypium Hirsutum
US-10-285-649A-9

```

```

Query Match      27.8%; Score 32; DB 4; Length 20;
Best Local Similarity 42.9%; Pred. No. 9.6e+02;
Matches 6; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

```

```

QY      2 IHPPTNIHKYLCE 15
      : ||||| : |
      6 LPPTPTHKCLTSD 19

```

```

RESULT 22
US-11-008-653-128
/ Sequence 128, Application US/11008653
/ Publication No. US20050175627A1
/ GENERAL INFORMATION:
/ APPLICANT: Schneider, Joerg
/ TITLE OF INVENTION: HIV Pharmacies
/ FILE REFERENCE: 3742.1001-000
/ CURRENT APPLICATION NUMBER: US/11/008,653
/ PRIOR FILING DATE: 2004-12-09
/ PRIOR APPLICATION NUMBER: PCT/GB2004/004038
/ PRIOR FILING DATE: 2004-09-23
/ PRIOR APPLICATION NUMBER: GB 0325011.5
/ PRIOR FILING DATE: 2003-10-27
/ PRIOR APPLICATION NUMBER: GB 0322637.0
/ PRIOR FILING DATE: 2003-09-26
/ PRIOR APPLICATION NUMBER: GB 0322402.9
/ PRIOR FILING DATE: 2003-09-24
/ NUMBER OF SEQ ID NOS: 174
/ SOFTWARE: FASTSEQ for Windows Version 4.0
/ SEQ ID NO 128
/ LENGTH: 20
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: peptide from pol pool 2
US-11-008-653-128

```

```

Query Match      27.8%; Score 32; DB 6; Length 20;
Best Local Similarity 55.6%; Pred. No. 9.6e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

```

```

QY      2 IHPPTNIHK 10
      ||||| : |
      5 IHPHAGLKK 13

```

```

RESULT 23
US-10-430-685-95
/ Sequence 95, Application US/10430685
/ Publication No. US20040039543A1
/ GENERAL INFORMATION:
/ APPLICANT: KECK, Peter
/ TITLE OF INVENTION: COMPUTER METHOD AND APPARATUS FOR CLASSIFYING OBJECTS
/ FILE REFERENCE: 63040-010210
/ CURRENT APPLICATION NUMBER: US/10/430,685
/ PRIOR FILING DATE: 2003-05-06
/ PRIOR APPLICATION NUMBER: PCT/US01/44000
/ PRIOR FILING DATE: 2001-11-06
/ PRIOR APPLICATION NUMBER: 60/246,196
/ PRIOR FILING DATE: 2000-11-06
/ NUMBER OF SEQ ID NOS: 240

```

```
/ SOFTWARE: Patentin version 3.2
/ SEQ ID NO 95
/ LENGTH: 17
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-430-685-95

Query Match
Best Local Similarity 66.7%; Score 31.5; DB 4; Length 17;
Matches 6; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

Qy 4 HPTNHHKL 12
   |||||
Db 1 HPTN-HAYI 8

RESULT 24
US-10-706-391-29
/ Sequence 29, Application US/10706391
/ Publication No. US20040137482A1
/ GENERAL INFORMATION:
/ APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
/ APPLICANT: WASHINGTON DENTAL SERVICE
/ APPLICANT: Eckert, Randall
/ APPLICANT: Qi, Fengxia
/ APPLICANT: Shi, Wenxuan
/ APPLICANT: Anderson, Maxwell H.
/ TITLE OF INVENTION: ANTI-MICROBIAL TARGETING CHIMERIC PHARMACEUTICAL
/ FILE REFERENCE: 2101363-991600
/ CURRENT APPLICATION NUMBER: US/10/706,391
/ CURRENT FILING DATE: 2003-06-16
/ PRIOR APPLICATION NUMBER: US 10/077,624
/ PRIOR FILING DATE: 2002-02-14
/ PRIOR FILING DATE: 2002-02-14
/ PRIOR APPLICATION NUMBER: US 09/910,358
/ PRIOR FILING DATE: 2001-07-19
/ PRIOR APPLICATION NUMBER: US 09/378,577
/ PRIOR FILING DATE: 1999-08-20
/ NUMBER OF SEQ ID NOS: 71
/ SOFTWARE: Patentin version 3.1
/ SEQ ID NO 29
/ LENGTH: 12
/ TYPE: PRT
/ ORGANISM: Artificial sequence
/ FEATURE:
/ OTHER INFORMATION: Peptide library
US-10-706-391-29

Query Match
Best Local Similarity 57.1%; Score 31; DB 4; Length 12;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 PPHPTNH 9
   |||||
Db 2 PPHKXH 8

RESULT 25
US-09-966-782A-58
/ Sequence 58, Application US/09966782A
/ Publication No. US2003002183A1
/ GENERAL INFORMATION:
/ APPLICANT: Battaglin, P.
/ APPLICANT: Feder, J.N.
/ APPLICANT: Mintier, G.
/ APPLICANT: Ramanathan, C. S.
/ APPLICANT: Westphal, R.
/ APPLICANT: Hawken, D. R.
/ APPLICANT: Cacace, A.
/ APPLICANT: Barber, L.
/ APPLICANT: Kornacker, M. G.
/ TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPBMY7,
/ EXPRESSED HIGHLY IN SPINAL CORD
/ FILE REFERENCE: D0044NP
```

```
/ CURRENT APPLICATION NUMBER: US/09/966,782A
/ CURRENT FILING DATE: 2001-09-26
/ PRIOR APPLICATION NUMBER: 60/235,731
/ PRIOR FILING DATE: 2000-09-27
/ PRIOR APPLICATION NUMBER: 60/268,580
/ PRIOR FILING DATE: 2001-02-14
/ PRIOR APPLICATION NUMBER: 60/315,423
/ PRIOR FILING DATE: 2001-08-28
/ NUMBER OF SEQ ID NOS: 64
/ SOFTWARE: Patentin Ver. 2.1
/ SEQ ID NO 58
/ LENGTH: 15
/ TYPE: PRT
/ ORGANISM: Artificial sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: : Synthetic
US-09-966-782A-58

Query Match
Best Local Similarity 40.0%; Score 31; DB 3; Length 15;
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 11 YLVCSVNGG 20
   |::||
Db 3 YVCSNDIHGG 12

RESULT 26
US-10-254-905-58
/ Sequence 58, Application US/10254905
/ Publication No. US20030186265A1
/ GENERAL INFORMATION:
/ APPLICANT: Bristol-Myers Squibb Company
/ TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPBMY7, EXPRESSED HI
/ FILE REFERENCE: D0044 CIP
/ CURRENT APPLICATION NUMBER: US/10/254,905
/ CURRENT FILING DATE: 2002-09-25
/ NUMBER OF SEQ ID NOS: 75
/ SOFTWARE: Patentin version 3.1
/ SEQ ID NO 58
/ LENGTH: 15
/ TYPE: PRT
/ ORGANISM: Artificial sequence
/ FEATURE:
/ OTHER INFORMATION: Synthetic polypeptide
US-10-254-905-58

Query Match
Best Local Similarity 40.0%; Score 31; DB 4; Length 15;
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 11 YLVCSVNGG 20
   |::||
Db 3 YVCSNDIHGG 12

RESULT 27
US-09-791-524-3
/ Sequence 3, Application US/09791524
/ Publication No. US20030143309A1
/ GENERAL INFORMATION:
/ APPLICANT: Aventis Pharmaceuticals Products Inc.
/ TITLE OF INVENTION: Targeted Adenovirus Vectors For Delivery Of Heterologous Genes
/ FILE REFERENCE: A3319A
/ CURRENT APPLICATION NUMBER: US/09/791,524
/ CURRENT FILING DATE: 2001-02-22
/ PRIOR APPLICATION NUMBER: 60/09828
/ PRIOR FILING DATE: 1998-08-27
/ NUMBER OF SEQ ID NOS: 150
/ SOFTWARE: Patentin version 3.0
/ SEQ ID NO 3
```

LENGTH: 16  
TYPE: PRT  
ORGANISM: Adenovirus  
US-09-791-524-3

Query Match 27.0%; Score 31; DB 3; Length 16;  
Best Local Similarity 45.5%; Pred. No. 1.1e+03;  
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 IPHPTNHKYL 12  
DB 4 MPHSLNFSQYL 14

RESULT 28  
US-09-791-524-4  
Sequence 4, Application US/09791524  
Publication No. US20030143209A1  
GENERAL INFORMATION:  
APPLICANT: Aventis Pharmaceuticals Products Inc.  
TITLE OF INVENTION: Targeted Adenovirus Vectors For Delivery Of Heterologous Genes  
FILE REFERENCE: A3319A  
CURRENT APPLICATION NUMBER: US/09/791,524  
PRIOR FILING DATE: 2001-02-22  
PRIOR APPLICATION NUMBER: 60/09828  
PRIOR FILING DATE: 1998-08-27  
NUMBER OF SEQ ID NOS: 150  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 4  
LENGTH: 17  
TYPE: PRT  
ORGANISM: Adenovirus  
US-09-791-524-4

Query Match 27.0%; Score 31; DB 3; Length 17;  
Best Local Similarity 45.5%; Pred. No. 1.2e+03;  
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 IPHPTNHKYL 12  
DB 4 MPHSLNFSQYL 14

RESULT 29  
US-10-609-217-196  
Sequence 196, Application US/10609217  
Publication No. US2004004188A1  
GENERAL INFORMATION:  
APPLICANT: FEIG, ULRICH  
APPLICANT: LIU, CHUAN-PA  
APPLICANT: CHEETHAM, JANET C.  
APPLICANT: BOONE, THOMAS CHARLES  
TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS  
FILE REFERENCE: A-527  
CURRENT APPLICATION NUMBER: US/10/609,217  
CURRENT FILING DATE: 2003-06-27  
PRIOR APPLICATION NUMBER: US/09/428,082B  
PRIOR FILING DATE: 1999-10-22  
PRIOR APPLICATION NUMBER: 60/105,371  
PRIOR FILING DATE: 1998-10-23  
NUMBER OF SEQ ID NOS: 1133  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 196  
LENGTH: 17  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: UKR ANTAGONIST PEPTIDE  
US-10-609-217-196

Query Match 27.0%; Score 31; DB 4; Length 17;  
Best Local Similarity 45.5%; Pred. No. 1.2e+03;  
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 IPHPTNHKYL 12  
DB 4 MPHSLNFSQYL 14

RESULT 30  
US-10-632-388-196  
Sequence 196, Application US/10632388  
Publication No. US20040053845A1  
GENERAL INFORMATION:  
APPLICANT: FEIG, ULRICH  
APPLICANT: LIU, CHUAN-PA  
APPLICANT: CHEETHAM, JANET C.  
APPLICANT: BOONE, THOMAS CHARLES  
TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS  
FILE REFERENCE: A-527  
CURRENT APPLICATION NUMBER: US/10/632,388  
CURRENT FILING DATE: 2003-07-31  
PRIOR APPLICATION NUMBER: US/09/428,082B  
PRIOR FILING DATE: 1999-10-22  
PRIOR APPLICATION NUMBER: 60/105,371  
PRIOR FILING DATE: 1998-10-23  
NUMBER OF SEQ ID NOS: 1133  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 196  
LENGTH: 17  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: UKR ANTAGONIST PEPTIDE  
US-10-632-388-196

Query Match 27.0%; Score 31; DB 4; Length 17;  
Best Local Similarity 45.5%; Pred. No. 1.2e+03;  
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 IPHPTNHKYL 12  
DB 4 MPHSLNFSQYL 14

RESULT 31  
US-10-651-723-196  
Sequence 196, Application US/10651723  
Publication No. US20040057953A1  
GENERAL INFORMATION:  
APPLICANT: FEIG, ULRICH  
APPLICANT: LIU, CHUAN-PA  
APPLICANT: CHEETHAM, JANET C.  
APPLICANT: BOONE, THOMAS CHARLES  
TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS  
FILE REFERENCE: A-527  
CURRENT APPLICATION NUMBER: US/10/651,723  
CURRENT FILING DATE: 2003-08-29  
PRIOR APPLICATION NUMBER: US/09/428,082B  
PRIOR FILING DATE: 1999-10-22  
PRIOR APPLICATION NUMBER: 60/105,371  
PRIOR FILING DATE: 1998-10-23  
NUMBER OF SEQ ID NOS: 1133  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 196  
LENGTH: 17  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: UKR ANTAGONIST PEPTIDE  
US-10-651-723-196

Query Match 27.0%; Score 31; DB 4; Length 17;  
Best Local Similarity 45.5%; Pred. No. 1.2e+03;  
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 2 IHPPTNIHKYL 12  
: || | : ||  
Db 4 MPHSLNFSQYL 14

RESULT 32  
US-10-645-761-196  
; Sequence 196, Application US/10645761  
; Publication No. US20040071712A1  
; GENERAL INFORMATION:  
; APPLICANT: FEIGE, ULRICH  
; APPLICANT: LIU, CHUAN-FA  
; APPLICANT: CHEETHAM, JANET C.  
; APPLICANT: BOONE, THOMAS CHARLES  
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS  
; FILE REFERENCE: A-527  
; CURRENT APPLICATION NUMBER: US/10/645,761  
; CURRENT FILING DATE: 2003-08-18  
; PRIOR APPLICATION NUMBER: US/09/428,082B  
; PRIOR FILING DATE: 1999-10-22  
; PRIOR APPLICATION NUMBER: 60/105,371  
; PRIOR FILING DATE: 1998-10-23  
; NUMBER OF SEQ ID NOS: 1133  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO 196  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: UKR ANTAGONIST PEPTIDE  
US-10-645-761-196

Query Match 27.0%; Score 31; DB 4; Length 17;  
Best Local Similarity 45.5%; Pred. No. 1.2e+03;  
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 2 IHPPTNIHKYL 12  
: || | : ||  
Db 4 MPHSLNFSQYL 14

RESULT 33  
US-10-666-696-196  
; Sequence 196, Application US/10666696  
; Publication No. US20040077022A1  
; GENERAL INFORMATION:  
; APPLICANT: FEIGE, ULRICH  
; APPLICANT: LIU, CHUAN-FA  
; APPLICANT: CHEETHAM, JANET C.  
; APPLICANT: BOONE, THOMAS CHARLES  
; APPLICANT: GUDAS, JEAN MARIE  
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS  
; FILE REFERENCE: A-527A  
; CURRENT APPLICATION NUMBER: US/10/666,696  
; CURRENT FILING DATE: 2003-09-19  
; PRIOR APPLICATION NUMBER: US/09/563,286C  
; PRIOR FILING DATE: 2000-05-03  
; PRIOR APPLICATION NUMBER: 09/428,082  
; PRIOR FILING DATE: 1999-10-22  
; PRIOR APPLICATION NUMBER: 60/105,371  
; PRIOR FILING DATE: 1998-10-23  
; NUMBER OF SEQ ID NOS: 1157  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO 196  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: UKR ANTAGONIST PEPTIDE  
US-10-666-696-196

Query Match 27.0%; Score 31; DB 4; Length 17;  
Best Local Similarity 45.5%; Pred. No. 1.2e+03;

Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 2 IHPPTNIHKYL 12  
: || | : ||  
Db 4 MPHSLNFSQYL 14

RESULT 34  
US-10-653-048-196  
; Sequence 196, Application US/10653048  
; Publication No. US2004008778A1  
; GENERAL INFORMATION:  
; APPLICANT: FEIGE, ULRICH  
; APPLICANT: LIU, CHUAN-FA  
; APPLICANT: CHEETHAM, JANET C.  
; APPLICANT: BOONE, THOMAS CHARLES  
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS  
; FILE REFERENCE: A-527  
; CURRENT APPLICATION NUMBER: US/10/653,048  
; CURRENT FILING DATE: 2003-08-29  
; PRIOR APPLICATION NUMBER: US/09/428,082B  
; PRIOR FILING DATE: 1999-10-22  
; PRIOR APPLICATION NUMBER: 60/105,371  
; PRIOR FILING DATE: 1998-10-23  
; NUMBER OF SEQ ID NOS: 1133  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO 196  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: UKR ANTAGONIST PEPTIDE  
US-10-653-048-196

Query Match 27.0%; Score 31; DB 4; Length 17;  
Best Local Similarity 45.5%; Pred. No. 1.2e+03;  
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 2 IHPPTNIHKYL 12  
: || | : ||  
Db 4 MPHSLNFSQYL 14

RESULT 35  
US-10-756-289-1  
; Sequence 1, Application US/10756289  
; Publication No. US20040138110A1  
; GENERAL INFORMATION:  
; APPLICANT: Kessler, Horst  
; APPLICANT: Graeff, Heinrich  
; APPLICANT: Schmitt, Manfred  
; APPLICANT: Magdolen, Viktor  
; APPLICANT: Wilhelm, Olaf G.  
; APPLICANT: Riemer, Christoph  
; APPLICANT: Burgle, Markus  
; TITLE OF INVENTION: Inhibitors for Urokinase Receptor  
; FILE REFERENCE: 100564-09040  
; CURRENT APPLICATION NUMBER: US/10/756,289  
; CURRENT FILING DATE: 2004-01-14  
; PRIOR APPLICATION NUMBER: US/09/402,464  
; PRIOR FILING DATE: 2000-01-07  
; PRIOR APPLICATION NUMBER: EP 97 106 024.9  
; PRIOR FILING DATE: 1997-04-11  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-756-289-1

Query Match 27.0%; Score 31; DB 4; Length 17;  
Best Local Similarity 45.5%; Pred. No. 1.2e+03;

Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 IPHPTNHYKL 12  
Db 4 MPHSLNFSQYL 14

## RESULT 36

US-10-821-544-16  
Sequence 16, Application US/10821544  
Publication No. US20040265797A1  
GENERAL INFORMATION:  
APPLICANT: ROSENBERG, STEVE  
APPLICANT: DOYLE, MICHAEL  
APPLICANT: CHAPMAN, HAROLD  
TITLE OF INVENTION: PEPTIDE LIGANDS OF THE UROKINASE RECEPTOR  
FILE REFERENCE: 014024-0284102  
CURRENT APPLICATION NUMBER: US/10/821,544  
PRIOR FILING DATE: 2004-04-09  
PRIOR APPLICATION NUMBER: US/09/155,260C  
PRIOR FILING DATE: 1998-09-23  
PRIOR FILING DATE: 1997-03-28  
PRIOR APPLICATION NUMBER: PCT/US97/05199  
PRIOR FILING DATE: 1997-03-28  
PRIOR APPLICATION NUMBER: 08/623,361  
PRIOR FILING DATE: 1996-03-28  
NUMBER OF SEQ ID NOS: 76  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 16  
LENGTH: 17  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-10-821-544-16

Query Match 27.0%; Score 31; DB 5; Length 17;  
Best Local Similarity 45.5%; Pred. No. 1.2e+03;  
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 IPHPTNHYKL 12  
Db 4 MPHSLNFSQYL 14

## RESULT 37

US-10-645-784-196  
Sequence 196, Application US/10645784  
Publication No. US20050123548A1  
GENERAL INFORMATION:  
APPLICANT: PEIGE, ULRICH  
APPLICANT: LIU, CHUAN-FA  
APPLICANT: CHESTNUT, JANET C.  
APPLICANT: BOONE, THOMAS CHARLES  
APPLICANT: GUIDAS, JEAN MARIE  
TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS  
FILE REFERENCE: A-527A  
CURRENT APPLICATION NUMBER: US/10/645,784  
PRIOR FILING DATE: 2003-08-18  
PRIOR APPLICATION NUMBER: US/09/563,286  
PRIOR FILING DATE: 2000-05-03  
PRIOR APPLICATION NUMBER: 09/428,082  
PRIOR FILING DATE: 1999-10-22  
PRIOR APPLICATION NUMBER: 60/105,371  
PRIOR FILING DATE: 1998-10-23  
NUMBER OF SEQ ID NOS: 1157  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 196  
LENGTH: 17  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: UKR ANTAGONIST PEPTIDE

US-10-645-784-196

Query Match 27.0%; Score 31; DB 5; Length 17;  
Best Local Similarity 45.5%; Pred. No. 1.2e+03;  
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 IPHPTNHYKL 12  
Db 4 MPHSLNFSQYL 14

## RESULT 38

US-09-864-761-44227  
Sequence 44227, Application US/09864761  
Patent No. US20020048763A1  
GENERAL INFORMATION:  
APPLICANT: Penn, Sharon G.  
APPLICANT: Rank, David R.  
APPLICANT: Hanzel, David K.  
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
FILE REFERENCE: Aeomica-X-1  
CURRENT APPLICATION NUMBER: US/09/864,761  
PRIOR FILING DATE: 2001-05-23  
PRIOR APPLICATION NUMBER: US 60/180,312  
PRIOR FILING DATE: 2000-02-04  
PRIOR APPLICATION NUMBER: US 60/207,456  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: US 09/632,366  
PRIOR FILING DATE: 2000-08-03  
PRIOR APPLICATION NUMBER: GB 24263.6  
PRIOR FILING DATE: 2000-10-04  
PRIOR APPLICATION NUMBER: US 60/236,359  
PRIOR FILING DATE: 2000-09-27  
PRIOR APPLICATION NUMBER: PCT/US01/00666  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00667  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00664  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00669  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00665  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00668  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00663  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00662  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00661  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00670  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: US 60/234,687  
PRIOR FILING DATE: 2000-09-21  
PRIOR APPLICATION NUMBER: US 09/608,408  
PRIOR FILING DATE: 2000-06-30  
PRIOR APPLICATION NUMBER: US 09/774,203  
PRIOR FILING DATE: 2001-01-29  
NUMBER OF SEQ ID NOS: 49117  
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1  
SEQ ID NO 44227  
LENGTH: 18  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: MAP TO AC005827.3  
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.84  
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.67  
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.95  
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.74

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.65  
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.79  
US-09-864-761-44227

Query Match 27.0%; Score 31; DB 3; Length 18;  
Best Local Similarity 44.4%; Pred. No. 1.2e+03;  
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 6 TNIHKYVC 14  
Db 9 SHIHVFLIC 17

RESULT 39  
US-09-791-524-9

Sequence 9, Application US/09791524  
Publication No. US20030143209A1  
GENERAL INFORMATION:  
APPLICANT: Aventis Pharmaceuticals Products Inc.  
TITLE OF INVENTION: Targeted Adenovirus Vectors For Delivery Of Heterologous Genes  
FILE REFERENCE: A3319A  
CURRENT APPLICATION NUMBER: US/09/791,524  
CURRENT FILING DATE: 2001-02-22  
PRIOR APPLICATION NUMBER: 60/09828  
PRIOR FILING DATE: 1998-08-27  
NUMBER OF SEQ ID NOS: 150  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 9  
LENGTH: 20  
TYPE: PRT  
ORGANISM: Adenovirus  
US-09-791-524-9

Query Match 27.0%; Score 31; DB 3; Length 20;  
Best Local Similarity 45.5%; Pred. No. 1.4e+03;  
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 2 IPHPTIHKYL 12  
Db 6 MPHSLNFSQYL 16

RESULT 40  
US-10-182-252A-787

Sequence 787, Application US/10182252A  
Publication No. US20040072162A1  
GENERAL INFORMATION:  
APPLICANT: FOMSGAARD, ANDERS  
APPLICANT: BRUNAK, SOREN  
APPLICANT: BUS, SOREN  
APPLICANT: CORBET, SYLVIE  
APPLICANT: LAUEMOLLER, SANNE LISE  
APPLICANT: HANSEN, JAN  
TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND  
TITLE OF INVENTION: CONTROL OF HIV INFECTIONS  
FILE REFERENCE: 030307/0205  
CURRENT APPLICATION NUMBER: US/10/182,252A  
CURRENT FILING DATE: 2003-04-10  
PRIOR APPLICATION NUMBER: PCT/DK01/00059  
PRIOR FILING DATE: 2001-01-29  
PRIOR APPLICATION NUMBER: EP 00610017.6  
PRIOR FILING DATE: 2000-01-28  
PRIOR APPLICATION NUMBER: US 60/179,333  
PRIOR FILING DATE: 2000-01-31  
NUMBER OF SEQ ID NOS: 1388  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 787  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: HIV peptide  
US-10-182-252A-787

Query Match 26.1%; Score 30; DB 4; Length 9;  
Best Local Similarity 71.4%; Pred. No. 1.7e+06;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 IPHPTNI 8  
Db 3 IPHPAGI 9

RESULT 41  
US-10-182-252A-830

Sequence 830, Application US/10182252A  
Publication No. US20040072162A1  
GENERAL INFORMATION:  
APPLICANT: FOMSGAARD, ANDERS  
APPLICANT: BRUNAK, SOREN  
APPLICANT: BUS, SOREN  
APPLICANT: CORBET, SYLVIE  
APPLICANT: LAUEMOLLER, SANNE LISE  
APPLICANT: HANSEN, JAN  
TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND  
TITLE OF INVENTION: CONTROL OF HIV INFECTIONS  
FILE REFERENCE: 030307/0205  
CURRENT APPLICATION NUMBER: US/10/182,252A  
CURRENT FILING DATE: 2003-04-10  
PRIOR APPLICATION NUMBER: PCT/DK01/00059  
PRIOR FILING DATE: 2001-01-29  
PRIOR APPLICATION NUMBER: EP 00610017.6  
PRIOR FILING DATE: 2000-01-28  
PRIOR APPLICATION NUMBER: US 60/179,333  
PRIOR FILING DATE: 2000-01-31  
NUMBER OF SEQ ID NOS: 1388  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 830  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: HIV peptide  
US-10-182-252A-830

Query Match 26.1%; Score 30; DB 4; Length 9;  
Best Local Similarity 71.4%; Pred. No. 1.7e+06;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 IPHPTNI 8  
Db 3 IPHPAGI 9

RESULT 42  
US-09-765-086-58

Sequence 58, Application US/09765086  
Patent No. US20010046498A1  
GENERAL INFORMATION:  
APPLICANT: Ruoslahti, Erkki  
APPLICANT: Paqualini, Renata  
APPLICANT: Wadli, Arap  
APPLICANT: Bredesen, Dale E.  
APPLICANT: Bledy, H. Michael  
TITLE OF INVENTION: Chimeric Prostate-Homing Peptides With  
TITLE OF INVENTION: Pro-Apoptotic Activity  
FILE REFERENCE: P-Id 3844  
CURRENT APPLICATION NUMBER: US/09/765,086  
CURRENT FILING DATE: 2001-01-17  
PRIOR APPLICATION NUMBER: US 09/489,582  
PRIOR FILING DATE: 2000-01-21  
NUMBER OF SEQ ID NOS: 235  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 58  
LENGTH: 10  
TYPE: PRT



ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: synthetic peptide  
US-09-765-086-58

Query Match 26.1%; Score 30; DB 3; Length 10;  
Best Local Similarity 83.3%; Pred. No. 9.3e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 14 CESVNG 19  
DB 1 CEGVNG 6

RESULT 43  
US-09-573-822C-160  
Sequence 160, Application US/09573822C  
Publication No. US2003019901A1  
GENERAL INFORMATION:  
APPLICANT: Proteom Ltd  
TITLE OF INVENTION: Complementary peptide ligands generated from microbial genome seq  
FILE REFERENCE: Microbe Patent  
CURRENT APPLICATION NUMBER: US/09/573,822C  
CURRENT FILING DATE: 2000-05-18  
NUMBER OF SEQ ID NOS: 804  
SOFTWARE: ProPatent version 1.0  
SEQ ID NO 160  
LENGTH: 10  
TYPE: PRT  
ORGANISM: mycoplasma genitalium  
FEATURE:  
OTHER INFORMATION: Sequence located in MG445 at 158-167 and may interact with Sequen  
US-09-573-822C-160

Query Match 26.1%; Score 30; DB 3; Length 10;  
Best Local Similarity 71.4%; Pred. No. 9.3e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 12 LVESVYV 18  
DB 4 LICESPV 10

RESULT 44  
US-10-264-374-58  
Sequence 58, Application US/10264374  
Publication No. US20030113320A1  
GENERAL INFORMATION:  
APPLICANT: Ruoslahti, Erkki  
TITLE OF INVENTION: NGR Receptor and Methods of Identifying Tumor Homing  
TITLE OF INVENTION: Molecules That Home to Angiogenic Vasculature Using  
FILE REFERENCE: P-LJ 3203  
CURRENT APPLICATION NUMBER: US/10/264,374  
CURRENT FILING DATE: 2002-10-03  
PRIOR APPLICATION NUMBER: US/09/139,802  
PRIOR FILING DATE: 1998-08-25  
PRIOR APPLICATION NUMBER: 08/926,914  
PRIOR FILING DATE: 1997-09-10  
PRIOR APPLICATION NUMBER: 08/710,067  
PRIOR FILING DATE: 1996-09-10  
NUMBER OF SEQ ID NOS: 226  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 58  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-10-264-374-58

Query Match 26.1%; Score 30; DB 4; Length 10;  
Best Local Similarity 83.3%; Pred. No. 9.3e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 14 CESVNG 19  
DB 1 CEGVNG 6

RESULT 45  
US-10-375-992-58  
Sequence 58, Application US/10375992  
Publication No. US20030152578A1  
GENERAL INFORMATION:  
APPLICANT: Ruoslahti, Erkki  
TITLE OF INVENTION: Tumor Homing Molecules, Conjugates  
DERIVED THEREFROM, and Methods of Using Same  
NUMBER OF SEQUENCES: 199  
CORRESPONDENCE ADDRESSES:  
ADDRESSER: Campbell & Flores  
STREET: 4370 La Jolla Village Drive, Suite 700  
CITY: San Diego  
STATE: California  
COUNTRY: United States  
ZIP: 92122  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/375,992  
FILING DATE: 27-Feb-2003  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/926,914  
FILING DATE: 10-SEP-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Campbell, Cathryn A.  
REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P-LJ 2725  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 535-9001  
TELEFAX: (619) 535-8949  
INFORMATION FOR SEQ ID NO: 58:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 58:  
US-10-375-992-58

Query Match 26.1%; Score 30; DB 4; Length 10;  
Best Local Similarity 83.3%; Pred. No. 9.3e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 14 CESVNG 19  
DB 1 CEGVNG 6

RESULT 46  
US-10-264-374-58  
Sequence 58, Application US/10264374  
Publication No. US20040096441A3  
GENERAL INFORMATION:  
APPLICANT: Ruoslahti, Erkki  
TITLE OF INVENTION: NGR Receptor and Methods of Identifying Tumor Homing  
TITLE OF INVENTION: Molecules That Home to Angiogenic Vasculature Using  
US-10-264-374-58

/ TITLE OF INVENTION: Same  
/ FILE REFERENCE: P-LJ 3203  
/ CURRENT APPLICATION NUMBER: US/10/264,374  
/ CURRENT FILING DATE: 2002-10-03  
/ PRIOR APPLICATION NUMBER: US/09/139,802  
/ PRIOR FILING DATE: 1998-08-25  
/ PRIOR APPLICATION NUMBER: 08/926,914  
/ PRIOR FILING DATE: 1997-09-10  
/ PRIOR APPLICATION NUMBER: 08/710,067  
/ PRIOR FILING DATE: 1996-09-10  
/ NUMBER OF SEQ ID NOS: 226  
/ SOFTWARE: PatentIn Ver. 2.0  
/ SEQ ID NO 58  
/ LENGTH: 10  
/ TYPE: PRT  
/ ORGANISM: Artificial Sequence  
/ FEATURE:  
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
/ US-10-264-374-58

Query Match 26.1%; Score 30; DB 4; Length 10;  
Best Local Similarity 83.3%; Pred. No. 9.3e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 14 CEGVNG 19  
|||  
1 CEGVNG 6

Db 1 CEGVNG 6

RESULT 47  
US-10-375-992-58  
/ Sequence 58, Application US/10375992  
/ Publication No. US20040131623A9  
/ GENERAL INFORMATION:  
/ APPLICANT: Ruoslahti, Erkki  
/ Pasqualini, Renata  
/ TITLE OF INVENTION: Tumor Homing Molecules, Conjugates  
/ Derived Therefrom, and Methods of Using Same  
/ NUMBER OF SEQUENCES: 199  
/ CORRESPONDENCE ADDRESS:  
/ ADDRESSEE: Campbell & Flores  
/ STREET: 4370 La Jolla Village Drive, Suite 700  
/ CITY: San Diego  
/ STATE: California  
/ COUNTRY: United States  
/ ZIP: 92122  
/ COMPUTER READABLE FORM:  
/ MEDIUM TYPE: Floppy disk  
/ COMPUTER: IBM PC compatible  
/ OPERATING SYSTEM: PC-DOS/MS-DOS  
/ SOFTWARE: PatentIn Release #1.0, Version #1.25  
/ CURRENT APPLICATION DATA:  
/ APPLICATION NUMBER: US/10/375,992  
/ FILING DATE: 27-Feb-2003  
/ CLASSIFICATION: 435  
/ PRIOR APPLICATION DATA:  
/ APPLICATION NUMBER: US/08/926,914  
/ FILING DATE: 10-SEP-1997  
/ ATTORNEY/AGENT INFORMATION:  
/ NAME: Campbell, Cathryn A.  
/ REGISTRATION NUMBER: 31,815  
/ REFERENCE/DOCKET NUMBER: P-LJ 2725  
/ TELECOMMUNICATION INFORMATION:  
/ TELEPHONE: (619) 535-9001  
/ TELEFAX: (619) 535-8949  
/ INFORMATION FOR SEQ ID NO: 58:  
/ SEQUENCE CHARACTERISTICS:  
/ LENGTH: 10 amino acids  
/ TYPE: amino acid  
/ TOPOLOGY: both  
/ MOLECULE TYPE: peptide  
/ SEQUENCE DESCRIPTION: SEQ ID NO: 58:

US-10-375-992-58

Query Match 26.1%; Score 30; DB 4; Length 10;  
Best Local Similarity 83.3%; Pred. No. 9.3e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 14 CEGVNG 19  
|||  
1 CEGVNG 6

Db 1 CEGVNG 6

RESULT 48  
US-10-838-289-549  
/ Sequence 549, Application US/10838289  
/ Publication No. US20050058603A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Ai, Hua  
/ APPLICANT: Gao, Jiming  
/ TITLE OF INVENTION: DRUG DELIVERY SYSTEM BASED ON POLYMER  
/ FILE REFERENCE: CMRU-P01-040  
/ CURRENT APPLICATION NUMBER: US/10/838,289  
/ CURRENT FILING DATE: 2004-05-03  
/ PRIOR APPLICATION NUMBER: US 60/502,429  
/ PRIOR FILING DATE: 2003-09-12  
/ PRIOR APPLICATION NUMBER: US 60/467,389  
/ PRIOR FILING DATE: 2003-05-02  
/ NUMBER OF SEQ ID NOS: 756  
/ SOFTWARE: FastSeq for Windows Version 4.0  
/ SEQ ID NO 549  
/ LENGTH: 10  
/ TYPE: PRT  
/ ORGANISM: Unknown  
/ FEATURE:  
/ OTHER INFORMATION: Tumor targeting peptide  
/ US-10-838-289-549

Query Match 26.1%; Score 30; DB 5; Length 10;  
Best Local Similarity 83.3%; Pred. No. 9.3e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 14 CEGVNG 19  
|||  
1 CEGVNG 6

Db 1 CEGVNG 6

RESULT 49  
US-10-490-911-4  
/ Sequence 4, Application US/10490911  
/ Publication No. US20040253636A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Soloviev, Mikhail  
/ APPLICANT: Terret, Jonathan Alexander  
/ TITLE OF INVENTION: A METHOD OF PROTEIN ANALYSIS  
/ FILE REFERENCE: 2543-1-035  
/ CURRENT APPLICATION NUMBER: US/10/490,911  
/ CURRENT FILING DATE: 2004-03-26  
/ PRIOR APPLICATION NUMBER: GB 0123295.8  
/ PRIOR FILING DATE: 2001-09-27  
/ PRIOR APPLICATION NUMBER: US 60/326177  
/ PRIOR FILING DATE: 2001-09-27  
/ NUMBER OF SEQ ID NOS: 10  
/ SOFTWARE: PatentIn version 3.1  
/ SEQ ID NO 4  
/ LENGTH: 11  
/ TYPE: PRT  
/ ORGANISM: Homosapiens  
/ FEATURE:  
/ NAME/KEY: MOD RES  
/ LOCATION: (1)-(1)  
/ OTHER INFORMATION: biotinylated at N-terminus  
/ US-10-490-911-4

Query Match 26.1%; Score 30; DB 5; Length 11;  
Best Local Similarity 50.0%; Pred. No. 1e+03;  
Matches 7; Conservative 1; Mismatches 2; Indels 4; Gaps 1;

QY 7 NIKHYLVCSVNGG 20  
DB 1 NPHQY----SVEGG 10

## RESULT 50

US-10-946-647-769  
; Sequence 769, Application US/10946647  
; Publication No. US20050186217A1  
; GENERAL INFORMATION:  
; APPLICANT: EMERY, DARYL A.  
; APPLICANT: STRAUB, DARREN E.  
; TITLE OF INVENTION: COMPOSITIONS PRODUCED USING ENTERIC PATHOGENS AND METHODS OF USE  
; FILE REFERENCE: 293.00340101  
; CURRENT APPLICATION NUMBER: US/10/946,647  
; CURRENT FILING DATE: 2004-09-20  
; PRIOR APPLICATION NUMBER: 60/504,119  
; PRIOR FILING DATE: 2003-09-19  
; NUMBER OF SEQ ID NOS: 1448  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 769  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Escherichia coli  
US-10-946-647-769

Query Match 26.1%; Score 30; DB 5; Length 15;  
Best Local Similarity 50.0%; Pred. No. 1.4e+03;  
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 IHPHTNIHKY 11  
DB 1 IHPYTESQNY 10

## RESULT 51

US-09-825-517A-7  
; Sequence 7, Application US/09825517A  
; Publication No. US20030203415A1  
; GENERAL INFORMATION:  
; APPLICANT: Rondon, Isaac J  
; APPLICANT: Ladner, Robert C  
; TITLE OF INVENTION: BINDING PEPTIDES FOR CARCINOEMBRIONIC  
; FILE REFERENCE: DTX-016.1 (3421.1005-001)  
; CURRENT APPLICATION NUMBER: US/09/825,517A  
; CURRENT FILING DATE: 2003-03-24  
; PRIOR APPLICATION NUMBER: US 09/541,345  
; PRIOR FILING DATE: 2000-04-03  
; NUMBER OF SEQ ID NOS: 151  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 7  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: CEA binding polypeptide  
US-09-825-517A-7

Query Match 26.1%; Score 30; DB 3; Length 16;  
Best Local Similarity 62.5%; Pred. No. 1.5e+03;  
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 13 VCESVNGG 20  
DB 3 VCEKTTGG 10

## RESULT 52

US-10-148-671-10  
; Sequence 10, Application US/10148671  
; Publication No. US20030186419A1  
; GENERAL INFORMATION:  
; APPLICANT: Jenseius, Jens Christian  
; APPLICANT: Thiel, Steffen  
; TITLE OF INVENTION: MASP-3, A complement-fixing enzyme, and uses for it  
; FILE REFERENCE: 10/148,671  
; CURRENT APPLICATION NUMBER: US/10/148,671  
; CURRENT FILING DATE: 2000-11-30  
; PRIOR APPLICATION NUMBER: PCT/DK00/00659  
; PRIOR FILING DATE: 2000-11-30  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 10  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Homo sapiens (fig. 4, cd13 and cd14)  
US-10-148-671-10

Query Match 26.1%; Score 30; DB 4; Length 16;  
Best Local Similarity 66.7%; Pred. No. 1.5e+03;  
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 PTNIHKYLV 13  
DB 6 PANIMNYLV 14

## RESULT 53

US-11-045-477-7  
; Sequence 7, Application US/11045477  
; Publication No. US20050201934A1  
; GENERAL INFORMATION:  
; APPLICANT: Rondon, Isaac J  
; APPLICANT: Ladner, Robert C  
; TITLE OF INVENTION: BINDING PEPTIDES FOR CARCINOEMBRIONIC  
; FILE REFERENCE: DTX-016.1 (3421.1005-001)  
; CURRENT APPLICATION NUMBER: US/11/045,477  
; CURRENT FILING DATE: 2005-01-26  
; PRIOR APPLICATION NUMBER: US/09/825,517  
; PRIOR FILING DATE: 2001-04-03  
; PRIOR APPLICATION NUMBER: US 09/541,345  
; PRIOR FILING DATE: 2000-04-03  
; NUMBER OF SEQ ID NOS: 151  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 7  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: CEA binding polypeptide  
US-11-045-477-7

Query Match 26.1%; Score 30; DB 6; Length 16;  
Best Local Similarity 62.5%; Pred. No. 1.5e+03;  
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 13 VCESVNGG 20  
DB 3 VCEKTTGG 10

## RESULT 54

US-10-280-066-34  
; Sequence 34, Application US/10280066  
; Publication No. US20030180718A1  
; GENERAL INFORMATION:  
; APPLICANT: Pillucola, Renuka C.  
; APPLICANT: Brissette, Renee  
; APPLICANT: Spruyt, Michael

```

/ APPLICANT: Dedova, Olga
/ APPLICANT: Blume, Arthur J.
/ APPLICANT: Prendergast, John
/ APPLICANT: Goldstein, Neil I
/ TITLE OF INVENTION: TARGET SPECIFIC SCREENING AND ITS USE FOR IDENTIFYING TARGET BIND
/ FILE REFERENCE: 2598-4009051
/ CURRENT APPLICATION NUMBER: US/10/280,066
/ CURRENT FILING DATE: 2002-10-24
/ PRIOR APPLICATION NUMBER: 60/345,471
/ PRIOR FILING DATE: 2001-10-24
/ NUMBER OF SEQ ID NOS: 537
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 34
/ LENGTH: 20
/ TYPE: PRT
/ ORGANISM: Escherichia coli
/ FEATURE:
/ NAME/KEY: MISC FEATURE
/ OTHER INFORMATION: DGI-2-20F-PP-B42
US-10-280-066-34

```

```

Query Match      26.1%; Score 30; DB 4; Length 20;
Best Local Similarity 55.6%; Pred. No. 2e+03;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

```

```

QY      12 LVCESVNGG 20
DB      5 VVCRPVSGG 13

```

```

RESULT 55
US-10-776-013-463
/ Sequence 463, Application US/10776013
/ Publication No. US20040226056A1
/ GENERAL INFORMATION:
/ APPLICANT: MYRIAD GENETICS, INC.
/ APPLICANT: Koch, Jean-Marc
/ APPLICANT: Barcel, Paul
/ APPLICANT: Heichman, Karen
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING NEUROLOGICAL DISORDERS AND
/ FILE REFERENCE: 1600.24
/ CURRENT APPLICATION NUMBER: US/10/776,013
/ CURRENT FILING DATE: 2004-02-09
/ PRIOR APPLICATION NUMBER: 09/948994
/ PRIOR FILING DATE: 2001-09-10
/ PRIOR APPLICATION NUMBER: 09/466139
/ PRIOR FILING DATE: 1999-12-21
/ PRIOR APPLICATION NUMBER: 60/113534
/ PRIOR FILING DATE: 1998-12-22
/ PRIOR APPLICATION NUMBER: 60/124120
/ PRIOR FILING DATE: 1999-03-12
/ PRIOR APPLICATION NUMBER: 60/141243
/ PRIOR FILING DATE: 1999-06-30
/ PRIOR APPLICATION NUMBER: 09/975072
/ PRIOR FILING DATE: 2001-10-12
/ PRIOR APPLICATION NUMBER: 60/240790
/ PRIOR FILING DATE: 2000-10-17
/ PRIOR APPLICATION NUMBER: 10/194967
/ PRIOR FILING DATE: 2002-07-15
/ PRIOR APPLICATION NUMBER: 60/304775
/ PRIOR FILING DATE: 2001-07-13
/ NUMBER OF SEQ ID NOS: 695
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 463
/ LENGTH: 20
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-776-013-463

```

```

Query Match      26.1%; Score 30; DB 5; Length 20;
Best Local Similarity 50.0%; Pred. No. 2e+03;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

```

```

QY      2 IPHPTNIH 9
DB      11 LPSPTRIH 18

```

```

RESULT 56
US-10-062-109A-123
/ Sequence 123, Application US/10062109A
/ Publication No. US20030165505A1
/ GENERAL INFORMATION:
/ APPLICANT: Agensys
/ APPLICANT: Chailita-Bid, Pia M.
/ APPLICANT: Raitano, Arthur B.
/ APPLICANT: Paris, Mary
/ APPLICANT: Hubert, Rene S.
/ APPLICANT: Morrison, Karen Jane Meyrick
/ APPLICANT: Jakobovits, Aya
/ TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
/ TITLE OF INVENTION: Entitled 161P2P10B Useful in Treatment and Detection of
/ FILE REFERENCE: 51158-20062.01
/ CURRENT APPLICATION NUMBER: US/10/062,109A
/ CURRENT FILING DATE: 2002-01-31
/ PRIOR APPLICATION NUMBER: US 10/005,480
/ PRIOR FILING DATE: 2001-11-07
/ NUMBER OF SEQ ID NOS: 765
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 123
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-062-109A-123

```

```

Query Match      25.7%; Score 29.5; DB 4; Length 9;
Best Local Similarity 75.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

```

```

QY      2 IPH-PTNI 8
DB      2 IPHRPTNV 9

```

```

RESULT 57
US-10-005-480A-123
/ Sequence 123, Application US/10005480A
/ Publication No. US20030191073A1
/ GENERAL INFORMATION:
/ APPLICANT: Agensys
/ APPLICANT: Chailita-Bid, Pia M.
/ APPLICANT: Raitano, Arthur B.
/ APPLICANT: Paris, Mary
/ APPLICANT: Hubert, Rene S.
/ APPLICANT: Morrison, Karen Jane Meyrick
/ APPLICANT: Jakobovits, Aya
/ TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
/ TITLE OF INVENTION: Entitled 161P2P10B Useful in Treatment and Detection of
/ FILE REFERENCE: 51158-20062.00
/ CURRENT APPLICATION NUMBER: US/10/005,480A
/ CURRENT FILING DATE: 2001-11-07
/ NUMBER OF SEQ ID NOS: 765
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 123
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-005-480A-123

```

```

Query Match      25.7%; Score 29.5; DB 4; Length 9;
Best Local Similarity 75.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

```

QY 2 IPH-PTNI 8  
 ||| |||:  
 Db 2 IPHRPTNV 9

RESULT 58  
 US-10-062-109A-164

; Sequence 164, Application US/10062109A  
 ; Publication No. US20030165505A1  
 ; GENERAL INFORMATION:

; APPLICANT: Agenysys  
 ; APPLICANT: Chailita-Bld, Pia M.  
 ; APPLICANT: Raitano, Arthur B.  
 ; APPLICANT: Paris, Mary  
 ; APPLICANT: Hubert, Rene S.  
 ; APPLICANT: Morrison, Karen Jane Meyrick

; APPLICANT: Jakobovits, Aya  
 ; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein  
 ; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of

; FILE REFERENCE: 51158-20062.01  
 ; CURRENT APPLICATION NUMBER: US/10/062,109A

; PRIOR FILING DATE: 2002-01-31  
 ; PRIOR FILING DATE: 2001-11-07

; NUMBER OF SEQ ID NOS: 765  
 ; SOFTWARE: PastSeq for Windows Version 4.0

; SEQ ID NO 164

; LENGTH: 10  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens

US-10-062-109A-164

Query Match 25.7%; Score 29.5; DB 4; Length 10;  
 Best Local Similarity 75.0%; Pred. No. 1.1e+03;  
 Matches 6; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 2 IPH-PTNI 8  
 ||| |||:  
 Db 3 IPHRPTNV 10

RESULT 59

US-10-005-480A-164

; Sequence 164, Application US/10005480A  
 ; Publication No. US20030191073A1  
 ; GENERAL INFORMATION:

; APPLICANT: Agenysys  
 ; APPLICANT: Chailita-Bld, Pia M.  
 ; APPLICANT: Raitano, Arthur B.  
 ; APPLICANT: Paris, Mary  
 ; APPLICANT: Hubert, Rene S.

; APPLICANT: Morrison, Karen Jane Meyrick  
 ; APPLICANT: Jakobovits, Aya

; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein  
 ; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of

; FILE REFERENCE: 51158-20062.00  
 ; CURRENT APPLICATION NUMBER: US/10/005,480A

; CURRENT FILING DATE: 2001-11-07  
 ; NUMBER OF SEQ ID NOS: 765

; SOFTWARE: PastSeq for Windows Version 4.0  
 ; SEQ ID NO 164

; LENGTH: 10  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens

US-10-005-480A-164

Query Match 25.7%; Score 29.5; DB 4; Length 10;  
 Best Local Similarity 75.0%; Pred. No. 1.1e+03;  
 Matches 6; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 2 IPH-PTNI 8

Db 3 IPHRPTNV 10  
 ||| |||:  
 ||| |||:

RESULT 60

US-10-485-758-89

; Sequence 89, Application US/10485758  
 ; Publication No. US20050129681A1  
 ; GENERAL INFORMATION:

; APPLICANT: Varner, Judith A.  
 ; TITLE OF INVENTION: Methods for Inhibiting Angiogenesis  
 ; FILE REFERENCE: UCSD-07325  
 ; CURRENT APPLICATION NUMBER: US/10/485,758

; CURRENT FILING DATE: 2004-02-03  
 ; PRIOR FILING DATE: 2001-08-06

; NUMBER OF SEQ ID NOS: 97  
 ; SOFTWARE: PatentIn Version 3.1

; SEQ ID NO 89

; LENGTH: 17  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens

US-10-485-758-89

Query Match 25.7%; Score 29.5; DB 5; Length 17;  
 Best Local Similarity 62.5%; Pred. No. 2e+03;  
 Matches 5; Conservative 2; Mismatches 0; Indels 1; Gaps 1;

QY 2 IPHPTNIH 9  
 :||| |||:  
 Db 3 LPHP-NLH 9

RESULT 61

US-10-285-394-408

; Sequence 408, Application US/10285394  
 ; Publication No. US20030228583A1  
 ; GENERAL INFORMATION:

; APPLICANT: AMACHER, DAVID E.  
 ; APPLICANT: PASULO, LISA M.  
 ; APPLICANT: HERATH, HERATH MUDIYANSelage ATHULA CHANDRASIRI

; APPLICANT: HOLT, GORDON DUANE  
 ; APPLICANT: STIGER, THOMAS R.  
 ; TITLE OF INVENTION: BIOMARKERS OF LIVER RESPONSE

; FILE REFERENCE: POA-003.01  
 ; CURRENT APPLICATION NUMBER: US/10/285,394

; CURRENT FILING DATE: 2003-02-07  
 ; PRIOR APPLICATION NUMBER: 60/335,964

; PRIOR FILING DATE: 2001-10-31  
 ; NUMBER OF SEQ ID NOS: 412

; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 408

; LENGTH: 8  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens

US-10-285-394-408

Query Match 25.2%; Score 29; DB 4; Length 8;  
 Best Local Similarity 71.4%; Pred. No. 1.7e+06;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 11 YLVCSV 17  
 ||| |||:  
 Db 1 YTVCDV 7

RESULT 62

US-09-826-290-41

; Sequence 41, Application US/09826290  
 ; Patent No. US2002016468A1  
 ; GENERAL INFORMATION:

; APPLICANT: Durham, L. Kathryn  
 ; APPLICANT: Friedman, David L.

```
/ APPLICANT: Herath, Herath Mudiyanselage Athula Chandrasiri
/ APPLICANT: Kimmel, Lida H.
/ APPLICANT: Parekh, Rajesh Bhikhu
/ APPLICANT: Potter, David M.
/ APPLICANT: Rohlf, Christian
/ APPLICANT: Silber, B. Michael
/ APPLICANT: Stigler, Thomas R.
/ APPLICANT: Sunderland, P. Trey
/ APPLICANT: Townsend, Robert Reid
/ APPLICANT: White, Frost
/ APPLICANT: Williams, Stephen A.
/ TITLE OF INVENTION: Nucleic Acid Molecules, Polypeptides and
/ TITLE OF INVENTION: Uses Therefor, Including Diagnosis and Treatment of
/ TITLE OF INVENTION: Alzheimer's Disease
/ FILE REFERENCE: 2572-1-001 N2
/ CURRENT APPLICATION NUMBER: US/09/826,230
/ CURRENT FILING DATE: 2001-04-30
/ PRIOR APPLICATION NUMBER: US 60/194,504
/ PRIOR FILING DATE: 2000-04-03
/ PRIOR APPLICATION NUMBER: US 60/253,647
/ PRIOR FILING DATE: 2000-11-28
/ NUMBER OF SEQ ID NOS: 492
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 41
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: homo sapien
US-09-826-290-41
```

```
Query Match      25.2%; Score 29; DB 3; Length 9;
Best Local Similarity 50.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy      12 LVCSVNG 19
Db      1 LICSELNG 8
```

```
RESULT 63
US-09-791-393-7
/ Sequence 7, Application US/09791389
/ Publication No. US20030032200A1
/ GENERAL INFORMATION:
/ APPLICANT: Herath, Herath Mudiyanselage Athula Chandrasiri
/ APPLICANT: Parekh, Rajesh Bhikhu
/ APPLICANT: Rohlf, Christian
/ TITLE OF INVENTION: Proteins, Genes and Their Use for
/ TITLE OF INVENTION: Diagnosis and Treatment of Bipolar Affective Disorder (BAD)
/ FILE REFERENCE: 2543-1-001 N1
/ CURRENT APPLICATION NUMBER: US/09/791,393
/ CURRENT FILING DATE: 2002-01-02
/ EARLIER APPLICATION NUMBER: GB 0004412.3
/ EARLIER FILING DATE: 2000-02-24
/ EARLIER APPLICATION NUMBER: GB 0030050.9
/ EARLIER FILING DATE: 2000-12-08
/ EARLIER APPLICATION NUMBER: US 60/254,830
/ EARLIER FILING DATE: 2000-12-12
/ NUMBER OF SEQ ID NOS: 308
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 7
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: homo sapien
US-09-791-393-7
```

```
Query Match      25.2%; Score 29; DB 3; Length 9;
Best Local Similarity 50.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy      12 LVCSVNG 19
Db      1 LICSELNG 8
```

```
RESULT 64
US-09-791-389-7
/ Sequence 7, Application US/09791389
/ Publication No. US20030032773A1
/ GENERAL INFORMATION:
/ APPLICANT: Herath, Herath Mudiyanselage Athula Chandrasiri
/ APPLICANT: Parekh, Rajesh Bhikhu
/ APPLICANT: Rohlf, Christian
/ APPLICANT: Terrett, Jonathan Alexander
/ APPLICANT: Tyson, Kerry Louise
/ TITLE OF INVENTION: Proteins, Genes and Their Use for
/ TITLE OF INVENTION: Diagnosis and Treatment of Bipolar Affective Disorder (BAD)
/ FILE REFERENCE: 2543-1-001 N2
/ CURRENT APPLICATION NUMBER: US/09/791,389
/ CURRENT FILING DATE: 2001-02-23
/ PRIOR APPLICATION NUMBER: GB 0004412.3
/ PRIOR FILING DATE: 2000-02-24
/ PRIOR APPLICATION NUMBER: GB 0030050.9
/ PRIOR FILING DATE: 2000-12-08
/ PRIOR APPLICATION NUMBER: US 60/254,830
/ PRIOR FILING DATE: 2000-12-12
/ NUMBER OF SEQ ID NOS: 308
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 7
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: homo sapien
US-09-791-389-7
```

```
Query Match      25.2%; Score 29; DB 3; Length 9;
Best Local Similarity 50.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy      12 LVCSVNG 19
Db      1 LICSELNG 8
```

```
RESULT 65
US-10-264-309-239
/ Sequence 239, Application US/10264309
/ Publication No. US20040022794A1
/ GENERAL INFORMATION:
/ APPLICANT: DURHAM, L. KATHRYN
/ APPLICANT: FRIEDMAN, DAVID L.
/ APPLICANT: HERATH, HERATH
/ APPLICANT: KIMMEL, LIDA H.
/ APPLICANT: PAREKH, RAJESH B.
/ APPLICANT: POTTER, DAVID M.
/ APPLICANT: ROHLF, CHRISTIAN
/ APPLICANT: SILBER, B. MICHAEL
/ APPLICANT: SNYDER, PETER J.
/ APPLICANT: SOARES, HOLLY D.
/ APPLICANT: STIGLER, THOMAS R.
/ APPLICANT: SUNDERLAND, P. TREY
/ APPLICANT: TOWNSEND, ROBERT R.
/ APPLICANT: WHITE, W. FROST
/ APPLICANT: WILLIAMS, STEPHEN A.
/ TITLE OF INVENTION: NUCLEIC ACID MOLECULES, POLYPEPTIDES AND USES THEREFOR,
/ TITLE OF INVENTION: INCLUDING DIAGNOSIS AND TREATMENT OF ALZHEIMER'S DISEASE
/ FILE REFERENCE: POA-002.01
/ CURRENT APPLICATION NUMBER: US/10/264,309
/ CURRENT FILING DATE: 2002-10-03
/ PRIOR APPLICATION NUMBER: 60/326,708
/ PRIOR FILING DATE: 2001-10-03
/ NUMBER OF SEQ ID NOS: 491
/ SOFTWARE: Patencin Version 2.1
/ SEQ ID NO 239
/ LENGTH: 9
/ TYPE: PRT
```

ORGANISM: Homo sapiens  
US-10-264-309-239

Query Match 25.2%; Score 29; DB 4; Length 9;  
Best Local Similarity 50.0%; Pred. No. 1.7e+06;  
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 12 LVCSYNG 19  
|:|:|:  
DB 1 LIGSELNG 8

## RESULT 66

US-10-182-252A-232  
Sequence 232, Application US/10182252A  
Publication No. US20040072162A1  
GENERAL INFORMATION:  
APPLICANT: FOMSGAARD, ANDERS  
APPLICANT: BRUNAK, SOREN  
APPLICANT: BUIJS, SOREN  
APPLICANT: CORBET, SYLVIE  
APPLICANT: LAUBMOLLER, SANNE LISE  
APPLICANT: HANSEN, JAN  
TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND  
FILE REFERENCE: 030307/0205  
CURRENT APPLICATION NUMBER: US/10/182,252A  
CURRENT FILING DATE: 2003-04-10  
PRIOR APPLICATION NUMBER: PCT/DK01/00059  
PRIOR FILING DATE: 2001-01-29  
PRIOR APPLICATION NUMBER: EP 00610017.6  
PRIOR FILING DATE: 2000-01-28  
PRIOR APPLICATION NUMBER: US 60/179,333  
PRIOR FILING DATE: 2000-01-31  
NUMBER OF SEQ ID NOS: 1388  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 232  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: HIV peptide  
US-10-182-252A-232

Query Match 25.2%; Score 29; DB 4; Length 9;  
Best Local Similarity 57.1%; Pred. No. 1.7e+06;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 IPHPTNI 8  
|:|:|:  
DB 3 IPHPAGV 9

## RESULT 67

US-10-182-252A-759  
Sequence 759, Application US/10182252A  
Publication No. US20040072162A1  
GENERAL INFORMATION:  
APPLICANT: FOMSGAARD, ANDERS  
APPLICANT: BRUNAK, SOREN  
APPLICANT: BUIJS, SOREN  
APPLICANT: CORBET, SYLVIE  
APPLICANT: LAUBMOLLER, SANNE LISE  
APPLICANT: HANSEN, JAN  
TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND  
FILE REFERENCE: 030307/0205  
CURRENT APPLICATION NUMBER: US/10/182,252A  
CURRENT FILING DATE: 2003-04-10  
PRIOR APPLICATION NUMBER: PCT/DK01/00059  
PRIOR FILING DATE: 2001-01-29  
PRIOR APPLICATION NUMBER: EP 00610017.6  
PRIOR FILING DATE: 2000-01-28

PRIOR APPLICATION NUMBER: US 60/179,333  
PRIOR FILING DATE: 2000-01-31

NUMBER OF SEQ ID NOS: 1388  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 759

LENGTH: 9  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: HIV peptide  
US-10-182-252A-759

Query Match 25.2%; Score 29; DB 4; Length 9;  
Best Local Similarity 57.1%; Pred. No. 1.7e+06;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 IPHPTNI 8  
|:|:|:  
DB 3 IPHPAGV 9

## RESULT 68

US-10-182-252A-832  
Sequence 832, Application US/10182252A  
Publication No. US20040072162A1  
GENERAL INFORMATION:  
APPLICANT: FOMSGAARD, ANDERS  
APPLICANT: BRUNAK, SOREN  
APPLICANT: BUIJS, SOREN  
APPLICANT: CORBET, SYLVIE  
APPLICANT: LAUBMOLLER, SANNE LISE  
APPLICANT: HANSEN, JAN  
TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND  
FILE REFERENCE: 030307/0205  
CURRENT APPLICATION NUMBER: US/10/182,252A  
CURRENT FILING DATE: 2003-04-10  
PRIOR APPLICATION NUMBER: PCT/DK01/00059  
PRIOR FILING DATE: 2001-01-29  
PRIOR APPLICATION NUMBER: EP 00610017.6  
PRIOR FILING DATE: 2000-01-28  
PRIOR APPLICATION NUMBER: US 60/179,333  
PRIOR FILING DATE: 2000-01-31  
NUMBER OF SEQ ID NOS: 1388  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 832  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: HIV peptide  
US-10-182-252A-832

Query Match 25.2%; Score 29; DB 4; Length 9;  
Best Local Similarity 57.1%; Pred. No. 1.7e+06;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 IPHPTNI 8  
|:|:|:  
DB 3 IPHPAGV 9

## RESULT 69

US-10-182-252A-866  
Sequence 866, Application US/10182252A  
Publication No. US20040072162A1  
GENERAL INFORMATION:  
APPLICANT: FOMSGAARD, ANDERS  
APPLICANT: BRUNAK, SOREN  
APPLICANT: BUIJS, SOREN  
APPLICANT: CORBET, SYLVIE  
APPLICANT: LAUBMOLLER, SANNE LISE  
APPLICANT: HANSEN, JAN

```
/ TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND
/ FILE OF INVENTION: CONTROL OF HIV INFECTIONS
/ FILE REFERENCE: 030307/0205
/ CURRENT APPLICATION NUMBER: US/10/182,252A
/ CURRENT FILING DATE: 2003-04-10
/ PRIOR APPLICATION NUMBER: PCT/DK01/00059
/ PRIOR FILING DATE: 2001-01-29
/ PRIOR APPLICATION NUMBER: EP 00610017.6
/ PRIOR FILING DATE: 2000-01-28
/ PRIOR APPLICATION NUMBER: US 60/179,333
/ PRIOR FILING DATE: 2000-01-31
/ NUMBER OF SEQ ID NOS: 1388
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 866
/ LENGTH: 9
/ TYPE: PRF
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: HIV peptide
US-10-182-252A-866
```

```
Query Match          25.2%; Score 29; DB 4; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      2 IHPPTNI 8
      |||||
DB      3 IHPHAGV 9
```

```
RESULT 70
US-10-264-309-239
/ Sequence 239, Application US/10264309
/ Publication No. US20050163789A9
/ GENERAL INFORMATION:
/ APPLICANT: DURHAM, L. KATHRYN
/ APPLICANT: FRIEDMAN, DAVID L.
/ APPLICANT: HERATH, HERATH
/ APPLICANT: KIMMEL, LIDA H.
/ APPLICANT: PAREKH, RAJESH B.
/ APPLICANT: POTTER, DAVID M.
/ APPLICANT: ROHLF, CHRISTIAN
/ APPLICANT: SILBER, B. MICHAEL
/ APPLICANT: SNYDER, PETER J.
/ APPLICANT: SOARES, HOLLY D.
/ APPLICANT: STIGER, THOMAS R.
/ APPLICANT: SUNDERLAND, P. TREV
/ APPLICANT: TOWNSEND, ROBERT R.
/ APPLICANT: WHITE, W. FROST
/ APPLICANT: WILLIAMS, STEPHEN A.
/ TITLE OF INVENTION: NUCLEIC ACID MOLECULES, POLYPEPTIDES AND USES THEREFOR,
/ TITLE OF INVENTION: INCLUDING DIAGNOSIS AND TREATMENT OF ALZHEIMER'S DISEASE
/ FILE REFERENCE: POA-002.01
/ CURRENT APPLICATION NUMBER: US/10/264,309
/ CURRENT FILING DATE: 2002-10-03
/ PRIOR APPLICATION NUMBER: 60/326,708
/ PRIOR FILING DATE: 2001-10-03
/ NUMBER OF SEQ ID NOS: 491
/ SOFTWARE: PatentIn Version 2.1
/ SEQ ID NO 239
/ LENGTH: 9
/ TYPE: PRF
/ ORGANISM: Homo sapiens
US-10-264-309-239
```

```
Query Match          25.2%; Score 29; DB 5; Length 9;
Best Local Similarity 50.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      12 LVCEVSG 19
      |||||
DB      1 LICSELNG 8
```

```
RESULT 71
US-08-996-140-16
/ Sequence 16, Application US/08996140
/ Publication No. US20030190318A1
/ GENERAL INFORMATION:
/ APPLICANT: TORIGOE, Kakuji
/ APPLICANT: USHIO, Shimpel
/ APPLICANT: KUNIKATA, Toshio
/ APPLICANT: KURIMOTO, Masashi
/ TITLE OF INVENTION: INTERLEUKIN-18 RECEPTOR PROTEINS
/ NUMBER OF SEQUENCES: 31
/ CORRESPONDENCE ADDRESS:
/ ADDRESSER: BROWDY AND NEIMARK
/ STREET: 419 Seventh Street, N.W., Suite 300
/ CITY: Washington
/ STATE: D.C.
/ COUNTRY: USA
/ ZIP: 20004
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/996,140
/ FILING DATE: 22-DEC-1997
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: JP 356,426/1996
/ FILING DATE: 26-DEC-1996
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: JP 52,526/1997
/ FILING DATE: 21-FEB-1997
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: JP 163,490/1997
/ FILING DATE: 6-JUN-1997
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: JP 215,490/1997
/ FILING DATE: 28-JUL-1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: BROWDY, Roger L.
/ REGISTRATION NUMBER: 25,618
/ REFERENCE/DOCKET NUMBER: TORIGOE=2
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 202-628-5197
/ TELEFAX: 202-737-3528
/ INFORMATION FOR SEQ ID NO: 16:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 11 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ FRAGMENT TYPE: internal fragment
US-08-996-140-16
```

```
Query Match          25.2%; Score 29; DB 2; Length 11;
Best Local Similarity 83.3%; Pred. No. 1.5e+03;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      7 NIKHYL 12
      |||||
DB      5 NIKHYL 10
```

```
RESULT 72
US-10-169-351-80
/ Sequence 80, Application US/10169351
/ Publication No. US20030157090A1
/ GENERAL INFORMATION:
/ APPLICANT: BENVENUTO, EUGENIO
/ APPLICANT: FRANCONI, ROSELLA
/ APPLICANT: DESIDERIO, ANGIOLA
/ APPLICANT: TAVLADORAKI, PARASKEVI
```



```
/ TITLE OF INVENTION: STABILIZING PEPTIDES, POLYPEPTIDES AND ANTIBODIES
/ TITLE OF INVENTION: WHICH INCLUDE THEM
/ FILE REFERENCE: 4161-4
/ CURRENT APPLICATION NUMBER: US/10/169,351
/ CURRENT FILING DATE: 2002-10-29
/ PRIOR APPLICATION NUMBER: PCT/IT00/00554
/ PRIOR FILING DATE: 2000-12-29
/ PRIOR APPLICATION NUMBER: IT RM99A000803
/ PRIOR FILING DATE: 1999-12-30
/ NUMBER OF SEQ ID NOS: 118
/ SOFTWARE: Patentin Ver. 2.1
/ SEQ ID NO 80
/ LENGTH: 11
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic
/ US-10-169-351-80
```

```
Query Match      25.2%; Score 29; DB 4; Length 11;
Best Local Similarity 83.3%; Pred. No. 1.5e+03;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      7 NIHKYL 12
        |||||
Db      5 NIHNVL 10
```

```
RESULT 73
US-10-239-656-9
/ Sequence 9, Application US/10239656
/ Publication No. US20040038339A1
/ GENERAL INFORMATION:
```

```
/ APPLICANT: KUFER, PETER
/ APPLICANT: RIETHMULLER, GERT
/ APPLICANT: LUTTERBUSCH, RALF
/ APPLICANT: BORSCHERT, KATRIN
/ APPLICANT: KISCHEL, ROMAN
/ APPLICANT: MAYER, MONIKA
/ APPLICANT: HOFMEISTER, ROBERT
/ TITLE OF INVENTION: MULTIFUNCTIONAL POLYPEPTIDES COMPRISING A BINDING SITE
/ TITLE OF INVENTION: TO AN EPIPOPE OF THE NKG2D RECEPTOR COMPLEX
/ FILE REFERENCE: 029976/0106
/ CURRENT APPLICATION NUMBER: US/10/239,656
/ CURRENT FILING DATE: 2003-03-06
/ PRIOR APPLICATION NUMBER: PCT/EP01/03414
/ PRIOR FILING DATE: 2001-03-26
/ PRIOR APPLICATION NUMBER: EP 00106467.4
/ PRIOR FILING DATE: 2000-03-24
/ NUMBER OF SEQ ID NOS: 92
/ SOFTWARE: Patentin Ver. 2.1
/ SEQ ID NO 9
/ LENGTH: 11
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic Anti-NKG2D
/ OTHER INFORMATION: hybriddoma 11B2D10 variable light chain CDRI
/ US-10-239-656-9
```

```
Query Match      25.2%; Score 29; DB 4; Length 11;
Best Local Similarity 83.3%; Pred. No. 1.5e+03;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      7 NIHKYL 12
        |||||
Db      5 NIHNVL 10
```

```
RESULT 74
US-10-879-994-59
/ Sequence 59, Application US/10879994
```

```
/ Publication No. US2005002175A1
/ GENERAL INFORMATION:
/ APPLICANT: Stahl, Neil
/ APPLICANT: Yancopoulos, George D.
/ APPLICANT: Karow, Margaret
/ APPLICANT: Smith, Eric
/ TITLE OF INVENTION: HIGH AFFINITY FUSION PROTEINS AND THERAPEUTIC AND DIAGNOSTIC MET
/ FILE REFERENCE: REG 20352
/ CURRENT APPLICATION NUMBER: US/10/879,994
/ CURRENT FILING DATE: 2004-06-29
/ PRIOR APPLICATION NUMBER: 10/610,452
/ PRIOR FILING DATE: 2003-06-30
/ NUMBER OF SEQ ID NOS: 112
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 59
/ LENGTH: 11
/ TYPE: PRT
/ ORGANISM: mus musculus
/ US-10-879-994-59
```

```
Query Match      25.2%; Score 29; DB 5; Length 11;
Best Local Similarity 83.3%; Pred. No. 1.5e+03;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      7 NIHKYL 12
        |||||
Db      5 NIHNVL 10
```

```
RESULT 75
US-10-411-869A-36
/ Sequence 36, Application US/10411869A
/ Publication No. US20030228605A1
/ GENERAL INFORMATION:
/ APPLICANT: Slocatara, Jelle Mouter
/ APPLICANT: Puljck, Mouter Cornelis
/ APPLICANT: Melsen, Robert Hans
/ APPLICANT: van Dijk, Pieter
/ APPLICANT: van Dijk, Pieter
/ TITLE OF INVENTION: IDENTIFICATION OF PROTEIN BINDING SITES
/ FILE REFERENCE: 2183-5921US (SVD/P54407US00)
/ CURRENT APPLICATION NUMBER: US/10/411,869A
/ CURRENT FILING DATE: 2003-04-10
/ PRIOR APPLICATION NUMBER: PCT/NL01/00744
/ PRIOR FILING DATE: 2001-10-10
/ PRIOR APPLICATION NUMBER: EP 00203518.6
/ PRIOR FILING DATE: 2000-10-11
/ NUMBER OF SEQ ID NOS: 65
/ SOFTWARE: Patentin version 3.2
/ SEQ ID NO 36
/ LENGTH: 12
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: LCDRI of 1fd1.pdb
/ US-10-411-869A-36
```

```
Query Match      25.2%; Score 29; DB 4; Length 12;
Best Local Similarity 83.3%; Pred. No. 1.6e+03;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      7 NIHKYL 12
        |||||
Db      5 NIHNVL 10
```

```
RESULT 76
US-10-283-940-59
/ Sequence 59, Application US/10283940
/ Publication No. US20030220394A1
/ GENERAL INFORMATION:
/ APPLICANT: Danisco A/S
```

```
/ APPLICANT: Morgan, Andrew J
/ APPLICANT: Yu, Shukun
/ APPLICANT: Weiergang, Inge
/ APPLICANT: Pedersen, Hans C
/ TITLE OF INVENTION: Sequences
/ FILE REFERENCE: 674509-2041.1
/ CURRENT APPLICATION NUMBER: US/10/283,940
/ PRIOR FILING DATE: 2002-10-30
/ PRIOR APPLICATION NUMBER: PCT/GB02/04916
/ PRIOR FILING DATE: 2002-10-30
/ PRIOR APPLICATION NUMBER: GB 0126164.3
/ PRIOR FILING DATE: 2001-10-31
/ PRIOR APPLICATION NUMBER: US 60/343,485
/ PRIOR FILING DATE: 2001-12-21
/ NUMBER OF SEQ ID NOS: 84
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 59
/ LENGTH: 15
/ TYPE: PRT
/ ORGANISM: Phanerochaete chrysosporium
/ US-10-283-940-59
```

```
Query Match      25.2% Score 29; DB 4; Length 15;
Best Local Similarity 54.5%; Pred. No. 2e+03;
Matches 6; Conservative 1; Mismatches 2; Indels 2; Gaps 1;
```

```
Qy 4 HPTNHHKYLVC 14
    |||
    6 HP--VMSYLVLC 14
```

```
RESULT 77
US-11-022-454-59
/ Sequence 59, Application US/11022454
/ Publication No. US20050164259A1
/ GENERAL INFORMATION:
/ APPLICANT: Morgan, Andrew John      Pedersen, Hans Christian
/ APPLICANT: Weiergang, Inge
/ APPLICANT: Yu, Shukun
/ TITLE OF INVENTION: Sequences
/ FILE REFERENCE: 674509-2041.2
/ CURRENT APPLICATION NUMBER: US/11/022,454
/ PRIOR FILING DATE: 2004-12-22
/ PRIOR APPLICATION NUMBER: US 10/283,940
/ PRIOR FILING DATE: 2002-10-30
/ PRIOR APPLICATION NUMBER: PCT/GB02/04916
/ PRIOR FILING DATE: 2002-10-30
/ PRIOR APPLICATION NUMBER: GB 0126164.3
/ PRIOR FILING DATE: 2001-10-31
/ PRIOR APPLICATION NUMBER: US 60/343,485
/ PRIOR FILING DATE: 2001-12-21
/ NUMBER OF SEQ ID NOS: 84
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 59
/ LENGTH: 15
/ TYPE: PRT
/ ORGANISM: Phanerochaete chrysosporium
/ US-11-022-454-59
```

```
Query Match      25.2% Score 29; DB 6; Length 15;
Best Local Similarity 54.5%; Pred. No. 2e+03;
Matches 6; Conservative 1; Mismatches 2; Indels 2; Gaps 1;
```

```
Qy 4 HPTNHHKYLVC 14
    |||
    6 HP--VMSYLVLC 14
```

```
RESULT 78
US-10-219-834-123
/ Sequence 123, Application US/10219834
/ Publication No. US20030096751A1
/ GENERAL INFORMATION:
```

```
/ APPLICANT: Bristol-Myers Squibb Company
/ TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTOR POLYNUCLEOTIDES AND METHODS OF USE THR
/ FILE REFERENCE: D0191 NP
/ CURRENT APPLICATION NUMBER: US/10/219,834
/ PRIOR FILING DATE: 2002-08-15
/ PRIOR APPLICATION NUMBER: US 60/313,658
/ PRIOR FILING DATE: 2001-08-20
/ PRIOR APPLICATION NUMBER: US 60/340,703
/ PRIOR FILING DATE: 2001-10-30
/ PRIOR APPLICATION NUMBER: US 60/318,675
/ PRIOR FILING DATE: 2001-09-12
/ PRIOR APPLICATION NUMBER: US 60/355,596
/ PRIOR FILING DATE: 2002-02-06
/ PRIOR APPLICATION NUMBER: US 60/333,417
/ PRIOR FILING DATE: 2001-11-26
/ PRIOR APPLICATION NUMBER: US 60/338,367
/ PRIOR FILING DATE: 2001-12-06
/ NUMBER OF SEQ ID NOS: 192
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 123
/ LENGTH: 16
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ US-10-219-834-123
```

```
Query Match      25.2% Score 29; DB 4; Length 16;
Best Local Similarity 66.7%; Pred. No. 2.2e+03;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy 12 LVCSVNGG 20
    |||
    7 LVCSAVHTG 15
```

```
RESULT 79
US-10-244-151-15
/ Sequence 15, Application US/10244151
/ Publication No. US2004005371A1
/ GENERAL INFORMATION:
/ APPLICANT: Grace Mareah and Alan Snow
/ TITLE OF INVENTION: Therapeutic and Diagnostic Applications
/ of Perlecan Domain I Splice Variants
/ NUMBER OF SEQUENCES: 20
/ CORRESPONDENCE ADDRESSES:
/ ADDRESS: Patrick M. Dwyer
/ STREET: 1816 Westlake Avenue N, Suite 114
/ CITY: Seattle
/ STATE: WA (Washington)
/ COUNTRY: United States of America
/ ZIP: 98109
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette - 3.50 inch, 1.44 Mb storage
/ COMPUTER: IBM PC
/ OPERATING SYSTEM: PC-DOS (Windows NT '95)
/ SOFTWARE: WordPerfect 9
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/244,151
/ FILING DATE: 13-Sep-2002
/ CLASSIFICATION: Unknown
/ PRIOR APPLICATION DATA:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Dwyer, Patrick M.
/ REGISTRATION NUMBER: 32,411
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (206) 343-7074
/ TELEFAX: (206) 343-7085
/ INFORMATION FOR SEQ ID NO: 15
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 17 AMINO ACIDS
/ TYPE: AMINO ACID
/ STRANDEDNESS: SINGLE
/ TOPOLOGY: LINEAR
```

```
/ MOLECULE TYPE: PROTEIN
/ SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-10-244-151-15

Query Match      25.2%; Score 29; DB 4; Length 17;
Best Local Similarity 43.8%; Pred. No. 2.3e+03;
Matches 7; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY      5 PTNHHKYLVCESVNGG 20
DB      1 PTPGSAVPKSLHGG 16

RESULT 80
US-09-988-493-136
/ Sequence 136, Application US/09988493
/ Publication No. US20030064419A1
/ GENERAL INFORMATION:
/ APPLICANT: Herath, Herath Mudiyanselage Athula Chandrasiri
/ APPLICANT: O'Hare, Michael John
/ APPLICANT: Page, Martin John
/ APPLICANT: Parekh, Rajesh Bhikhu
/ APPLICANT: Waterfield, Michael Derek
/ TITLE OF INVENTION: Proteins, Genes, and Their Use for
/ FILE REFERENCE: 2543-1-024
/ CURRENT APPLICATION NUMBER: US/09/988,493
/ PRIOR FILING DATE: 2002-05-21
/ PRIOR APPLICATION NUMBER: PCT/GB01/01219
/ PRIOR FILING DATE: 2001-03-20
/ PRIOR APPLICATION NUMBER: GB 0006695.1
/ PRIOR FILING DATE: 2000-03-20
/ PRIOR APPLICATION NUMBER: GB 0007265.2
/ PRIOR FILING DATE: 2000-02-24
/ NUMBER OF SEQ ID NOS: 308
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 136
/ LENGTH: 18
/ TYPE: PRT
/ ORGANISM: homo sapien
US-09-988-493-136

Query Match      25.2%; Score 29; DB 3; Length 18;
Best Local Similarity 60.0%; Pred. No. 2.5e+03;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      11 YLVCSVNGG 20
DB      4 PLVTVEVNGG 13

RESULT 81
US-10-481-180-280
/ Sequence 280, Application US/10481180
/ Publication No. US20040171821A1
/ GENERAL INFORMATION:
/ APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS
/ APPLICANT: REPRESENTED BY THE SECRETARY OF THE DEPARTMENT OF HEALTH AND
/ APPLICANT: HUMAN SERVICES
/ APPLICANT: Valenzuela, Jesus G.
/ APPLICANT: Belkaid, Yasmine
/ APPLICANT: Kamhawi, Shaden
/ APPLICANT: Sacks, David
/ APPLICANT: Ribeiro, Jose M. C.
/ TITLE OF INVENTION: ANTI-ARTHOPOD VECTOR VACCINES, METHODS
/ FILE REFERENCE: 4239-67347
/ CURRENT APPLICATION NUMBER: US/10/481,180
/ PRIOR FILING DATE: 2003-12-17
/ PRIOR APPLICATION NUMBER: PCT/US02/19663
/ PRIOR FILING DATE: 2002-06-18
/ PRIOR APPLICATION NUMBER: US 60/299,391
/ PRIOR FILING DATE: 2001-06-19
```

```
/ NUMBER OF SEQ ID NOS: 884
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 280
/ LENGTH: 19
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence; NOTE =
US-10-481-180-280

Query Match      25.2%; Score 29; DB 4; Length 19;
Best Local Similarity 28.6%; Pred. No. 2.6e+03;
Matches 4; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY      1 DIPPTNHHKYLVC 14
DB      6 ELFNDKHTCYVAC 19

RESULT 82
US-09-466-035-84
/ Sequence 84, Application US/09466035
/ Patent No. US20020165172A1
/ GENERAL INFORMATION:
/ APPLICANT: SALIBERG, MATTI
/ APPLICANT: MILICH, DAVID R.
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
/ INTRACELLULAR DISEASES
/ NUMBER OF SEQUENCES: 86
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Robine & Pasternak LLP
/ STREET: 545 Middlefield Road, Suite 180
/ CITY: Menlo Park
/ STATE: California
/ COUNTRY: U.S.
/ ZIP: 94025
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Releasee #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/466,035
/ FILING DATE: 17-Dec-1999
/ CLASSIFICATION: <Unknown>
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Pasternak, Dana S.
/ REGISTRATION NUMBER: 41,411
/ REFERENCE/DOCKET NUMBER: 2300-1231.01
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 650-325-7812
/ TELEFAX: 650-325-7823
/ TELEX: <Unknown>
/ INFORMATION FOR SEQ ID NO: 84:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 20 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: <Unknown>
/ TOPOLOGY: linear
/ SEQUENCE DESCRIPTION: SEQ ID NO: 84:
US-09-466-035-84

Query Match      25.2%; Score 29; DB 3; Length 20;
Best Local Similarity 33.3%; Pred. No. 2.8e+03;
Matches 4; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY      3 PPHPTNHHKYLVC 14
DB      1 PPHPTNHHKYLVC 12
```

RESULT 83  
US-10-103-395-195  
; Sequence 195, Application US/10103395  
; Publication No. US20020160019A1  
; GENERAL INFORMATION:  
; APPLICANT: EPIMUNE, Inc.  
; APPLICANT: Sette, Alessandro  
; APPLICANT: Sidney, John  
; APPLICANT: Southwood, Scott  
; TITLE OF INVENTION: IDENTIFICATION OF BROADLY REACTIVE DR  
; TITLE OF INVENTION: RESTRICTED EPITOPES  
; FILE REFERENCE: 3963-20016.01  
; CURRENT APPLICATION NUMBER: US/10/103,395  
; PRIOR FILING DATE: 2003-01-03  
; PRIOR APPLICATION NUMBER: US 09/009,953  
; PRIOR FILING DATE: 1998-01-21  
; PRIOR APPLICATION NUMBER: PCT/US98/01373  
; PRIOR FILING DATE: 1998-01-23  
; PRIOR APPLICATION NUMBER: US 60/036,713  
; PRIOR FILING DATE: 1997-01-23  
; PRIOR APPLICATION NUMBER: US 60/037,432  
; PRIOR FILING DATE: 1997-02-07  
; NUMBER OF SEQ ID NOS: 274  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 195  
; LENGTH: 20  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-103-395-195

Query Match 25.2%; Score 29; DB 4; Length 20;  
Best Local Similarity 33.3%; Pred. No. 2.8e+03;  
Matches 4; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 3 PPHPTNIHKYLVLC 14  
|||:|:  
DB 1 PPHPTALRQAILC 12

RESULT 84  
US-10-225-567A-2221  
; Sequence 2221, Application US/10225567A  
; Publication No. US20030113798A1  
; GENERAL INFORMATION:  
; APPLICANT: Lifespan Biosciences  
; APPLICANT: Brown, Joseph P.  
; APPLICANT: Burner, Glenn C.  
; APPLICANT: Roush, Christine L.  
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS  
; FILE REFERENCE: 1920-4-4  
; CURRENT APPLICATION NUMBER: US/10/225,567A  
; PRIOR FILING DATE: 2001-12-19  
; PRIOR APPLICATION NUMBER: 60/257,144  
; PRIOR FILING DATE: 2000-12-19  
; NUMBER OF SEQ ID NOS: 2292  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2221  
; LENGTH: 20  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-225-567A-2221

Query Match 25.2%; Score 29; DB 4; Length 20;  
Best Local Similarity 35.3%; Pred. No. 2.8e+03;  
Matches 6; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 3 PPHPTNIHKYLVCSVNG 19  
|||:|:  
DB 2 PRSSGSHKAYSRPQG 18

RESULT 85  
US-10-029-386-33390

; Sequence 33390, Application US/10029386  
; Publication No. US20030194704A1  
; GENERAL INFORMATION:  
; APPLICANT: Penn, Sharon G.  
; APPLICANT: Rank, David R.  
; APPLICANT: Hanzel, David K.  
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G  
; TITLE OF INVENTION: EXPRESSION ANALYSIS TWO  
; FILE REFERENCE: A60MICA-X-2  
; CURRENT APPLICATION NUMBER: US/10/029,386  
; PRIOR FILING DATE: 2001-12-20  
; NUMBER OF SEQ ID NOS: 34288  
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1  
; SEQ ID NO 33390  
; LENGTH: 20  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: MAP TO AC001237.1  
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.8  
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.3  
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.9  
US-10-029-386-33390

Query Match 25.2%; Score 29; DB 4; Length 20;  
Best Local Similarity 66.7%; Pred. No. 2.8e+03;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 HPTNTH 9  
|||:|:  
DB 3 HATNVH 8

RESULT 86  
US-10-371-525-150  
; Sequence 150, Application US/10371525  
; Publication No. US20030203869A1  
; GENERAL INFORMATION:  
; APPLICANT: Pike, John D.  
; APPLICANT: Hermanson, Gary G.  
; APPLICANT: Sette, Alessandro  
; APPLICANT: Ishioke, Glenn Y.  
; APPLICANT: Livingston, Brian  
; APPLICANT: Chesnut, Robert W.  
; TITLE OF INVENTION: Expression Vectors for Stimulating an  
; TITLE OF INVENTION: Immune Response and Methods of Using the Same  
; FILE REFERENCE: 3963-20022.01  
; CURRENT APPLICATION NUMBER: US/10/371,525  
; PRIOR FILING DATE: 2003-02-21  
; PRIOR APPLICATION NUMBER: US 09/311,784  
; PRIOR FILING DATE: 1999-05-13  
; PRIOR APPLICATION NUMBER: US 60/085,751  
; PRIOR FILING DATE: 1998-05-15  
; NUMBER OF SEQ ID NOS: 463  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 150  
; LENGTH: 20  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: HBV CORE 50 (peptide 857.02)  
US-10-371-525-150

Query Match 25.2%; Score 29; DB 4; Length 20;  
Best Local Similarity 33.3%; Pred. No. 2.8e+03;  
Matches 4; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 3 PPHPTNIHKYLVLC 14  
|||:|:  
DB 1 PPHPTALRQAILC 12

```
RESULT 87
US-10-371-069-150
; Sequence 150, Application US/10371069
; Publication No. US20030216342A1
; GENERAL INFORMATION:
; APPLICANT: EPIMUNE Inc.
; APPLICANT: Fikes, John D.
; APPLICANT: Hermanson, Gary G.
; APPLICANT: Sette, Alessandro
; APPLICANT: Iehloka, Glenn Y.
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert W.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Expression Vectors for Stimulating an
; FILE REFERENCE: 39963-20022.10
; CURRENT APPLICATION NUMBER: US/10/371,069
; PRIOR FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US 09/078,904
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: US 60/085,751
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 150
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HBV CORE 50 (peptide 857.02)
US-10-371-069-150

Query Match          25.2%; Score 29; DB 4; Length 20;
Best Local Similarity 33.3%; Pred. No. 2.8e+03;
Matches 4; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY      3 PHEPTNIHKYLVLC 14
      |||:|:|:|
      1 PHTTALRQAIIIC 12

RESULT 88
US-10-371-645-150
; Sequence 150, Application US/10371645
; Publication No. US20030216343A1
; GENERAL INFORMATION:
; APPLICANT: EPIMUNE Inc.
; APPLICANT: Fikes, John D.
; APPLICANT: Hermanson, Gary G.
; APPLICANT: Sette, Alessandro
; APPLICANT: Iehloka, Glenn Y.
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert W.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Expression Vectors for Stimulating an
; FILE REFERENCE: 39963-20022.11
; CURRENT APPLICATION NUMBER: US/10/371,645
; PRIOR FILING DATE: 2003-06-20
; PRIOR APPLICATION NUMBER: US 09/078,904
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: US 60/085,751
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 150
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HBV CORE 50 (peptide 857.02)
US-10-371-645-150
```

```
Query Match          25.2%; Score 29; DB 4; Length 20;
Best Local Similarity 33.3%; Pred. No. 2.8e+03;
Matches 4; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY      3 PHEPTNIHKYLVLC 14
      |||:|:|:|
      1 PHTTALRQAIIIC 12

RESULT 89
US-10-371-260-150
; Sequence 150, Application US/10371260
; Publication No. US20030220285A1
; GENERAL INFORMATION:
; APPLICANT: EPIMUNE Inc.
; APPLICANT: Fikes, John D.
; APPLICANT: Hermanson, Gary G.
; APPLICANT: Sette, Alessandro
; APPLICANT: Iehloka, Glenn Y.
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert W.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Expression Vectors for Stimulating an
; FILE REFERENCE: 39963-20022.13
; CURRENT APPLICATION NUMBER: US/10/371,260
; PRIOR FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US 09/078,904
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: US 60/085,751
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 150
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HBV CORE 50 (peptide 857.02)
US-10-371-260-150

Query Match          25.2%; Score 29; DB 4; Length 20;
Best Local Similarity 33.3%; Pred. No. 2.8e+03;
Matches 4; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY      3 PHEPTNIHKYLVLC 14
      |||:|:~|:|
      1 PHTTALRQAIIIC 12

RESULT 90
US-10-666-480-5
; Sequence 5, Application US/1066480
; Publication No. US20040121959A1
; GENERAL INFORMATION:
; APPLICANT: Boone, Thomas C
; APPLICANT: Wild, Kenneth D
; APPLICANT: Stiney, Karen C
; APPLICANT: Min, Hosing
; APPLICANT: Kimmel, Bruce
; TITLE OF INVENTION: Peptides and Related Molecules That Modulate Nerve Growth Factor
; FILE REFERENCE: A-82705
; CURRENT APPLICATION NUMBER: US/10/666,480
; PRIOR FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: 60/412,524
; PRIOR FILING DATE: 2002-09-19
; NUMBER OF SEQ ID NOS: 286
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
```

```
/ OTHER INFORMATION: Therapeutically active peptide of randomly generated, non-natural
/ OTHER INFORMATION: ly occurring sequence
US-10-666-480-5

Query Match      25.2% Score 29; DB 4; Length 20;
Best Local Similarity 44.4%; Pred. No. 2.8e+03;
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY      5 PTNHHKLV 13
DB      10 PSNIDRYML 18

RESULT 91
US-10-732-862A-232
/ Sequence 232, Application US/10732862A
/ Publication No. US20040146524A1
/ GENERAL INFORMATION:
/ APPLICANT: ASHLEY, BIRKETT J.
/ APPLICANT: Lyons, Katelynne J.
/ APPLICANT: Jay, Haron J.
/ TITLE OF INVENTION: STABILIZED IMMUNOGENIC HBC CHIMER PARTICLES
/ FILE REFERENCE: ICC-136.0 (4564-88881)
/ CURRENT APPLICATION NUMBER: US/10/732,862A
/ PRIOR FILING DATE: 2003-12-10
/ PRIOR APPLICATION NUMBER: US 60/432,123
/ PRIOR FILING DATE: 2002-12-10
/ PRIOR APPLICATION NUMBER: US 10/274,616
/ PRIOR FILING DATE: 2002-10-21
/ PRIOR APPLICATION NUMBER: US 10/080,299
/ PRIOR FILING DATE: 2002-02-21
/ PRIOR APPLICATION NUMBER: US 10/082,014
/ PRIOR FILING DATE: 2002-02-22
/ NUMBER OF SEQ ID NOS: 455
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 232
/ LENGTH: 20
/ TYPE: PRT
/ ORGANISM: Hepatitis B virus
US-10-732-862A-232

Query Match      25.2% Score 29; DB 4; Length 20;
Best Local Similarity 33.3%; Pred. No. 2.8e+03;
Matches 4; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY      3 PPHTHKLV 14
DB      1 PPHTHKLV 12

RESULT 92
US-10-481-180-283
/ Sequence 283, Application US/10481180
/ Publication No. US20040171821A1
/ GENERAL INFORMATION:
/ APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS
/ APPLICANT: REPRESENTED BY THE SECRETARY OF THE DEPARTMENT OF HEALTH AND
/ APPLICANT: HUMAN SERVICES
/ APPLICANT: Valenzuela, Jesus G.
/ APPLICANT: Belkaid, Yasmine
/ APPLICANT: Kamhawi, Shaden
/ APPLICANT: Sacke, David
/ APPLICANT: Ribeiro, Jose M. C.
/ TITLE OF INVENTION: ANTI-ARTHROPOD VECTOR VACCINES, METHODS
/ TITLE OF INVENTION: OF SELECTING AND USES THEREOF
/ FILE REFERENCE: 4239-67347
/ CURRENT APPLICATION NUMBER: US/10/481,180
/ PRIOR FILING DATE: 2003-12-17
/ PRIOR APPLICATION NUMBER: PCT/US02/19663
/ PRIOR FILING DATE: 2002-06-18
/ PRIOR APPLICATION NUMBER: US 60/299,391
/ PRIOR FILING DATE: 2001-06-19
/ NUMBER OF SEQ ID NOS: 884
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/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 283
/ LENGTH: 20
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence; NOTE =
US-10-481-180-283

Query Match      25.2% Score 29; DB 4; Length 20;
Best Local Similarity 28.6%; Pred. No. 2.8e+03;
Matches 4; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY      1 DIPHTNHHKLV 14
DB      7 ELPNDEKTHCYKC 20

RESULT 93
US-10-474-960A-403
/ Sequence 403, Application US/10474960A
/ Publication No. US20040248113A1
/ GENERAL INFORMATION:
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Livingston, Brian
/ APPLICANT: Baker, Denise
/ APPLICANT: Newman, Mark
/ APPLICANT: Brown, David
/ TITLE OF INVENTION: Methods and System for Optimizing Multi-epitope Nucleic
/ TITLE OF INVENTION: Acid Constructors and Peptides Encoded Thereby
/ FILE REFERENCE: 2060.0320004
/ CURRENT APPLICATION NUMBER: US/10/474,960A
/ PRIOR FILING DATE: 2003-10-16
/ PRIOR APPLICATION NUMBER: PCT/US02/09877
/ PRIOR FILING DATE: 2002-03-28
/ PRIOR APPLICATION NUMBER: US 09/894,018
/ PRIOR FILING DATE: 2001-06-27
/ PRIOR APPLICATION NUMBER: US 60/284,221
/ PRIOR FILING DATE: 2001-04-16
/ NUMBER OF SEQ ID NOS: 419
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 403
/ LENGTH: 20
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-474-960A-403

Query Match      25.2% Score 29; DB 5; Length 20;
Best Local Similarity 33.3%; Pred. No. 2.8e+03;
Matches 4; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY      3 PPHTHKLV 14
DB      1 PPHTHKLV 12

RESULT 94
US-10-654-601-2566
/ Sequence 2566, Application US/10654601
/ Publication No. US20050063983A1
/ GENERAL INFORMATION:
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Vitiello, Maria A.
/ APPLICANT: Livingston, Brian D.
/ APPLICANT: Cells, Berhan
/ APPLICANT: Kubo, Ralph T.
/ APPLICANT: Grey, Howard M.
/ APPLICANT: Chesnut, Robert
/ APPLICANT: EpiImmune Inc.
```

```
/ TITLE OF INVENTION: Inducing Cellular Immune Responses to Hepatitis B Virus
/ FILE OF INVENTION: Using Peptide and Nucleic Acid Compositions
/ FILE REFERENCE: 2060.006007
/ CURRENT APPLICATION NUMBER: US/10/654,601
/ PRIOR FILING DATE: 2003-09-04
/ PRIOR APPLICATION NUMBER: US/09/239,043
/ PRIOR FILING DATE: 1999-01-27
/ PRIOR APPLICATION NUMBER: US 09/189,702
/ PRIOR FILING DATE: 1998-11-10
/ PRIOR APPLICATION NUMBER: US 08/978,291
/ PRIOR FILING DATE: 1997-11-25
/ PRIOR APPLICATION NUMBER: US 08/820,360
/ PRIOR FILING DATE: 1997-03-12
/ PRIOR APPLICATION NUMBER: US 60/013,363
/ PRIOR FILING DATE: 1996-03-13
/ PRIOR APPLICATION NUMBER: US 08/461,603
/ PRIOR FILING DATE: 1995-06-05
/ PRIOR APPLICATION NUMBER: US 08/347,610
/ PRIOR FILING DATE: 1994-12-01
/ PRIOR APPLICATION NUMBER: US 08/344,824
/ PRIOR FILING DATE: 1994-11-23
/ PRIOR APPLICATION NUMBER: US 08/278,634
/ PRIOR FILING DATE: 1994-07-21
/ PRIOR APPLICATION NUMBER: US 08/205,713
/ PRIOR FILING DATE: 1994-03-04
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 2579
/ SOFTWARE: PatSeq for Windows Version 4.0
/ SEQ ID NO 2566
/ LENGTH: 20
/ TYPE: PRT
/ ORGANISM: Orthohepadnaviridae hepatitis B virus
US-10-654-601-2566

Query Match          25.2%; Score 29; DB 5; Length 20;
Best Local Similarity 33.3%; Pred. No. 2.8e+03;
Matches 4; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 3 PPHTHIKTLVC 14
DB 1 PPHHTALRQALIC 12

RESULT 95
US-11-127-702-5
/ Sequence 5, Application US/11127702
/ Publication No. US20050222035A1
/ GENERAL INFORMATION:
/ APPLICANT: Boone, Thomas C
/ APPLICANT: Wild, Kenneth D
/ APPLICANT: Stiney, Karen C
/ APPLICANT: Min, Hoesung
/ APPLICANT: Kimmel, Bruce
/ TITLE OF INVENTION: Peptides and Related Molecules That Modulate Nerve Growth Factor
/ FILE REFERENCE: A-827US
/ CURRENT APPLICATION NUMBER: US/11/127,702
/ PRIOR FILING DATE: 2005-05-11
/ PRIOR APPLICATION NUMBER: US/10/666,480
/ PRIOR FILING DATE: 2003-09-18
/ PRIOR APPLICATION NUMBER: 60/412,524
/ PRIOR FILING DATE: 2002-09-19
/ NUMBER OF SEQ ID NOS: 286
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 5
/ LENGTH: 20
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Therapeutically active peptide of randomly generated, non-natural
US-11-127-702-5

Query Match          25.2%; Score 29; DB 6; Length 20;
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Best Local Similarity 44.4%; Pred. No. 2.8e+03;
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 5 PTNIHKTLV 13
DB 10 PSNIDRYML 18

RESULT 96
US-10-469-304-106
/ Sequence 106, Application US/10469304
/ Publication No. US20040091974A1
/ GENERAL INFORMATION:
/ APPLICANT: KIRIN BEER KABUSHIKI KAISHA
/ TITLE OF INVENTION: Anti HLA-DR antibody
/ FILE REFERENCE: PH-1646-PCF
/ CURRENT APPLICATION NUMBER: US/10/469,304
/ PRIOR FILING DATE: 2003-08-29
/ PRIOR APPLICATION NUMBER: JP2001/317054
/ PRIOR FILING DATE: 2001-10-15
/ NUMBER OF SEQ ID NOS: 147
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 106
/ LENGTH: 13
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence:peptide
US-10-469-304-106

Query Match          24.8%; Score 28.5; DB 4; Length 13;
Best Local Similarity 63.6%; Pred. No. 2.1e+03;
Matches 7; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

QY 9 HKYLVCESYNG 19
DB 4 HNLVLC-SVSG 13

RESULT 97
US-10-469-304-107
/ Sequence 107, Application US/10469304
/ Publication No. US20040091974A1
/ GENERAL INFORMATION:
/ APPLICANT: KIRIN BEER KABUSHIKI KAISHA
/ TITLE OF INVENTION: Anti HLA-DR antibody
/ FILE REFERENCE: PH-1646-PCF
/ CURRENT APPLICATION NUMBER: US/10/469,304
/ PRIOR FILING DATE: 2003-08-29
/ PRIOR APPLICATION NUMBER: JP2001/317054
/ PRIOR FILING DATE: 2001-10-15
/ NUMBER OF SEQ ID NOS: 147
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 107
/ LENGTH: 13
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence:peptide
US-10-469-304-107

Query Match          24.8%; Score 28.5; DB 4; Length 13;
Best Local Similarity 63.6%; Pred. No. 2.1e+03;
Matches 7; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

QY 9 HKYLVCESYNG 19
DB 2 HNLVLC-SVSG 11

RESULT 98
US-10-133-210-83
/ Sequence 83, Application US/10133210
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/ Publication No. US20030103964A1
/ GENERAL INFORMATION:
/ APPLICANT: Delisle, Charles
/ APPLICANT: Berzofsky, Jay
/ APPLICANT: Gulukota, Kamalakara
/ APPLICANT: Vaccaro, Dennis
/ APPLICANT: Weng, Zhipling
/ APPLICANT: Zhang, Chao
/ TITLE OF INVENTION: METHODS FOR DESIGNING MOLECULAR CONJUGATES AND
/ TITLE OF INVENTION: COMPOSITIONS THEREOF
/ FILE REFERENCE: BU-035AX
/ CURRENT APPLICATION NUMBER: US/10/133,210
/ CURRENT FILING DATE: 2002-04-26
/ NUMBER OF SEQ ID NOS: 281
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 83
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-133-210-83

Query Match          24.3%; Score 28; DB 4; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 IPHPTNI 8
   |||||
   :
Db 2 IPHPAGL 8

RESULT 99
US-10-442-909-4
/ Sequence 4, Application US/10442909
/ Publication No. US20040001845A1
/ GENERAL INFORMATION:
/ APPLICANT: Altfield, Marcus
/ APPLICANT: Yu, Xu
/ APPLICANT: Walker, Bruce
/ APPLICANT: Adde, Marylyn
/ TITLE OF INVENTION: Cytotoxic T-Cell Epitopes of HIV-1 Virus
/ FILE REFERENCE: 24028-010
/ CURRENT APPLICATION NUMBER: US/10/442,909
/ CURRENT FILING DATE: 2003-05-20
/ PRIOR APPLICATION NUMBER: 60/382,120
/ PRIOR FILING DATE: 2002-05-20
/ NUMBER OF SEQ ID NOS: 77
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 4
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Human immunodeficiency virus type 1
US-10-442-909-4

Query Match          24.3%; Score 28; DB 4; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 IPHPTNI 8
   |||||
   :
Db 2 IPHPAGL 8

RESULT 100
US-10-182-252A-758
/ Sequence 758, Application US/10182252A
/ Publication No. US20040072162A1
/ GENERAL INFORMATION:
/ APPLICANT: FOMSGAARD, ANDERS
/ APPLICANT: BRUNAK, SOREN
/ APPLICANT: BUSU, SOREN
/ APPLICANT: CORBERT, SYLVIE
```

```
/ APPLICANT: LAUEMOLLER, SANNE LISE
/ APPLICANT: HANSEN, JAN
/ TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND
/ TITLE OF INVENTION: CONTROL OF HIV INFECTIONS
/ FILE REFERENCE: 030307/0205
/ CURRENT APPLICATION NUMBER: US/10/182,252A
/ CURRENT FILING DATE: 2003-04-10
/ PRIOR APPLICATION NUMBER: PCT/DK01/00059
/ PRIOR FILING DATE: 2001-01-29
/ PRIOR APPLICATION NUMBER: EP 00610017.6
/ PRIOR FILING DATE: 2000-01-28
/ PRIOR APPLICATION NUMBER: US 60/179,333
/ PRIOR FILING DATE: 2000-01-31
/ NUMBER OF SEQ ID NOS: 1388
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 758
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: HIV peptide
US-10-182-252A-758

Query Match          24.3%; Score 28; DB 4; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 IPHPTNI 8
   |||||
   :
Db 3 IPHPAGL 9
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Search completed: January 20, 2006, 19:45:38  
Job time : 74.1154 Secs



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OM protein - protein search, using sw model

Run on: January 20, 2006, 19:12:21 / Search time 8.07692 Seconds  
(without alignments)  
25.093 Million cell updates/sec

Title: US-09-662-293-3

Perfect score: 115  
Sequence: 1 DIPHPNTHKYLVCESVNGG 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 70606 seqs, 10133881 residues

Total number of hits satisfying chosen parameters: 34662

Minimum DB seq length: 0  
Maximum DB seq length: 20

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 100 summaries

Database :

Published Applications AA, New:\*  
1: /cgn2\_6/prodata/1/pubppa/US08\_NEW\_PUB.pep:\*  
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3: /cgn2\_6/prodata/1/pubppa/US07\_NEW\_PUB.pep:\*  
4: /cgn2\_6/prodata/1/pubppa/PCF\_NEW\_PUB.pep:\*  
5: /cgn2\_6/prodata/1/pubppa/US09\_NEW\_PUB.pep:\*  
6: /cgn2\_6/prodata/1/pubppa/US10\_NEW\_PUB.pep:\*  
7: /cgn2\_6/prodata/1/pubppa/US11\_NEW\_PUB.pep:\*  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

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1	32	27.8	10	7	US-11-045-024-3294
2	32	27.8	10	7	US-11-045-024-12014
3	32	27.8	10	7	US-11-045-024-12085
4	32	27.8	11	7	US-11-045-024-3376
5	32	27.8	11	7	US-11-045-024-10191
6	32	27.8	11	7	US-11-045-024-10215
7	32	27.8	11	7	US-11-045-024-12063
8	32	27.8	11	7	US-11-045-024-12086
9	32	27.8	15	7	US-11-045-024-13140
10	31	27.0	16	7	US-11-038-980-3
11	31	27.0	17	7	US-11-038-980-4
12	31	27.0	20	6	US-11-038-980-9
13	29.5	25.7	9	6	US-10-859-643-123
14	29.5	25.7	9	7	US-11-097-864-123
15	29.5	25.7	9	7	US-11-097-864-123
16	29.5	25.7	10	6	US-10-859-643-123
17	29.5	25.7	10	7	US-11-097-864-164
18	29.5	25.7	10	7	US-11-097-864-164
19	29	25.2	13	6	US-10-966-483-17
20	29	25.2	13	6	US-10-966-483-17
21	28	24.3	8	7	US-11-023-207-71
22	28	24.3	8	7	US-11-045-024-1657
23	28	24.3	8	7	US-11-045-024-4340
24	28	24.3	9	7	US-11-045-024-3222
25	28	24.3	9	7	US-11-045-024-10229
			9	7	US-11-045-024-12094

26	28	24.3	9	7	US-11-045-024-13796	Sequence 13796, A
27	28	24.3	10	7	US-11-045-024-2073	Sequence 2073, Ap
28	28	24.3	10	7	US-11-045-024-4608	Sequence 4608, Ap
29	28	24.3	10	7	US-11-045-024-10231	Sequence 10231, A
30	28	24.3	11	7	US-11-045-024-12095	Sequence 12095, A
31	28	24.3	10	7	US-11-045-024-2288	Sequence 2288, Ap
32	28	24.3	11	7	US-11-045-024-3375	Sequence 3375, Ap
33	28	24.3	11	7	US-11-045-024-10232	Sequence 10232, A
34	28	24.3	11	7	US-11-045-024-12096	Sequence 12096, A
35	28	24.3	15	7	US-11-045-024-13150	Sequence 13150, A
36	28	24.3	16	6	US-10-967-671-10	Sequence 10, Appl
37	27	23.5	13	7	US-11-033-039-792	Sequence 792, App
38	27	23.5	19	6	US-10-880-238-115	Sequence 115, App
39	27	23.5	19	7	US-11-033-039-794	Sequence 794, App
40	27	23.5	20	6	US-10-467-657-9183	Sequence 9183, Ap
41	26.5	23.0	18	7	US-11-119-581-113	Sequence 113, App
42	26	22.6	5	6	US-10-956-755A-55	Sequence 55, Appl
43	26	22.6	5	6	US-10-956-755A-73	Sequence 73, Appl
44	26	22.6	5	6	US-10-956-755A-91	Sequence 91, Appl
45	26	22.6	8	7	US-11-045-024-1626	Sequence 1626, Ap
46	26	22.6	8	7	US-11-045-024-10228	Sequence 10228, A
47	26	22.6	9	6	US-10-859-643-17	Sequence 17, Appl
48	26	22.6	9	7	US-11-097-864-117	Sequence 17, Appl
49	26	22.6	9	7	US-11-097-864-117	Sequence 17, Appl
50	26	22.6	9	7	US-11-045-024-1831	Sequence 1831, Ap
51	26	22.6	9	7	US-11-045-024-13806	Sequence 13806, A
52	26	22.6	10	6	US-11-041-893-64	Sequence 64, Appl
53	26	22.6	10	6	US-10-859-643-53	Sequence 53, Appl
54	26	22.6	10	7	US-11-097-864-53	Sequence 53, Appl
55	26	22.6	10	7	US-11-097-864-53	Sequence 53, Appl
56	26	22.6	10	7	US-11-045-024-2072	Sequence 2072, Ap
57	26	22.6	10	7	US-11-045-024-10220	Sequence 10220, A
58	26	22.6	10	7	US-11-033-039-381	Sequence 381, App
59	26	22.6	13	6	US-10-511-559-126	Sequence 126, App
60	26	22.6	13	6	US-10-511-559-127	Sequence 127, App
61	26	22.6	13	6	US-10-511-559-128	Sequence 128, App
62	26	22.6	13	6	US-10-511-559-129	Sequence 129, App
63	26	22.6	13	7	US-11-116-144-64	Sequence 64, Appl
64	26	22.6	15	6	US-10-929-988-189	Sequence 189, App
65	26	22.6	15	7	US-11-045-024-13137	Sequence 13137, A
66	26	22.6	20	6	US-10-623-155-247	Sequence 247, App
67	25	21.7	7	7	US-11-084-717-55	Sequence 55, Appl
68	25	21.7	9	7	US-11-010-7488-856	Sequence 856, App
69	25	21.7	9	7	US-11-010-7488-860	Sequence 860, App
70	25	21.7	9	7	US-11-010-7488-861	Sequence 861, App
71	25	21.7	9	7	US-11-010-7488-864	Sequence 864, App
72	25	21.7	9	7	US-11-010-7488-866	Sequence 866, App
73	25	21.7	9	7	US-11-010-7488-868	Sequence 868, App
74	25	21.7	12	6	US-10-929-988-163	Sequence 163, App
75	25	21.7	17	7	US-11-010-7488-855	Sequence 855, App
76	25	21.7	18	7	US-11-033-039-1223	Sequence 1223, Ap
77	25	21.7	20	6	US-10-485-788A-580	Sequence 580, App
78	25	21.7	20	7	US-11-022-562-141	Sequence 141, App
79	25	21.7	20	7	US-11-022-562-142	Sequence 142, App
80	25	21.7	8	7	US-11-064-416-5	Sequence 4, Appl1
81	24	20.9	8	7	US-11-064-416-5	Sequence 4, Appl1
82	24	20.9	9	6	US-10-966-483-14	Sequence 14, Appl
83	24	20.9	10	6	US-10-614-599-26	Sequence 26, Appl
84	24	20.9	11	6	US-10-929-988-102	Sequence 102, App
85	24	20.9	12	6	US-10-966-371-7	Sequence 7, Appl1
86	24	20.9	12	7	US-11-180-997-5	Sequence 5, Appl1
87	24	20.9	12	7	US-11-180-997-5	Sequence 5, Appl1
88	24	20.9	12	7	US-11-180-997-19	Sequence 19, Appl
89	24	20.9	14	6	US-10-939-890-44	Sequence 44, Appl
90	24	20.9	16	7	US-11-033-039-1428	Sequence 1428, Ap
91	24	20.9	17	7	US-11-033-039-1427	Sequence 1427, Ap
92	24	20.9	17	7	US-11-041-893-132	Sequence 132, App
93	24	20.9	18	7	US-11-033-039-1426	Sequence 1426, Ap
94	24	20.9	19	7	US-11-033-039-1425	Sequence 1425, Ap
95	24	20.9	20	6	US-10-623-155-514	Sequence 514, App
96	24	20.9	20	7	US-11-022-562-173	Sequence 173, App
97	24	20.9	20	7	US-11-033-039-1424	Sequence 1424, Ap
98	23	20.0	7	7	US-11-226-701-28	Sequence 28, Appl

99 23 20.0 8 7 US-11-140-417-18  
100 23 20.0 11 7 US-11-108-135-8

Sequence 18, Appl  
Sequence 8, Appl

## ALIGNMENTS

RESULT 1  
US-11-045-024-3294

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/ Sequence 3294, Application US/11045024
/ Publication No. US20050271676A1
/ GENERAL INFORMATION:
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Livingston, Brian
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Baker, Denise Marie
/ APPLICANT: Cells, Esteban
/ APPLICANT: Kubo, Ralph
/ APPLICANT: Grey, Howard M.
/ APPLICANT: EpiImmune Inc.
/ TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
/ TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
/ FILE REFERENCE: 2060.0040007
/ CURRENT APPLICATION NUMBER: US/11/045,024
/ PRIOR FILING DATE: 2005-01-28
/ PRIOR APPLICATION NUMBER: US 09/412,863
/ PRIOR FILING DATE: 1999-10-05
/ PRIOR APPLICATION NUMBER: US 08/027,146
/ PRIOR FILING DATE: 1993-03-05
/ PRIOR APPLICATION NUMBER: US 08/073,205
/ PRIOR FILING DATE: 1993-06-04
/ PRIOR APPLICATION NUMBER: US 08/103,396
/ PRIOR FILING DATE: 1993-08-06
/ PRIOR APPLICATION NUMBER: US 08/159,184
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/159,339
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/205,713
/ PRIOR FILING DATE: 1994-03-04
/ PRIOR APPLICATION NUMBER: US 08/347,610
/ PRIOR FILING DATE: 1994-12-01
/ NUMBER OF SEQ ID NOS: 14528
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 3294
/ LENGTH: 10
/ TYPE: PRT
/ ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
/ US-11-045-024-3294
```

Query Match 27.8%; Score 32; DB 7; Length 10;  
Best Local Similarity 55.6%; Pred. No. 13;  
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 IPHPTNIRK 10  
||| : |  
Db 2 IPHPAGLRK 10

## RESULT 2

```
US-11-045-024-10214
/ Sequence 10214, Application US/11045024
/ Publication No. US20050271676A1
/ GENERAL INFORMATION:
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Livingston, Brian
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Baker, Denise Marie
/ APPLICANT: Cells, Esteban
/ APPLICANT: Kubo, Ralph
```

```
/ APPLICANT: Grey, Howard M.
/ APPLICANT: EpiImmune Inc.
/ TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
/ TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
/ FILE REFERENCE: 2060.0040007
/ CURRENT APPLICATION NUMBER: US/11/045,024
/ PRIOR FILING DATE: 2005-01-28
/ PRIOR APPLICATION NUMBER: US 09/412,863
/ PRIOR FILING DATE: 1999-10-05
/ PRIOR APPLICATION NUMBER: US 08/027,146
/ PRIOR FILING DATE: 1993-03-05
/ PRIOR APPLICATION NUMBER: US 08/073,205
/ PRIOR FILING DATE: 1993-06-04
/ PRIOR APPLICATION NUMBER: US 08/103,396
/ PRIOR FILING DATE: 1993-08-06
/ PRIOR APPLICATION NUMBER: US 08/159,184
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/159,339
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/205,713
/ PRIOR FILING DATE: 1994-03-04
/ PRIOR APPLICATION NUMBER: US 08/347,610
/ PRIOR FILING DATE: 1994-12-01
/ NUMBER OF SEQ ID NOS: 14528
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 10214
/ LENGTH: 10
/ TYPE: PRT
/ ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
/ US-11-045-024-10214
```

Query Match 27.8%; Score 32; DB 7; Length 10;  
Best Local Similarity 55.6%; Pred. No. 13;  
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 IPHPTNIRK 10  
||| : |  
Db 2 IPHPAGLRK 10

## RESULT 3

```
US-11-045-024-12085
/ Sequence 12085, Application US/11045024
/ Publication No. US20050271676A1
/ GENERAL INFORMATION:
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Livingston, Brian
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Baker, Denise Marie
/ APPLICANT: Cells, Esteban
/ APPLICANT: Kubo, Ralph
/ APPLICANT: Grey, Howard M.
/ APPLICANT: EpiImmune Inc.
/ TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
/ TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
/ FILE REFERENCE: 2060.0040007
/ CURRENT APPLICATION NUMBER: US/11/045,024
/ PRIOR FILING DATE: 2005-01-28
/ PRIOR APPLICATION NUMBER: US 09/412,863
/ PRIOR FILING DATE: 1999-10-05
/ PRIOR APPLICATION NUMBER: US 08/027,146
/ PRIOR FILING DATE: 1993-03-05
/ PRIOR APPLICATION NUMBER: US 08/073,205
/ PRIOR FILING DATE: 1993-06-04
/ PRIOR APPLICATION NUMBER: US 08/103,396
/ PRIOR FILING DATE: 1993-08-06
/ PRIOR APPLICATION NUMBER: US 08/159,184
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/159,339
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/205,713
```

```
/ PRIOR FILING DATE: 1994-03-04
/ PRIOR APPLICATION NUMBER: US 08/347,610
/ PRIOR FILING DATE: 1994-12-01
/ NUMBER OF SEQ ID NOS: 14528
/ SOFTWARE: PaacSeq for Windows Version 4.0
/ SEQ ID NO 12085
/ LENGTH: 10
/ TYPE: PRT
/ ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-12085
```

```
Query Match      27.8%; Score 32; DB 7; Length 10;
Best Local Similarity 55.6%; Pred. No. 13;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      2 IHPPTNHHK 10
DB      2 IHPAGLKK 10
```

```
RESULT 4
US-11-045-024-3376
/ Sequence 3376, Application US/11045024
/ Publication No. US20050271676A1
/ GENERAL INFORMATION:
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Livingston, Brian
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Baker, Denise Marie
/ APPLICANT: Cells, Bateban
/ APPLICANT: Kubo, Ralph
/ APPLICANT: Grey, Howard M.
/ APPLICANT: BpImmune Inc.
/ TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
/ TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
/ FILE REFERENCE: 2060.0040007
/ CURRENT APPLICATION NUMBER: US/11/045,024
/ CURRENT FILING DATE: 2005-01-28
/ PRIOR APPLICATION NUMBER: US 09/412,863
/ PRIOR FILING DATE: 1999-10-05
/ PRIOR APPLICATION NUMBER: US 08/027,146
/ PRIOR FILING DATE: 1993-03-05
/ PRIOR APPLICATION NUMBER: US 08/073,205
/ PRIOR FILING DATE: 1993-06-04
/ PRIOR APPLICATION NUMBER: US 08/103,396
/ PRIOR FILING DATE: 1993-08-06
/ PRIOR APPLICATION NUMBER: US 08/159,184
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/159,339
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/205,713
/ PRIOR FILING DATE: 1994-03-04
/ PRIOR APPLICATION NUMBER: US 08/347,610
/ PRIOR FILING DATE: 1994-12-01
/ NUMBER OF SEQ ID NOS: 14528
/ SOFTWARE: PaacSeq for Windows Version 4.0
/ SEQ ID NO 3376
/ TYPE: PRT
/ ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-3376
```

```
Query Match      27.8%; Score 32; DB 7; Length 11;
Best Local Similarity 55.6%; Pred. No. 15;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      2 IHPPTNHHK 10
DB      2 IHPAGLKK 10
```

```
RESULT 5
US-11-045-024-10191
/ Sequence 10191, Application US/11045024
/ Publication No. US20050271676A1
/ GENERAL INFORMATION:
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Livingston, Brian
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Baker, Denise Marie
/ APPLICANT: Cells, Bateban
/ APPLICANT: Kubo, Ralph
/ APPLICANT: Grey, Howard M.
/ APPLICANT: BpImmune Inc.
/ TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
/ TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
/ FILE REFERENCE: 2060.0040007
/ CURRENT APPLICATION NUMBER: US/11/045,024
/ CURRENT FILING DATE: 2005-01-28
/ PRIOR APPLICATION NUMBER: US 09/412,863
/ PRIOR FILING DATE: 1999-10-05
/ PRIOR APPLICATION NUMBER: US 08/027,146
/ PRIOR FILING DATE: 1993-03-05
/ PRIOR APPLICATION NUMBER: US 08/073,205
/ PRIOR FILING DATE: 1993-06-04
/ PRIOR APPLICATION NUMBER: US 08/103,396
/ PRIOR FILING DATE: 1993-08-06
/ PRIOR APPLICATION NUMBER: US 08/159,184
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/159,339
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/205,713
/ PRIOR FILING DATE: 1994-03-04
/ PRIOR APPLICATION NUMBER: US 08/347,610
/ PRIOR FILING DATE: 1994-12-01
/ NUMBER OF SEQ ID NOS: 14528
/ SOFTWARE: PaacSeq for Windows Version 4.0
/ SEQ ID NO 10191
/ LENGTH: 11
/ TYPE: PRT
/ ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-10191
```

```
Query Match      27.8%; Score 32; DB 7; Length 11;
Best Local Similarity 55.6%; Pred. No. 15;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      2 IHPPTNHHK 10
DB      2 IHPAGLKK 10
```

```
RESULT 6
US-11-045-024-10215
/ Sequence 10215, Application US/11045024
/ Publication No. US20050271676A1
/ GENERAL INFORMATION:
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Livingston, Brian
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Baker, Denise Marie
/ APPLICANT: Cells, Bateban
/ APPLICANT: Kubo, Ralph
/ APPLICANT: Grey, Howard M.
/ APPLICANT: BpImmune Inc.
/ TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
/ TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
/ FILE REFERENCE: 2060.0040007
/ CURRENT APPLICATION NUMBER: US/11/045,024
/ CURRENT FILING DATE: 2005-01-28
```

```
/ TYPE: PRT
/ ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-12063
/ PRIOR APPLICATION NUMBER: US 09/412,863
/ PRIOR FILING DATE: 1999-10-05
/ PRIOR APPLICATION NUMBER: US 08/027,146
/ PRIOR FILING DATE: 1993-03-05
/ PRIOR APPLICATION NUMBER: US 08/073,205
/ PRIOR FILING DATE: 1993-06-04
/ PRIOR APPLICATION NUMBER: US 08/103,396
/ PRIOR FILING DATE: 1993-08-06
/ PRIOR APPLICATION NUMBER: US 08/159,184
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/159,339
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/205,713
/ PRIOR FILING DATE: 1994-03-04
/ PRIOR APPLICATION NUMBER: US 08/347,610
/ PRIOR FILING DATE: 1994-12-01
/ NUMBER OF SEQ ID NOS: 14528
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 10215
/ LENGTH: 11
/ TYPE: PRT
/ ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-10215

Query Match          27.8%; Score 32; DB 7; Length 11;
Best Local Similarity 55.6%; Pred. No. 15;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 IPHPTNHHK 10
DB 3 IPHPAGLKK 11

RESULT 7
US-11-045-024-12063
/ Sequence 12063, Application US/11045024
/ Publication No. US20050271676A1
/ GENERAL INFORMATION:
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Livingston, Brian
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Baker, Denise Marie
/ APPLICANT: Cells, Esteban
/ APPLICANT: Kubo, Ralph
/ APPLICANT: Grey, Howard M.
/ APPLICANT: EpiImmune Inc.
/ TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
/ FILE REFERENCE: 2060.0040007
/ CURRENT APPLICATION NUMBER: US/11/045,024
/ PRIOR FILING DATE: 2005-01-28
/ PRIOR APPLICATION NUMBER: US 09/412,863
/ PRIOR FILING DATE: 1999-10-05
/ PRIOR APPLICATION NUMBER: US 08/027,146
/ PRIOR FILING DATE: 1993-03-05
/ PRIOR APPLICATION NUMBER: US 08/073,205
/ PRIOR FILING DATE: 1993-06-04
/ PRIOR APPLICATION NUMBER: US 08/103,396
/ PRIOR FILING DATE: 1993-08-06
/ PRIOR APPLICATION NUMBER: US 08/159,184
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/159,339
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/205,713
/ PRIOR FILING DATE: 1994-03-04
/ PRIOR APPLICATION NUMBER: US 08/347,610
/ PRIOR FILING DATE: 1994-12-01
/ NUMBER OF SEQ ID NOS: 14528
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 12063
/ LENGTH: 11
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```
/ TYPE: PRT
/ ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-12063

Query Match          27.8%; Score 32; DB 7; Length 11;
Best Local Similarity 55.6%; Pred. No. 15;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 IPHPTNHHK 10
DB 3 IPHPAGLKK 11

RESULT 8
US-11-045-024-12066
/ Sequence 12066, Application US/11045024
/ Publication No. US20050271676A1
/ GENERAL INFORMATION:
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Livingston, Brian
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Baker, Denise Marie
/ APPLICANT: Cells, Esteban
/ APPLICANT: Kubo, Ralph
/ APPLICANT: Grey, Howard M.
/ APPLICANT: EpiImmune Inc.
/ TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
/ FILE REFERENCE: 2060.0040007
/ CURRENT APPLICATION NUMBER: US/11/045,024
/ PRIOR FILING DATE: 2005-01-28
/ PRIOR APPLICATION NUMBER: US 09/412,863
/ PRIOR FILING DATE: 1999-10-05
/ PRIOR APPLICATION NUMBER: US 08/027,146
/ PRIOR FILING DATE: 1993-03-05
/ PRIOR APPLICATION NUMBER: US 08/073,205
/ PRIOR FILING DATE: 1993-06-04
/ PRIOR APPLICATION NUMBER: US 08/103,396
/ PRIOR FILING DATE: 1993-08-06
/ PRIOR APPLICATION NUMBER: US 08/159,184
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/159,339
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/205,713
/ PRIOR FILING DATE: 1994-03-04
/ PRIOR APPLICATION NUMBER: US 08/347,610
/ PRIOR FILING DATE: 1994-12-01
/ NUMBER OF SEQ ID NOS: 14528
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 12066
/ LENGTH: 11
/ TYPE: PRT
/ ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-12066

Query Match          27.8%; Score 32; DB 7; Length 11;
Best Local Similarity 55.6%; Pred. No. 15;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 IPHPTNHHK 10
DB 3 IPHPAGLKK 11

RESULT 9
US-11-045-024-13140
/ Sequence 13140, Application US/11045024
/ Publication No. US20050271676A1
/ GENERAL INFORMATION:
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
```

```
/ APPLICANT: Southwood, Scott
/ APPLICANT: Livingston, Brian
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Baker, Denise Marie
/ APPLICANT: Cella, Ebediah
/ APPLICANT: Kubo, Ralph
/ APPLICANT: Grey, Howard M.
/ APPLICANT: Epiimmune Inc.
/ TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
/ TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
/ FILE REFERENCE: 2060.0040007
/ CURRENT APPLICATION NUMBER: US/11/045.024
/ PRIOR FILING DATE: 2005-01-28
/ PRIOR APPLICATION NUMBER: US 09/412,863
/ PRIOR FILING DATE: 1999-10-05
/ PRIOR APPLICATION NUMBER: US 08/027,146
/ PRIOR FILING DATE: 1993-03-05
/ PRIOR APPLICATION NUMBER: US 08/073,205
/ PRIOR FILING DATE: 1993-06-04
/ PRIOR APPLICATION NUMBER: US 08/103,396
/ PRIOR FILING DATE: 1993-08-06
/ PRIOR APPLICATION NUMBER: US 08/159,184
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/159,339
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/205,713
/ PRIOR FILING DATE: 1994-03-04
/ PRIOR APPLICATION NUMBER: US 08/347,610
/ PRIOR FILING DATE: 1994-12-01
/ NUMBER OF SEQ ID NOS: 14528
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 13140
/ LENGTH: 15
/ TYPE: PRT
/ ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
/ US-11-045-024-13140

Query Match      27.8%; Score 32; DB 7; Length 15;
Best Local Similarity 55.6%; Pred. No. 20;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      2 IHPHTNIHK 10
      ||| | : ||
      6 IHPHAGLKK 14

RESULT 10
/ US-11-038-980-3
/ Sequence 3, Application US/11038980
/ Publication No. US20060002893A1
/ GENERAL INFORMATION:
/ APPLICANT: Centellon SAS
/ APPLICANT: Emmanuelle Vigne
/ APPLICANT: Jean-Francois Dedieu
/ APPLICANT: Martine Latra
/ APPLICANT: Patrice Yeh
/ APPLICANT: Michel Perricaudet
/ TITLE OF INVENTION: Targeted Adenovirus Vectors For Delivery Of Heterologous Genes
/ FILE REFERENCE: P26,992-C USA
/ CURRENT APPLICATION NUMBER: US/11/038,980
/ PRIOR FILING DATE: 2005-01-20
/ PRIOR APPLICATION NUMBER: US 09/791,524
/ PRIOR FILING DATE: 2001-02-22
/ PRIOR APPLICATION NUMBER: PCT/IB99/01524
/ PRIOR FILING DATE: 1999-08-27
/ PRIOR APPLICATION NUMBER: US 60/098,028
/ PRIOR FILING DATE: 1998-08-27
/ NUMBER OF SEQ ID NOS: 165
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 3
/ LENGTH: 16
/ TYPE: PRT
/ ORGANISM: Adenovirus
```

```
US-11-038-980-3

Query Match      27.0%; Score 31; DB 7; Length 16;
Best Local Similarity 45.5%; Pred. No. 31;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY      2 IHPHTNIHKYL 12
      ||| | : ||
      4 MPHSLNPSQYL 14

RESULT 11
/ US-11-038-980-4
/ Sequence 4, Application US/11038980
/ Publication No. US20060002893A1
/ GENERAL INFORMATION:
/ APPLICANT: Centellon SAS
/ APPLICANT: Emmanuelle Vigne
/ APPLICANT: Jean-Francois Dedieu
/ APPLICANT: Martine Latra
/ APPLICANT: Patrice Yeh
/ APPLICANT: Michel Perricaudet
/ TITLE OF INVENTION: Targeted Adenovirus Vectors For Delivery Of Heterologous Genes
/ FILE REFERENCE: P26,992-C USA
/ CURRENT APPLICATION NUMBER: US/11/038,980
/ PRIOR FILING DATE: 2005-01-20
/ PRIOR APPLICATION NUMBER: US 09/791,524
/ PRIOR FILING DATE: 2001-02-22
/ PRIOR APPLICATION NUMBER: PCT/IB99/01524
/ PRIOR FILING DATE: 1999-08-27
/ PRIOR APPLICATION NUMBER: US 60/098,028
/ PRIOR FILING DATE: 1998-08-27
/ NUMBER OF SEQ ID NOS: 165
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 4
/ LENGTH: 17
/ TYPE: PRT
/ ORGANISM: Adenovirus
/ US-11-038-980-4

Query Match      27.0%; Score 31; DB 7; Length 17;
Best Local Similarity 45.5%; Pred. No. 33;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY      2 IHPHTNIHKYL 12
      ||| | : ||
      4 MPHSLNPSQYL 14

RESULT 12
/ US-11-038-980-9
/ Sequence 9, Application US/11038980
/ Publication No. US20060002893A1
/ GENERAL INFORMATION:
/ APPLICANT: Centellon SAS
/ APPLICANT: Emmanuelle Vigne
/ APPLICANT: Jean-Francois Dedieu
/ APPLICANT: Martine Latra
/ APPLICANT: Patrice Yeh
/ APPLICANT: Michel Perricaudet
/ TITLE OF INVENTION: Targeted Adenovirus Vectors For Delivery Of Heterologous Genes
/ FILE REFERENCE: P26,992-C USA
/ CURRENT APPLICATION NUMBER: US/11/038,980
/ PRIOR FILING DATE: 2005-01-20
/ PRIOR APPLICATION NUMBER: US 09/791,524
/ PRIOR FILING DATE: 2001-02-22
/ PRIOR APPLICATION NUMBER: PCT/IB99/01524
/ PRIOR FILING DATE: 1999-08-27
/ PRIOR APPLICATION NUMBER: US 60/098,028
/ PRIOR FILING DATE: 1998-08-27
/ NUMBER OF SEQ ID NOS: 165
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 9
```

/ LENGTH: 20  
/ TYPE: PRT  
/ ORGANISM: Adenovirus  
US-11-038-980-9

Query Match 27.0% Score 31, DB 7, Length 20;  
Best Local Similarity 45.5%; Pred. No. 39;  
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 IPHPTNHYKL 12  
:|||||:|  
Db 6 MPHSLNFSQYL 16

RESULT 13  
US-10-859-643-123  
/ Sequence 123, Application US/10859643  
/ Publication No. US20060002993A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Challita-Bid, Pia M.  
/ APPLICANT: Raitano, Arthur B.  
/ APPLICANT: Paris, Mary  
/ APPLICANT: Hubert, Rene S.  
/ APPLICANT: Morrison, Karen Jane Meyrick  
/ APPLICANT: Jakobovits, Aya  
/ TITLE OF INVENTION: Nucleic Acid and Corresponding Protein  
/ TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of  
/ FILE REFERENCE: 511582006203  
/ CURRENT APPLICATION NUMBER: US/10/859,643  
/ CURRENT FILING DATE: 2004-06-02  
/ PRIOR APPLICATION NUMBER: US 10/005,480  
/ PRIOR FILING DATE: 2001-11-07  
/ NUMBER OF SEQ ID NOS: 765  
/ SOFTWARE: FastSeq for Windows Version 4.0  
/ SEQ ID NO 123  
/ LENGTH: 9  
/ TYPE: PRT  
/ ORGANISM: Homo Sapien  
US-10-859-643-123

Query Match 25.7% Score 29.5; DB 6; Length 9;  
Best Local Similarity 75.0%; Pred. No. 5.5e+04;  
Matches 6; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 2 IPH-PTNI 8  
:|||||:  
Db 2 IPHRPTNV 9

RESULT 14  
US-11-097-864-123  
/ Sequence 123, Application US/11097864  
/ Publication No. US20050265924A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Challita-Bid, Pia M.  
/ APPLICANT: Raitano, Arthur B.  
/ APPLICANT: Paris, Mary  
/ APPLICANT: Hubert, Rene S.  
/ APPLICANT: Morrison, Karen Jane Meyrick  
/ APPLICANT: Jakobovits, Aya  
/ TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 161P2F10B  
/ TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF CANCER  
/ FILE REFERENCE: 511582006205  
/ CURRENT APPLICATION NUMBER: US/11/097,864  
/ CURRENT FILING DATE: 2005-04-01  
/ PRIOR APPLICATION NUMBER: US 10/062,109  
/ PRIOR FILING DATE: 2002-01-31  
/ PRIOR APPLICATION NUMBER: US 10/005,480  
/ PRIOR FILING DATE: 2001-11-07  
/ NUMBER OF SEQ ID NOS: 765  
/ SOFTWARE: FastSeq for Windows Version 4.0  
/ SEQ ID NO 123

/ LENGTH: 9  
/ TYPE: PRT  
/ ORGANISM: Homo Sapien  
US-11-097-864-123

Query Match 25.7% Score 29.5; DB 7; Length 9;  
Best Local Similarity 75.0%; Pred. No. 5.5e+04;  
Matches 6; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 2 IPH-PTNI 8  
:|||||:  
Db 2 IPHRPTNV 9

RESULT 15  
US-11-097-912-123  
/ Sequence 123, Application US/11097912  
/ Publication No. US20050265921A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Challita-Bid, Pia M.  
/ APPLICANT: Raitano, Arthur B.  
/ APPLICANT: Paris, Mary  
/ APPLICANT: Hubert, Rene S.  
/ APPLICANT: Morrison, Karen Jane Meyrick  
/ APPLICANT: Jakobovits, Aya  
/ TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 161P2F10B  
/ TITLE OF INVENTION: USEFUL IN TREATMENT AND DETECTION OF CANCER  
/ FILE REFERENCE: 511582006204  
/ CURRENT APPLICATION NUMBER: US/11/097,912  
/ CURRENT FILING DATE: 2005-04-01  
/ PRIOR APPLICATION NUMBER: US 10/062,109  
/ PRIOR FILING DATE: 2002-01-31  
/ PRIOR APPLICATION NUMBER: US 10/005,480  
/ PRIOR FILING DATE: 2001-11-07  
/ NUMBER OF SEQ ID NOS: 765  
/ SOFTWARE: FastSeq for Windows Version 4.0  
/ SEQ ID NO 123  
/ LENGTH: 9  
/ TYPE: PRT  
/ ORGANISM: Homo Sapien  
US-11-097-912-123

Query Match 25.7% Score 29.5; DB 7; Length 9;  
Best Local Similarity 75.0%; Pred. No. 5.5e+04;  
Matches 6; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 2 IPH-PTNI 8  
:|||||:  
Db 2 IPHRPTNV 9

RESULT 16  
US-10-859-643-164  
/ Sequence 164, Application US/10859643  
/ Publication No. US20060002993A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Challita-Bid, Pia M.  
/ APPLICANT: Raitano, Arthur B.  
/ APPLICANT: Paris, Mary  
/ APPLICANT: Hubert, Rene S.  
/ APPLICANT: Morrison, Karen Jane Meyrick  
/ APPLICANT: Jakobovits, Aya  
/ TITLE OF INVENTION: Nucleic Acid and Corresponding Protein  
/ TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of  
/ FILE REFERENCE: 511582006203  
/ CURRENT APPLICATION NUMBER: US/10/859,643  
/ CURRENT FILING DATE: 2004-06-02  
/ PRIOR APPLICATION NUMBER: US 10/005,480  
/ PRIOR FILING DATE: 2001-11-07  
/ NUMBER OF SEQ ID NOS: 765  
/ SOFTWARE: FastSeq for Windows Version 4.0  
/ SEQ ID NO 164

LENGTH: 10  
TYPE: PRT  
ORGANISM: Homo Sapien  
US-10-859-643-164

Query Match 25.7% Score 29.5; DB 6; Length 10;  
Best Local Similarity 75.0%; Pred. No. 33;  
Matches 6; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 2 IPR-PTNI 8  
Db 3 IPRPTNV 10

RESULT 17  
US-11-097-864-164

Sequence 164, Application US/11097864  
Publication No. US20050265924A1  
GENERAL INFORMATION:  
APPLICANT: Challita-Bid, Pia M.  
APPLICANT: Raitano, Arthur B.  
APPLICANT: Paris, Mary  
APPLICANT: Hubert, Rene S.  
APPLICANT: Morrison, Karen Jane Meyrick  
APPLICANT: Jakobovits, Aya  
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 161P2P10B  
TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF CANCER  
FILE REFERENCE: 511582006205  
CURRENT APPLICATION NUMBER: US/11/097,864  
CURRENT FILING DATE: 2005-04-01  
PRIOR APPLICATION NUMBER: US 10/062,109  
PRIOR FILING DATE: 2002-01-31  
PRIOR APPLICATION NUMBER: US 10/005,480  
PRIOR FILING DATE: 2001-11-07  
NUMBER OF SEQ ID NOS: 765  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 164  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Homo Sapien  
US-11-097-864-164

Query Match 25.7% Score 29.5; DB 7; Length 10;  
Best Local Similarity 75.0%; Pred. No. 33;  
Matches 6; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 2 IPR-PTNI 8  
Db 3 IPRPTNV 10

RESULT 18  
US-11-097-912-164

Sequence 164, Application US/11097912  
Publication No. US20050265921A1  
GENERAL INFORMATION:  
APPLICANT: Challita-Bid, Pia M.  
APPLICANT: Raitano, Arthur B.  
APPLICANT: Paris, Mary  
APPLICANT: Hubert, Rene S.  
APPLICANT: Morrison, Karen Jane Meyrick  
APPLICANT: Jakobovits, Aya  
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 161P2P10B  
TITLE OF INVENTION: USEFUL IN TREATMENT AND DETECTION OF CANCER  
FILE REFERENCE: 511582006204  
CURRENT APPLICATION NUMBER: US/11/097,912  
CURRENT FILING DATE: 2005-04-01  
PRIOR APPLICATION NUMBER: US 10/062,109  
PRIOR FILING DATE: 2002-01-31  
PRIOR APPLICATION NUMBER: US 10/005,480  
PRIOR FILING DATE: 2001-11-07  
NUMBER OF SEQ ID NOS: 765  
SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 164  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Homo Sapien  
US-11-097-912-164

Query Match 25.7% Score 29.5; DB 7; Length 10;  
Best Local Similarity 75.0%; Pred. No. 33;  
Matches 6; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 2 IPR-PTNI 8  
Db 3 IPRPTNV 10

RESULT 19  
US-10-966-483-17

Sequence 17, Application US/10966483  
Publication No. US20050281783A1  
GENERAL INFORMATION:  
APPLICANT: Kinch, Michael S.  
APPLICANT: Klenner, Peter A.  
APPLICANT: Bruckheimer, Elizabeth  
APPLICANT: Dubensky, Jr. Thomas W.  
APPLICANT: Cook, David N.  
TITLE OF INVENTION: LISTERIA-BASED BphA2 VACCINES  
FILE REFERENCE: 10271-146  
CURRENT APPLICATION NUMBER: US/10/966,483  
CURRENT FILING DATE: 2004-10-15  
PRIOR APPLICATION NUMBER: US 60/511,919  
PRIOR FILING DATE: 2003-10-15  
PRIOR APPLICATION NUMBER: US 60/511,719  
PRIOR FILING DATE: 2003-10-15  
PRIOR APPLICATION NUMBER: US 60/532,666  
PRIOR FILING DATE: 2003-12-24  
PRIOR APPLICATION NUMBER: US 60/556,631  
PRIOR FILING DATE: 2004-03-26  
PRIOR APPLICATION NUMBER:  
PRIOR FILING DATE: 2004-10-01  
PRIOR APPLICATION NUMBER:  
PRIOR FILING DATE: 2004-10-07  
NUMBER OF SEQ ID NOS: 72  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 17  
LENGTH: 13  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-966-483-17

Query Match 25.2% Score 29; DB 6; Length 13;  
Best Local Similarity 41.7%; Pred. No. 53;  
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 8 IHKLYCBESVNG 19  
Db 2 IYMSVCNWSG 13

RESULT 20  
US-10-723-207-71

Sequence 71, Application US/10723207  
Publication No. US20050250934A1  
GENERAL INFORMATION:  
APPLICANT: Wang, Chang Yi  
APPLICANT: Walfield, Alan M.  
TITLE OF INVENTION: PEPTIDE COMPOSITION AS IMMUNOGEN FOR THE TREATMENT OF  
TITLE OF INVENTION: ALLERGY  
FILE REFERENCE: 1151-4153US2  
CURRENT APPLICATION NUMBER: US/10/723,207  
CURRENT FILING DATE: 2003-11-24  
PRIOR APPLICATION NUMBER: 09/701,623  
PRIOR FILING DATE: 2000-12-01  
PRIOR APPLICATION NUMBER: PCT/US99/13959

;; PRIOR FILING DATE: 1999-06-21  
;; PRIOR APPLICATION NUMBER: 09/100,287  
;; PRIOR FILING DATE: 1998-06-20  
;; NUMBER OF SEQ ID NOS: 91  
;; SOFTWARE: PatentIn Ver. 2.1  
;; SEQ ID NO 71  
;; LENGTH: 20  
;; TYPE: PRT  
;; ORGANISM: Artificial Sequence  
;; FEATURE: Description of Artificial Sequence: Peptide  
;; OTHER INFORMATION: synthesized from amino acids with no genetic  
;; OTHER INFORMATION: material as source  
US-10-723-207-71

Query Match 25.2%; Score 29; DB 6; Length 20;  
Best Local Similarity 33.3%; Pred. No. 81;  
Matches 4; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 3 PPHPTNKHXYLVC 14  
Db 1 PPHPTALRQXILC 12

RESULT 21  
US-11-045-024-1627  
; Sequence 1627, Application US/11045024  
; Publication No. US20050271676A1  
; GENERAL INFORMATION:  
; APPLICANT: Sette, Alessandro  
; APPLICANT: Sidney, John  
; APPLICANT: Southwood, Scott  
; APPLICANT: Livingston, Brian  
; APPLICANT: Chesnut, Robert  
; APPLICANT: Baker, Denise Marie  
; APPLICANT: Cells, Esteban  
; APPLICANT: Kubo, Ralph  
; APPLICANT: Grey, Howard M.  
; APPLICANT: Eplimmune Inc.  
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency  
; TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions  
; FILE REFERENCE: 2060.0040007  
; CURRENT APPLICATION NUMBER: US/11/045,024  
; PRIOR FILING DATE: 2005-01-28  
; PRIOR APPLICATION NUMBER: US 09/412,863  
; PRIOR FILING DATE: 1999-10-05  
; PRIOR APPLICATION NUMBER: US 08/027,146  
; PRIOR FILING DATE: 1993-03-05  
; PRIOR APPLICATION NUMBER: US 08/073,205  
; PRIOR FILING DATE: 1993-06-04  
; PRIOR APPLICATION NUMBER: US 08/103,396  
; PRIOR FILING DATE: 1993-08-06  
; PRIOR APPLICATION NUMBER: US 08/159,184  
; PRIOR FILING DATE: 1993-11-29  
; PRIOR APPLICATION NUMBER: US 08/159,339  
; PRIOR FILING DATE: 1993-11-29  
; PRIOR APPLICATION NUMBER: US 08/205,713  
; PRIOR FILING DATE: 1994-03-04  
; PRIOR APPLICATION NUMBER: US 08/347,610  
; PRIOR FILING DATE: 1994-12-01  
; NUMBER OF SEQ ID NOS: 14528  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1627  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS  
US-11-045-024-1627

Query Match 24.3%; Score 28; DB 7; Length 8;  
Best Local Similarity 57.1%; Pred. No. 5.5e+04;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
Qy 2 IPHPTNI 8

Db 2 IPHPTNI 8

RESULT 22  
US-11-045-024-4340  
; Sequence 4340, Application US/11045024  
; Publication No. US20050271676A1  
; GENERAL INFORMATION:  
; APPLICANT: Sette, Alessandro  
; APPLICANT: Sidney, John  
; APPLICANT: Southwood, Scott  
; APPLICANT: Livingston, Brian  
; APPLICANT: Chesnut, Robert  
; APPLICANT: Baker, Denise Marie  
; APPLICANT: Cells, Esteban  
; APPLICANT: Kubo, Ralph  
; APPLICANT: Grey, Howard M.  
; APPLICANT: Eplimmune Inc.  
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency  
; TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions  
; FILE REFERENCE: 2060.0040007  
; CURRENT APPLICATION NUMBER: US/11/045,024  
; PRIOR FILING DATE: 2005-01-28  
; PRIOR APPLICATION NUMBER: US 09/412,863  
; PRIOR FILING DATE: 1999-10-05  
; PRIOR APPLICATION NUMBER: US 08/027,146  
; PRIOR FILING DATE: 1993-03-05  
; PRIOR APPLICATION NUMBER: US 08/073,205  
; PRIOR FILING DATE: 1993-06-04  
; PRIOR APPLICATION NUMBER: US 08/103,396  
; PRIOR FILING DATE: 1993-08-06  
; PRIOR APPLICATION NUMBER: US 08/159,184  
; PRIOR FILING DATE: 1993-11-29  
; PRIOR APPLICATION NUMBER: US 08/159,339  
; PRIOR FILING DATE: 1993-11-29  
; PRIOR APPLICATION NUMBER: US 08/205,713  
; PRIOR FILING DATE: 1994-03-04  
; PRIOR APPLICATION NUMBER: US 08/347,610  
; PRIOR FILING DATE: 1994-12-01  
; NUMBER OF SEQ ID NOS: 14528  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4340  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS  
US-11-045-024-4340

Query Match 24.3%; Score 28; DB 7; Length 8;  
Best Local Similarity 57.1%; Pred. No. 5.5e+04;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
Qy 2 IPHPTNI 8

Db 2 IPHPTNI 8

RESULT 23  
US-11-045-024-3222  
; Sequence 3222, Application US/11045024  
; Publication No. US20050271676A1  
; GENERAL INFORMATION:  
; APPLICANT: Sette, Alessandro  
; APPLICANT: Sidney, John  
; APPLICANT: Southwood, Scott  
; APPLICANT: Livingston, Brian  
; APPLICANT: Chesnut, Robert  
; APPLICANT: Baker, Denise Marie  
; APPLICANT: Cells, Esteban  
; APPLICANT: Kubo, Ralph  
; APPLICANT: Grey, Howard M.  
; APPLICANT: Eplimmune Inc.  
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency



```
/ TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
/ FILE REFERENCE: 2060.0040007
/ CURRENT APPLICATION NUMBER: US/11/045,024
/ CURRENT FILING DATE: 2005-01-28
/ PRIOR APPLICATION NUMBER: US 09/412,863
/ PRIOR FILING DATE: 1999-10-05
/ PRIOR APPLICATION NUMBER: US 08/027,146
/ PRIOR FILING DATE: 1993-03-05
/ PRIOR APPLICATION NUMBER: US 08/073,205
/ PRIOR FILING DATE: 1993-06-04
/ PRIOR APPLICATION NUMBER: US 08/103,396
/ PRIOR FILING DATE: 1993-08-06
/ PRIOR APPLICATION NUMBER: US 08/159,184
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/159,339
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/205,713
/ PRIOR FILING DATE: 1994-03-04
/ PRIOR APPLICATION NUMBER: US 08/347,610
/ PRIOR FILING DATE: 1994-12-01
/ NUMBER OF SEQ ID NOS: 14528
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 3222
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-3222
```

```
Query Match      24.3% Score 28; DB 7; Length 9;
Best Local Similarity 57.1%; Pred. No. 5.5e+04;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      2 IPHPINI 8
DB      2 IPHPAGL 8
```

```
RESULT 24
US-11-045-024-10229
/ Sequence 10229, Application US/11045024
/ Publication No. US20050271676A1
/ GENERAL INFORMATION:
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Livingston, Brian
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Baker, Denise Marie
/ APPLICANT: Celis, Betteban
/ APPLICANT: Kubo, Ralph
/ APPLICANT: Grey, Howard M.
/ APPLICANT: EpiImmune Inc.
/ TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
/ FILE REFERENCE: 2060.0040007
/ CURRENT APPLICATION NUMBER: US/11/045,024
/ CURRENT FILING DATE: 2005-01-28
/ PRIOR APPLICATION NUMBER: US 09/412,863
/ PRIOR FILING DATE: 1999-10-05
/ PRIOR APPLICATION NUMBER: US 08/027,146
/ PRIOR FILING DATE: 1993-03-05
/ PRIOR APPLICATION NUMBER: US 08/073,205
/ PRIOR FILING DATE: 1993-06-04
/ PRIOR APPLICATION NUMBER: US 08/103,396
/ PRIOR FILING DATE: 1993-08-06
/ PRIOR APPLICATION NUMBER: US 08/159,184
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/159,339
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/205,713
/ PRIOR FILING DATE: 1994-03-04
/ PRIOR APPLICATION NUMBER: US 08/347,610
/ PRIOR FILING DATE: 1994-12-01
```

```
/ NUMBER OF SEQ ID NOS: 14528
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 10229
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-10229
```

```
Query Match      24.3% Score 28; DB 7; Length 9;
Best Local Similarity 57.1%; Pred. No. 5.5e+04;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      2 IPHPINI 8
DB      2 IPHPAGL 8
```

```
RESULT 25
US-11-045-024-12094
/ Sequence 12094, Application US/11045024
/ Publication No. US20050271676A1
/ GENERAL INFORMATION:
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Livingston, Brian
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Baker, Denise Marie
/ APPLICANT: Celis, Betteban
/ APPLICANT: Kubo, Ralph
/ APPLICANT: Grey, Howard M.
/ APPLICANT: EpiImmune Inc.
/ TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
/ FILE REFERENCE: 2060.0040007
/ CURRENT APPLICATION NUMBER: US/11/045,024
/ CURRENT FILING DATE: 2005-01-28
/ PRIOR APPLICATION NUMBER: US 09/412,863
/ PRIOR FILING DATE: 1999-10-05
/ PRIOR APPLICATION NUMBER: US 08/027,146
/ PRIOR FILING DATE: 1993-03-05
/ PRIOR APPLICATION NUMBER: US 08/073,205
/ PRIOR FILING DATE: 1993-06-04
/ PRIOR APPLICATION NUMBER: US 08/103,396
/ PRIOR FILING DATE: 1993-08-06
/ PRIOR APPLICATION NUMBER: US 08/159,184
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/159,339
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/205,713
/ PRIOR FILING DATE: 1994-03-04
/ PRIOR APPLICATION NUMBER: US 08/347,610
/ PRIOR FILING DATE: 1994-12-01
/ NUMBER OF SEQ ID NOS: 14528
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 12094
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-12094
```

```
Query Match      24.3% Score 28; DB 7; Length 9;
Best Local Similarity 57.1%; Pred. No. 5.5e+04;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      2 IPHPINI 8
DB      2 IPHPAGL 8
```

```
RESULT 26
US-11-045-024-13796
/ Sequence 13796, Application US/11045024
```

```
/ Publication No. US20050271676A1
/ GENERAL INFORMATION:
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Livingston, Brian
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Baker, Denise Marie
/ APPLICANT: Cella, Esteban
/ APPLICANT: Kubo, Ralph
/ APPLICANT: Grey, Howard M.
/ APPLICANT: EpiImmune Inc.
/ TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
/ FILE REFERENCE: 2060.0040007
/ CURRENT APPLICATION NUMBER: US/11/045,024
/ PRIOR FILING DATE: 2005-01-28
/ PRIOR APPLICATION NUMBER: US 09/412,863
/ PRIOR FILING DATE: 1999-10-05
/ PRIOR APPLICATION NUMBER: US 08/205,713
/ PRIOR FILING DATE: 1993-03-05
/ PRIOR APPLICATION NUMBER: US 08/073,205
/ PRIOR FILING DATE: 1993-06-04
/ PRIOR APPLICATION NUMBER: US 08/103,396
/ PRIOR FILING DATE: 1993-08-06
/ PRIOR APPLICATION NUMBER: US 08/159,184
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/159,339
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/205,713
/ PRIOR FILING DATE: 1994-03-04
/ PRIOR APPLICATION NUMBER: US 08/347,610
/ PRIOR FILING DATE: 1994-12-01
/ NUMBER OF SEQ ID NOS: 14528
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 13796
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-13796

Query Match          24.3%; Score 28; DB 7; Length 9;
Best Local Similarity 57.1%; Pred. No. 5.5e+04;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      2 IPHPNTI 8
      |||||
      :
DB      3 IPHPAGL 9

RESULT 27
US-11-045-024-2073
/ Sequence 2073, Application US/11045024
/ Publication No. US20050271676A1
/ GENERAL INFORMATION:
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Livingston, Brian
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Baker, Denise Marie
/ APPLICANT: Cella, Esteban
/ APPLICANT: Kubo, Ralph
/ APPLICANT: Grey, Howard M.
/ APPLICANT: EpiImmune Inc.
/ TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
/ FILE REFERENCE: 2060.0040007
/ CURRENT APPLICATION NUMBER: US/11/045,024
/ PRIOR FILING DATE: 2005-01-28
/ PRIOR APPLICATION NUMBER: US 09/412,863
/ PRIOR FILING DATE: 1999-10-05
/ PRIOR APPLICATION NUMBER: US 08/207,146
```

```
/ PRIOR FILING DATE: 1993-03-05
/ PRIOR APPLICATION NUMBER: US 08/073,205
/ PRIOR FILING DATE: 1993-06-04
/ PRIOR APPLICATION NUMBER: US 08/103,396
/ PRIOR FILING DATE: 1993-08-06
/ PRIOR APPLICATION NUMBER: US 08/159,184
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/159,339
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/205,713
/ PRIOR FILING DATE: 1994-03-04
/ PRIOR APPLICATION NUMBER: US 08/347,610
/ PRIOR FILING DATE: 1994-12-01
/ NUMBER OF SEQ ID NOS: 14528
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 2073
/ LENGTH: 10
/ TYPE: PRT
/ ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-2073

Query Match          24.3%; Score 28; DB 7; Length 10;
Best Local Similarity 57.1%; Pred. No. 58;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      2 IPHPNTI 8
      |||||
      :
DB      4 IPHPAGL 10

RESULT 28
US-11-045-024-4608
/ Sequence 4608, Application US/11045024
/ Publication No. US20050271676A1
/ GENERAL INFORMATION:
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Livingston, Brian
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Baker, Denise Marie
/ APPLICANT: Cella, Esteban
/ APPLICANT: Kubo, Ralph
/ APPLICANT: Grey, Howard M.
/ APPLICANT: EpiImmune Inc.
/ TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
/ FILE REFERENCE: 2060.0040007
/ CURRENT APPLICATION NUMBER: US/11/045,024
/ PRIOR FILING DATE: 2005-01-28
/ PRIOR APPLICATION NUMBER: US 09/412,863
/ PRIOR FILING DATE: 1999-10-05
/ PRIOR APPLICATION NUMBER: US 08/027,146
/ PRIOR FILING DATE: 1993-03-05
/ PRIOR APPLICATION NUMBER: US 08/073,205
/ PRIOR FILING DATE: 1993-06-04
/ PRIOR APPLICATION NUMBER: US 08/103,396
/ PRIOR FILING DATE: 1993-08-06
/ PRIOR APPLICATION NUMBER: US 08/159,184
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/159,339
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/205,713
/ PRIOR FILING DATE: 1994-03-04
/ PRIOR APPLICATION NUMBER: US 08/347,610
/ PRIOR FILING DATE: 1994-12-01
/ NUMBER OF SEQ ID NOS: 14528
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 4608
/ LENGTH: 10
/ TYPE: PRT
/ ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-4608
```

Query Match 24.3%; Score 28; DB 7; Length 10;  
Best Local Similarity 57.1%; Pred. No. 58;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 IPHPTNI 8  
| | | | :  
Db 4 IPHPAGL 10

## RESULT 29

US-11-045-024-10231  
Sequence 10231, Application US/11045024  
Publication No. US20050271676A1  
GENERAL INFORMATION:

APPLICANT: Sette, Alessandro  
APPLICANT: Sidney, John  
APPLICANT: Southwood, Scott  
APPLICANT: Livingston, Brian  
APPLICANT: Cheenut, Robert  
APPLICANT: Baker, Denise Marie  
APPLICANT: Cello, Esteban  
APPLICANT: Kubo, Ralph  
APPLICANT: Grey, Howard M.  
APPLICANT: EpiImmune Inc.  
TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency  
TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions  
FILE REFERENCE: 2060.0040007  
CURRENT APPLICATION NUMBER: US/11/045,024  
CURRENT FILING DATE: 2005-01-28  
PRIOR APPLICATION NUMBER: US 09/412,863  
PRIOR FILING DATE: 1999-10-05  
PRIOR APPLICATION NUMBER: US 08/027,146  
PRIOR FILING DATE: 1993-03-05  
PRIOR APPLICATION NUMBER: US 08/073,205  
PRIOR FILING DATE: 1993-06-04  
PRIOR APPLICATION NUMBER: US 08/103,396  
PRIOR FILING DATE: 1993-08-06  
PRIOR APPLICATION NUMBER: US 08/159,184  
PRIOR FILING DATE: 1993-11-29  
PRIOR APPLICATION NUMBER: US 08/159,339  
PRIOR FILING DATE: 1993-11-29  
PRIOR APPLICATION NUMBER: US 08/205,713  
PRIOR FILING DATE: 1994-03-04  
PRIOR APPLICATION NUMBER: US 08/347,610  
PRIOR FILING DATE: 1994-12-01  
NUMBER OF SEQ ID NOS: 14528  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 10231  
LENGTH: 10  
TYPE: PRT  
ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS  
US-11-045-024-10231

Query Match 24.3%; Score 28; DB 7; Length 10;  
Best Local Similarity 57.1%; Pred. No. 58;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 IPHPTNI 8  
| | | | :  
Db 3 IPHPAGL 9

## RESULT 30

US-11-045-024-12095  
Sequence 12095, Application US/11045024  
Publication No. US20050271676A1  
GENERAL INFORMATION:

APPLICANT: Sette, Alessandro  
APPLICANT: Sidney, John  
APPLICANT: Southwood, Scott  
APPLICANT: Livingston, Brian  
APPLICANT: Cheenut, Robert

APPLICANT: Baker, Denise Marie  
APPLICANT: Cello, Esteban  
APPLICANT: Kubo, Ralph  
APPLICANT: Grey, Howard M.  
APPLICANT: EpiImmune Inc.  
TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency  
TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions  
FILE REFERENCE: 2060.0040007  
CURRENT APPLICATION NUMBER: US/11/045,024  
CURRENT FILING DATE: 2005-01-28  
PRIOR APPLICATION NUMBER: US 09/412,863  
PRIOR FILING DATE: 1999-10-05  
PRIOR APPLICATION NUMBER: US 08/027,146  
PRIOR FILING DATE: 1993-03-05  
PRIOR APPLICATION NUMBER: US 08/073,205  
PRIOR FILING DATE: 1993-06-04  
PRIOR APPLICATION NUMBER: US 08/103,396  
PRIOR FILING DATE: 1993-08-06  
PRIOR APPLICATION NUMBER: US 08/159,184  
PRIOR FILING DATE: 1993-11-29  
PRIOR APPLICATION NUMBER: US 08/159,339  
PRIOR FILING DATE: 1993-11-29  
PRIOR APPLICATION NUMBER: US 08/205,713  
PRIOR FILING DATE: 1994-03-04  
PRIOR APPLICATION NUMBER: US 08/347,610  
PRIOR FILING DATE: 1994-12-01  
NUMBER OF SEQ ID NOS: 14528  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 12095  
LENGTH: 10  
TYPE: PRT  
ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS  
US-11-045-024-12095

Query Match 24.3%; Score 28; DB 7; Length 10;  
Best Local Similarity 57.1%; Pred. No. 58;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 IPHPTNI 8  
| | | | :  
Db 3 IPHPAGL 9

## RESULT 31

US-11-045-024-2288  
Sequence 2288, Application US/11045024  
Publication No. US20050271676A1  
GENERAL INFORMATION:

APPLICANT: Sette, Alessandro  
APPLICANT: Sidney, John  
APPLICANT: Southwood, Scott  
APPLICANT: Livingston, Brian  
APPLICANT: Cheenut, Robert  
APPLICANT: Baker, Denise Marie  
APPLICANT: Cello, Esteban  
APPLICANT: Kubo, Ralph  
APPLICANT: Grey, Howard M.  
APPLICANT: EpiImmune Inc.  
TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency  
TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions  
FILE REFERENCE: 2060.0040007  
CURRENT APPLICATION NUMBER: US/11/045,024  
CURRENT FILING DATE: 2005-01-28  
PRIOR APPLICATION NUMBER: US 09/412,863  
PRIOR FILING DATE: 1999-10-05  
PRIOR APPLICATION NUMBER: US 08/027,146  
PRIOR FILING DATE: 1993-03-05  
PRIOR APPLICATION NUMBER: US 08/073,205  
PRIOR FILING DATE: 1993-06-04  
PRIOR APPLICATION NUMBER: US 08/103,396  
PRIOR FILING DATE: 1993-08-06  
PRIOR APPLICATION NUMBER: US 08/159,184  
PRIOR FILING DATE: 1993-11-29

```
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2288
; LENGTH: 11
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-2288
```

```
Query Match      24.3% Score 28; DB 7; Length 11;
Best Local Similarity 57.1%; Pred. No. 64;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      2 IPHPTVI 8
      |||||
      :
Db      5 IPHPAGL 11
```

```
RESULT 32
US-11-045-024-3375
; Sequence 3375, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Cheenut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Celis, Esteban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3375
; LENGTH: 11
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-3375
```

```
Query Match      24.3% Score 28; DB 7; Length 11;
Best Local Similarity 57.1%; Pred. No. 64;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      2 IPHPTVI 8
      |||||
      :
```

```
Db      4 IPHPAGL 10
```

```
RESULT 33
US-11-045-024-10232
; Sequence 10232, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Cheenut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Celis, Esteban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10232
; LENGTH: 11
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-10232
```

```
Query Match      24.3% Score 28; DB 7; Length 11;
Best Local Similarity 57.1%; Pred. No. 64;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      2 IPHPTVI 8
      |||||
      :
Db      4 IPHPAGL 10
```

```
RESULT 34
US-11-045-024-12096
; Sequence 12096, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Cheenut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Celis, Esteban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
```

```
/ FILE REFERENCE: 2060.0040007
/ CURRENT APPLICATION NUMBER: US/11/045.024
/ CURRENT FILING DATE: 2005-01-28
/ PRIOR APPLICATION NUMBER: US 09/412,863
/ PRIOR FILING DATE: 1999-10-05
/ PRIOR APPLICATION NUMBER: US 08/027,146
/ PRIOR FILING DATE: 1993-03-05
/ PRIOR APPLICATION NUMBER: US 08/073,205
/ PRIOR FILING DATE: 1993-06-04
/ PRIOR APPLICATION NUMBER: US 08/103,396
/ PRIOR FILING DATE: 1993-08-06
/ PRIOR APPLICATION NUMBER: US 08/159,184
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/159,339
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/205,713
/ PRIOR FILING DATE: 1994-03-04
/ PRIOR APPLICATION NUMBER: US 08/347,610
/ PRIOR FILING DATE: 1994-12-01
/ NUMBER OF SEQ ID NOS: 14528
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 12096
/ LENGTH: 11
/ TYPE: PRT
/ ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-12096
```

```
Query Match          24.3% Score 28; DB 7; Length 11;
Best Local Similarity 57.1%; Pred. No. 64;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 2 IHPPTNI 8
DB 4 IHPPTAGL 10
```

```
RESULT 35
US-11-045-024-13150
/ Sequence 13150, Application US/11045024
/ Publication No. US20050271676A1
/ GENERAL INFORMATION:
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Livingston, Brian
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Baker, Denise Marie
/ APPLICANT: Celis, Sørensen
/ APPLICANT: Kubo, Ralph
/ APPLICANT: Grey, Howard M.
/ APPLICANT: EpiMune Inc.
/ TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
/ TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
/ FILE REFERENCE: 2060.0040007
/ CURRENT APPLICATION NUMBER: US/11/045.024
/ CURRENT FILING DATE: 2005-01-28
/ PRIOR APPLICATION NUMBER: US 09/412,863
/ PRIOR FILING DATE: 1999-10-05
/ PRIOR APPLICATION NUMBER: US 08/027,146
/ PRIOR FILING DATE: 1993-03-05
/ PRIOR APPLICATION NUMBER: US 08/073,205
/ PRIOR FILING DATE: 1993-06-04
/ PRIOR APPLICATION NUMBER: US 08/103,396
/ PRIOR FILING DATE: 1993-08-06
/ PRIOR APPLICATION NUMBER: US 08/159,184
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/159,339
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/205,713
/ PRIOR FILING DATE: 1994-03-04
/ PRIOR APPLICATION NUMBER: US 08/347,610
/ PRIOR FILING DATE: 1994-12-01
/ NUMBER OF SEQ ID NOS: 14528
```

```
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 13150
/ LENGTH: 15
/ TYPE: PRT
/ ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-13150
```

```
Query Match          24.3% Score 28; DB 7; Length 15;
Best Local Similarity 57.1%; Pred. No. 88;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 2 IHPPTNI 8
DB 8 IHPPTAGL 14
```

```
RESULT 36
US-10-967-671-10
/ Sequence 10, Application US/10967671
/ Publication No. US20050245728A1
/ GENERAL INFORMATION:
/ APPLICANT: EDWARDS, ALBD
/ APPLICANT: DHARAMSI, AKIL
/ APPLICANT: VEDADI, MASOUD
/ APPLICANT: KIMBER, MATTHEW
/ APPLICANT: VALDES, FRANCIS
/ TITLE OF INVENTION: NOVEL PURIFIED POLYPEPTIDES FROM PSEUDOMONAS AERUGINOSA
/ FILE REFERENCE: IPT-261.01
/ CURRENT APPLICATION NUMBER: US/10/967,671
/ CURRENT FILING DATE: 2004-10-18
/ PRIOR APPLICATION NUMBER: PCT/CA03/00714
/ PRIOR FILING DATE: 2003-05-21
/ PRIOR APPLICATION NUMBER: 60/382,443
/ PRIOR FILING DATE: 2002-05-21
/ NUMBER OF SEQ ID NOS: 18
/ SOFTWARE: PatentIn Ver. 3.3
/ SEQ ID NO 10
/ LENGTH: 16
/ TYPE: PRT
/ ORGANISM: Pseudomonas aeruginosa
US-10-967-671-10
```

```
Query Match          24.3% Score 28; DB 6; Length 16;
Best Local Similarity 44.4%; Pred. No. 94;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 11 YLVCSGNG 19
DB 7 YLVCSGNG 15
```

```
RESULT 37
US-11-033-039-792
/ Sequence 792, Application US/11033039
/ Publication No. US20060002947A1
/ GENERAL INFORMATION:
/ APPLICANT: HUMPHREYS, ROBERT
/ APPLICANT: XU, MINZHEN
/ TITLE OF INVENTION: LI-KEY/ANTIGENIC EPIOTOPE HYBRID PEPTIDE VACCINES
/ FILE REFERENCE: RH-2017US01
/ CURRENT APPLICATION NUMBER: US/11/033,039
/ CURRENT FILING DATE: 2005-01-11
/ PRIOR APPLICATION NUMBER: 10/245,871
/ PRIOR FILING DATE: 2002-09-17
/ PRIOR APPLICATION NUMBER: 10/197,000
/ PRIOR FILING DATE: 2002-07-17
/ PRIOR APPLICATION NUMBER: 09/396,813
/ PRIOR FILING DATE: 1999-09-14
/ NUMBER OF SEQ ID NOS: 1452
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 792
/ LENGTH: 13
/ TYPE: PRT
```

ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
OTHER INFORMATION: hybrid peptide  
US-11-033-039-792

Query Match 23.5%; Score 27; DB 7; Length 13;  
Best Local Similarity 40.0%; Pred. No. 1.1e+02;  
Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 10 KLVCSVNG 19  
|:|:|:|:  
Db 4 KFLVSGTIQG 13

RESULT 38  
US-10-880-238-115  
Sequence 115, Application US/10880238  
Publication No. US20050287538A1  
GENERAL INFORMATION:

APPLICANT: Cheng, Ming-Tai  
TITLE OF INVENTION: FRAME-SHIFTING PCR FOR GERMLINE  
TITLE OF INVENTION: IMMUNOGLOBULIN GENES RETRIEVAL AND ANTIBODY ENGINEERING  
FILE REFERENCE: 17329-003001  
CURRENT APPLICATION NUMBER: US/10/880,238  
CURRENT FILING DATE: 2004-06-29  
NUMBER OF SEQ ID NOS: 214  
SOFTWARE: PaeSeq for windows Version 4.0  
SEQ ID NO 115  
LENGTH: 19  
TYPE: PRF  
ORGANISM: Artificial Sequence  
FEATURE:

OTHER INFORMATION: Synthetically generated peptide  
US-10-880-238-115

Query Match 23.5%; Score 27; DB 6; Length 19;  
Best Local Similarity 36.8%; Pred. No. 1.6e+02;  
Matches 7; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

Qy 1 DIPHTNHHKLVCSVNG 19  
|:|:|:|:  
Db 1 EIRSKANMHTYAAESVKG 19

RESULT 39  
US-11-033-039-794  
Sequence 794, Application US/11033039  
Publication No. US20060002947A1  
GENERAL INFORMATION:

APPLICANT: HUMPHREYS, ROBERT  
APPLICANT: XU, MINZHEN  
TITLE OF INVENTION: LI-KEY/ANTIGENIC EPIOTOPE HYBRID PEPTIDE VACCINES  
FILE REFERENCE: REH-2017US01  
CURRENT APPLICATION NUMBER: US/11/033,039  
CURRENT FILING DATE: 2005-01-11  
PRIOR APPLICATION NUMBER: 10/245,871  
PRIOR FILING DATE: 2002-09-17  
PRIOR APPLICATION NUMBER: 10/197,000  
PRIOR FILING DATE: 2002-07-17  
PRIOR APPLICATION NUMBER: 09/396,813  
PRIOR FILING DATE: 1999-09-14  
NUMBER OF SEQ ID NOS: 1452  
SOFTWARE: Patentin version 3.3  
SEQ ID NO 794  
LENGTH: 19  
TYPE: PRF  
ORGANISM: Artificial Sequence  
FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
OTHER INFORMATION: hybrid peptide  
US-11-033-039-794

Query Match 23.5%; Score 27; DB 7; Length 19;  
Best Local Similarity 40.0%; Pred. No. 1.6e+02;  
Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 10 KLVCSVNG 19  
|:|:|:|:  
Db 4 KFLVSGTIQG 13

RESULT 40  
US-10-467-657-9183  
Sequence 9183, Application US/10467657  
Publication No. US20050260581A1  
GENERAL INFORMATION:

APPLICANT: CHIRON SPA  
APPLICANT: FONTANA Maria Rita  
APPLICANT: PIZZA Mariagrazia  
APPLICANT: MASNIGANI Vega  
APPLICANT: MONACI Elisabetta  
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS  
FILE REFERENCE:  
CURRENT APPLICATION NUMBER: US/10/467,657  
CURRENT FILING DATE: 2003-08-11  
PRIOR APPLICATION NUMBER: GB-0103424.8  
PRIOR FILING DATE: 2001-02-12  
NUMBER OF SEQ ID NOS: 9218  
SOFTWARE: SeqWin99, version 1.04  
SEQ ID NO 9183  
LENGTH: 20  
TYPE: PRF  
ORGANISM: Neisseria gonorrhoeae  
US-10-467-657-9183

Query Match 23.5%; Score 27; DB 6; Length 20;  
Best Local Similarity 31.2%; Pred. No. 1.7e+02;  
Matches 5; Conservative 2; Mismatches 9; Indels 0; Gaps 0;

Qy 5 PTNHHKLVCSVNG 20  
|:|:|:|:  
Db 1 PATISCKIYCVIRINNG 16

RESULT 41  
US-11-119-581-113

Sequence 113, Application US/11119581  
Publication No. US20050250699A1  
GENERAL INFORMATION:  
APPLICANT: Hogenhaug, Hans-Henrik Kristensen  
APPLICANT: Myglind, Per Holse  
APPLICANT: Segura, Dorotea Raventos  
APPLICANT: Taboureau, Olivier  
APPLICANT: Sonksen, Carsten Peter  
TITLE OF INVENTION: Antimicrobial Peptides  
FILE REFERENCE: 10646.200-US  
CURRENT APPLICATION NUMBER: US/11/119,581  
CURRENT FILING DATE: 2005-05-02  
NUMBER OF SEQ ID NOS: 114  
SOFTWARE: Patentin version 3.3  
SEQ ID NO 113  
LENGTH: 18  
TYPE: PRF  
ORGANISM: Artificial

FEATURE:  
OTHER INFORMATION: Synthetic antimicrobial polypeptide  
US-11-119-581-113

Query Match 23.0%; Score 26.5; DB 7; Length 18;  
Best Local Similarity 25.0%; Pred. No. 1.9e+02;  
Matches 3; Conservative 7; Mismatches 1; Indels 1; Gaps 1;

Qy 7 NHHKLVCSVN 18  
|:|:|:|:|:  
|:|:|:|:|:

Db 2 NLHR-IICKGTH 12

## RESULT 42

US-10-956-755A-55  
; Sequence 55, Application US/10956755A  
; Publication No. US20050282747A1  
; GENERAL INFORMATION:  
; APPLICANT: Clark, Richard A.  
; TITLE OF INVENTION: Methods and Compositions for Wound Healing  
; FILE REFERENCE: STONYB-09223  
; CURRENT APPLICATION NUMBER: US/10/956, 755A  
; CURRENT FILING DATE: 2004-10-01  
; NUMBER OF SEQ ID NOS: 100  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 55  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
US-10-956-755A-55

Query Match 22.6%; Score 26; DB 6; Length 5;  
Best Local Similarity 100.0%; Pred. No. 5.5e+04;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 HPTN 7  
|||||  
Db 1 HPTN 4

## RESULT 43

US-10-956-755A-73  
; Sequence 73, Application US/10956755A  
; Publication No. US20050282747A1  
; GENERAL INFORMATION:  
; APPLICANT: Clark, Richard A.  
; TITLE OF INVENTION: Methods and Compositions for Wound Healing  
; FILE REFERENCE: STONYB-09223  
; CURRENT APPLICATION NUMBER: US/10/956, 755A  
; CURRENT FILING DATE: 2004-10-01  
; NUMBER OF SEQ ID NOS: 100  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 73  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
US-10-956-755A-73

Query Match 22.6%; Score 26; DB 6; Length 5;  
Best Local Similarity 100.0%; Pred. No. 5.5e+04;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 HPTN 7  
|||||  
Db 1 HPTN 4

## RESULT 44

US-10-956-755A-91  
; Sequence 91, Application US/10956755A  
; Publication No. US20050282747A1  
; GENERAL INFORMATION:  
; APPLICANT: Clark, Richard A.  
; TITLE OF INVENTION: Methods and Compositions for Wound Healing  
; FILE REFERENCE: STONYB-09223  
; CURRENT APPLICATION NUMBER: US/10/956, 755A

; CURRENT FILING DATE: 2004-10-01

; NUMBER OF SEQ ID NOS: 100

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 91

; LENGTH: 5

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:  
; OTHER INFORMATION: Synthetic  
US-10-956-755A-91

Query Match 22.6%; Score 26; DB 6; Length 5;  
Best Local Similarity 100.0%; Pred. No. 5.5e+04;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 HPTN 7  
|||||  
Db 1 HPTN 4

## RESULT 45

US-11-045-024-1626  
; Sequence 1626, Application US/11045024  
; Publication No. US20050271676A1  
; GENERAL INFORMATION:  
; APPLICANT: Sette, Alessandro  
; APPLICANT: Sidney, John  
; APPLICANT: Southwood, Scott  
; APPLICANT: Livingston, Brian  
; APPLICANT: Chesnut, Robert  
; APPLICANT: Baker, Denise Marie  
; APPLICANT: Celis, Betteban  
; APPLICANT: Kudo, Ralph  
; APPLICANT: Grey, Howard M.  
; APPLICANT: Bpimmune Inc.  
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency  
; FILE REFERENCE: 2060, 0040007  
; CURRENT APPLICATION NUMBER: US/11/045, 024  
; CURRENT FILING DATE: 2005-01-28  
; PRIOR APPLICATION NUMBER: US 09/412, 863  
; PRIOR FILING DATE: 1999-10-05  
; PRIOR APPLICATION NUMBER: US 08/027, 146  
; PRIOR FILING DATE: 1993-03-05  
; PRIOR APPLICATION NUMBER: US 08/073, 205  
; PRIOR FILING DATE: 1993-06-04  
; PRIOR APPLICATION NUMBER: US 08/103, 396  
; PRIOR FILING DATE: 1993-08-06  
; PRIOR APPLICATION NUMBER: US 08/159, 184  
; PRIOR FILING DATE: 1993-11-29  
; PRIOR APPLICATION NUMBER: US 08/159, 339  
; PRIOR FILING DATE: 1993-11-29  
; PRIOR APPLICATION NUMBER: US 08/205, 713  
; PRIOR FILING DATE: 1994-03-04  
; PRIOR APPLICATION NUMBER: US 08/347, 610  
; PRIOR FILING DATE: 1994-12-01  
; NUMBER OF SEQ ID NOS: 14528  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1626  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS  
US-11-045-024-1626

Query Match 22.6%; Score 26; DB 7; Length 8;  
Best Local Similarity 100.0%; Pred. No. 5.5e+04;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 IHPH 5  
|||||  
Db 4 IHPH 7

```
RESULT 46
US-11-045-024-10228
; Sequence 10228, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Cells, Esteban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: EpiMune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0040007
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US/11/045,024
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10228
; LENGTH: 8
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-10228

Query Match          22.6%; Score 26; DB 7; Length 8;
Best Local Similarity 100.0%; Pred. No. 5.5e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-859-643-17

Query Match          22.6%; Score 26; DB 6; Length 9;
Best Local Similarity 57.1%; Pred. No. 5.5e+04;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      1 DIPPTN 7
|:|:|:
Db      3 DVPIPTH 9

RESULT 48
US-11-097-864-17
; Sequence 17, Application US/11097864
; Publication No. US20050265924A1
; GENERAL INFORMATION:
; APPLICANT: Chailita-Bid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 161P2FI0B
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF CANCER
; FILE REFERENCE: 511582006205
; CURRENT FILING DATE: 2005-04-01
; PRIOR APPLICATION NUMBER: US/11/097,864
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 10/062,109
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapien
US-11-097-864-17

Query Match          22.6%; Score 26; DB 7; Length 9;
Best Local Similarity 57.1%; Pred. No. 5.5e+04;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      1 DIPPTN 7
|:|:|:
Db      3 DVPIPTH 9

RESULT 49
US-11-097-912-17
; Sequence 17, Application US/11097912
; Publication No. US20050265921A1
; GENERAL INFORMATION:
; APPLICANT: Chailita-Bid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 161P2FI0B
; TITLE OF INVENTION: USEFUL IN TREATMENT AND DETECTION OF CANCER
; FILE REFERENCE: 511582006204
; CURRENT FILING DATE: US/11/097,912
; PRIOR APPLICATION NUMBER: US 10/062,109
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
```



```
/ NUMBER OF SEQ ID NOS: 765
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 17
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Homo Sapien
US-11-097-912-17
```

```
Query Match          22.6%; Score 26; DB 7; Length 9;
Best Local Similarity 57.1%; Pred. No. 5.5e+04;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 DHPPTN 7
        |||||
Db       3 DVPDPTH 9
```

```
RESULT 50
US-11-045-024-1831
/ Sequence 1831, Application US/11045024
/ Publication No. US20050271676A1
/ GENERAL INFORMATION:
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Livingston, Brian
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Baker, Denise Marie
/ APPLICANT: Celis, Bstedan
/ APPLICANT: Kubo, Ralph
/ APPLICANT: Grey, Howard M.
/ APPLICANT: Bpimmune Inc.
/ TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
/ TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
/ FILE REFERENCE: 2060.0040007
/ CURRENT APPLICATION NUMBER: US/11/045,024
/ CURRENT FILING DATE: 2005-01-28
/ PRIOR APPLICATION NUMBER: US 09/412,863
/ PRIOR FILING DATE: 1999-10-05
/ PRIOR APPLICATION NUMBER: US 08/027,146
/ PRIOR FILING DATE: 1993-03-05
/ PRIOR APPLICATION NUMBER: US 08/073,205
/ PRIOR FILING DATE: 1993-06-04
/ PRIOR APPLICATION NUMBER: US 08/103,396
/ PRIOR FILING DATE: 1993-08-06
/ PRIOR APPLICATION NUMBER: US 08/159,184
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/159,339
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/205,713
/ PRIOR FILING DATE: 1994-03-04
/ PRIOR APPLICATION NUMBER: US 08/347,610
/ NUMBER OF SEQ ID NOS: 14528
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 1831
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-1831
```

```
Query Match          22.6%; Score 26; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 5.5e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      2 IPHP 5
        |||||
Db       5 IPHP 8
```

```
RESULT 51
US-11-045-024-13806
/ Sequence 13806, Application US/11045024
```

```
/ Publication No. US20050271676A1
/ GENERAL INFORMATION:
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Livingston, Brian
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Baker, Denise Marie
/ APPLICANT: Celis, Bstedan
/ APPLICANT: Kubo, Ralph
/ APPLICANT: Grey, Howard M.
/ APPLICANT: Bpimmune Inc.
/ TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
/ TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
/ FILE REFERENCE: 2060.0040007
/ CURRENT APPLICATION NUMBER: US/11/045,024
/ CURRENT FILING DATE: 2005-01-28
/ PRIOR APPLICATION NUMBER: US 09/412,863
/ PRIOR FILING DATE: 1999-10-05
/ PRIOR APPLICATION NUMBER: US 08/027,146
/ PRIOR FILING DATE: 1993-03-05
/ PRIOR APPLICATION NUMBER: US 08/073,205
/ PRIOR FILING DATE: 1993-06-04
/ PRIOR APPLICATION NUMBER: US 08/103,396
/ PRIOR FILING DATE: 1993-08-06
/ PRIOR APPLICATION NUMBER: US 08/159,184
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/159,339
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/205,713
/ PRIOR FILING DATE: 1994-03-04
/ PRIOR APPLICATION NUMBER: US 08/347,610
/ PRIOR FILING DATE: 1994-12-01
/ NUMBER OF SEQ ID NOS: 14528
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 13806
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-13806
```

```
Query Match          22.6%; Score 26; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 5.5e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      2 IPHP 5
        |||||
Db       5 IPHP 8
```

```
RESULT 52
US-11-041-893-64
/ Sequence 64, Application US/11041893
/ Publication No. US20060002941A1
/ GENERAL INFORMATION:
/ APPLICANT: Mahatra, Gregory G.
/ TITLE OF INVENTION: COMPOSITIONS COMPRISING IMMUNE RESPONSE
/ TITLE OF INVENTION: ALTERING AGENTS AND METHODS OF USE
/ FILE REFERENCE: 100123.401
/ CURRENT APPLICATION NUMBER: US/11/041,893
/ CURRENT FILING DATE: 2005-01-24
/ PRIOR APPLICATION NUMBER: US 60/616,855
/ PRIOR FILING DATE: 2004-10-06
/ PRIOR APPLICATION NUMBER: US 60/538,713
/ PRIOR FILING DATE: 2004-01-23
/ NUMBER OF SEQ ID NOS: 295
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 64
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Bacterioides coli
US-11-041-893-64
```

Query Match 22.6%; Score 26; DB 7; Length 9;  
Best Local Similarity 66.7%; Pred. No. 5.5e+04;  
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 DHPPTN 8  
|:|:|:  
DB 2 PHPPTN 7

RESULT 53  
US-10-859-643-53  
; Sequence 53, Application US/10859643  
; Publication No. US20060002993A1  
; GENERAL INFORMATION:  
; APPLICANT: Chailita-Bid, Pia M.  
; APPLICANT: Raitano, Arthur B.  
; APPLICANT: Farris, Mary  
; APPLICANT: Hubert, Rene S.  
; APPLICANT: Morrison, Karen Jane Meyrick  
; APPLICANT: Jakobovits, Aya  
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein  
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of  
; TITLES OF INVENTION: Cancer  
; FILE REFERENCE: 511582006203  
; CURRENT APPLICATION NUMBER: US/10/859,643  
; CURRENT FILING DATE: 2004-06-02  
; PRIOR APPLICATION NUMBER: US 10/005,480  
; PRIOR FILING DATE: 2001-11-07  
; NUMBER OF SEQ ID NOS: 765  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 53  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-859-643-53

Query Match 22.6%; Score 26; DB 6; Length 10;  
Best Local Similarity 57.1%; Pred. No. 1.2e+02;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 DHPPTN 7  
|:|:|:  
DB 3 DVPIPTH 9

RESULT 54  
US-11-097-864-53  
; Sequence 53, Application US/11097864  
; Publication No. US20050265924A1  
; GENERAL INFORMATION:  
; APPLICANT: Chailita-Bid, Pia M.  
; APPLICANT: Raitano, Arthur B.  
; APPLICANT: Farris, Mary  
; APPLICANT: Hubert, Rene S.  
; APPLICANT: Morrison, Karen Jane Meyrick  
; APPLICANT: Jakobovits, Aya  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 161P2F10B  
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF CANCER  
; FILE REFERENCE: 511582006205  
; CURRENT APPLICATION NUMBER: US/11/097,864  
; CURRENT FILING DATE: 2005-04-01  
; PRIOR APPLICATION NUMBER: US 10/062,109  
; PRIOR FILING DATE: 2002-01-31  
; PRIOR APPLICATION NUMBER: US 10/005,480  
; PRIOR FILING DATE: 2001-11-07  
; NUMBER OF SEQ ID NOS: 765  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 53  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-11-097-864-53

Query Match 22.6%; Score 26; DB 7; Length 10;  
Best Local Similarity 57.1%; Pred. No. 1.2e+02;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 DHPPTN 7  
|:|:|:  
DB 3 DVPIPTH 9

RESULT 55  
US-11-097-912-53  
; Sequence 53, Application US/11097912  
; Publication No. US20050265921A1  
; GENERAL INFORMATION:  
; APPLICANT: Chailita-Bid, Pia M.  
; APPLICANT: Raitano, Arthur B.  
; APPLICANT: Farris, Mary  
; APPLICANT: Hubert, Rene S.  
; APPLICANT: Morrison, Karen Jane Meyrick  
; APPLICANT: Jakobovits, Aya  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 161P2F10B  
; TITLE OF INVENTION: USEFUL IN TREATMENT AND DETECTION OF CANCER  
; FILE REFERENCE: 511582006204  
; CURRENT APPLICATION NUMBER: US/11/097,912  
; CURRENT FILING DATE: 2005-04-01  
; PRIOR APPLICATION NUMBER: US 10/062,109  
; PRIOR FILING DATE: 2002-01-31  
; PRIOR APPLICATION NUMBER: US 10/005,480  
; PRIOR FILING DATE: 2001-11-07  
; NUMBER OF SEQ ID NOS: 765  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 53  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-11-097-912-53

Query Match 22.6%; Score 26; DB 7; Length 10;  
Best Local Similarity 57.1%; Pred. No. 1.2e+02;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 DHPPTN 7  
|:|:|:  
DB 3 DVPIPTH 9

RESULT 56  
US-11-045-024-2072  
; Sequence 2072, Application US/11045024  
; Publication No. US20050271676A1  
; GENERAL INFORMATION:  
; APPLICANT: Sette, Alessandro  
; APPLICANT: Sidney, John  
; APPLICANT: Southwood, Scott  
; APPLICANT: Livingston, Brian  
; APPLICANT: Chesnut, Robert  
; APPLICANT: Baker, Denise Marie  
; APPLICANT: Celis, Eusebio  
; APPLICANT: Kubo, Ralph  
; APPLICANT: Grey, Howard M.  
; APPLICANT: EpiImmune Inc.  
; TITLE OF INVENTION: Reducing Cellular Responses to Human Immunodeficiency  
; TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions  
; FILE REFERENCE: 2060.0040007  
; CURRENT APPLICATION NUMBER: US/11/045,024  
; CURRENT FILING DATE: 2005-01-28  
; PRIOR APPLICATION NUMBER: US 09/412,863  
; PRIOR FILING DATE: 1999-10-05  
; PRIOR APPLICATION NUMBER: US 08/027,146  
; PRIOR FILING DATE: 1993-03-05  
; PRIOR APPLICATION NUMBER: US 08/073,205  
; PRIOR FILING DATE: 1993-06-04  
; PRIOR APPLICATION NUMBER: US 08/103,396

PRIOR FILING DATE: 1993-08-06  
PRIOR APPLICATION NUMBER: US 08/159,184  
PRIOR FILING DATE: 1993-11-29  
PRIOR APPLICATION NUMBER: US 08/159,339  
PRIOR FILING DATE: 1993-11-29  
PRIOR APPLICATION NUMBER: US 08/205,713  
PRIOR FILING DATE: 1994-03-04  
PRIOR APPLICATION NUMBER: US 08/347,610  
PRIOR FILING DATE: 1994-12-01  
NUMBER OF SEQ ID NOS: 14528  
SOFTWARE: PaSeq for Windows Version 4.0  
SEQ ID NO 2072  
LENGTH: 10  
TYPE: PRT  
ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS  
US-11-045-024-2072

Query Match 22.6%; Score 26; DB 7; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 IHPH 5  
DB 6 IHPH 9

RESULT 57  
US-11-045-024-10220  
Sequence 10220, Application US/11045024  
Publication No. US20050271676A1  
GENERAL INFORMATION:  
APPLICANT: Sette, Alessandro  
APPLICANT: Sidney, John  
APPLICANT: Southwood, Scott  
APPLICANT: Livingston, Brian  
APPLICANT: Chesnut, Robert  
APPLICANT: Baker, Denise Marie  
APPLICANT: Celis, Basteen  
APPLICANT: Kubo, Ralph  
APPLICANT: Grey, Howard M.  
APPLICANT: Eptimmune Inc.  
TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency  
TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions  
FILE REFERENCE: 2060, 0040007  
CURRENT APPLICATION NUMBER: US/11/045,024  
CURRENT FILING DATE: 2005-01-28  
PRIOR APPLICATION NUMBER: US 09/412,863  
PRIOR FILING DATE: 1999-10-05  
PRIOR APPLICATION NUMBER: US 08/027,146  
PRIOR FILING DATE: 1993-03-05  
PRIOR APPLICATION NUMBER: US 08/073,205  
PRIOR FILING DATE: 1993-06-04  
PRIOR APPLICATION NUMBER: US 08/103,396  
PRIOR FILING DATE: 1993-08-06  
PRIOR APPLICATION NUMBER: US 08/159,184  
PRIOR FILING DATE: 1993-11-29  
PRIOR APPLICATION NUMBER: US 08/159,339  
PRIOR FILING DATE: 1993-11-29  
PRIOR APPLICATION NUMBER: US 08/205,713  
PRIOR FILING DATE: 1994-03-04  
PRIOR APPLICATION NUMBER: US 08/347,610  
PRIOR FILING DATE: 1994-12-01  
NUMBER OF SEQ ID NOS: 14528  
SOFTWARE: PaSeq for Windows Version 4.0  
SEQ ID NO 10220  
LENGTH: 10  
TYPE: PRT  
ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS  
US-11-045-024-10220

Query Match 22.6%; Score 26; DB 7; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 IHPH 5  
DB 6 IHPH 9

RESULT 58  
US-11-033-039-381  
Sequence 381, Application US/11033039  
Publication No. US20060002947A1  
GENERAL INFORMATION:  
APPLICANT: HUMPHREYS, ROBERT  
APPLICANT: XU, MINZHEN  
TITLE OF INVENTION: LI-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES  
FILE REFERENCE: RSH-201/US01  
CURRENT APPLICATION NUMBER: US/11/033,039  
CURRENT FILING DATE: 2005-01-11  
PRIOR APPLICATION NUMBER: 10/245,871  
PRIOR FILING DATE: 2002-09-17  
PRIOR APPLICATION NUMBER: 10/197,000  
PRIOR FILING DATE: 2002-07-17  
PRIOR APPLICATION NUMBER: 09/396,813  
PRIOR FILING DATE: 1999-09-14  
NUMBER OF SEQ ID NOS: 1452  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 381  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-11-033-039-381

Query Match 22.6%; Score 26; DB 7; Length 10;  
Best Local Similarity 30.0%; Pred. No. 1.2e+02;  
Matches 3; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 4 HPTNHLYV 13  
DB 1 HPQKTKFMH 10

RESULT 59  
US-10-511-559-126  
Sequence 126, Application US/10511559  
Publication No. US20050256304A1  
GENERAL INFORMATION:  
APPLICANT: JONES, Tim  
APPLICANT: BAKER, Matthew  
APPLICANT: CARR, Francis J.  
TITLE OF INVENTION: MODIFIED FACTOR VIII  
FILE REFERENCE: MER-133  
CURRENT APPLICATION NUMBER: US/10/511,559  
CURRENT FILING DATE: 2004-10-15  
PRIOR APPLICATION NUMBER: PCT/EP03/04063  
PRIOR FILING DATE: 2003-04-17  
PRIOR APPLICATION NUMBER: EP 02008712.8  
PRIOR FILING DATE: 2002-04-18  
PRIOR APPLICATION NUMBER: EP 03006554.4  
PRIOR FILING DATE: 2003-03-24  
NUMBER OF SEQ ID NOS: 1147  
SOFTWARE: PaSeq for Windows Version 4.0  
SEQ ID NO 126  
LENGTH: 13  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Potential Epitope of human Factor VIII  
US-10-511-559-126

Query Match 22.6%; Score 26; DB 6; Length 13;  
Best Local Similarity 50.0%; Pred. No. 1.6e+02;  
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 HPTNH 9

Db 8 HPVSLH 13

```
RESULT 60
US-10-511-559-127
; Sequence 127, Application US/10511559
; Publication No. US20050256304A1
; GENERAL INFORMATION:
; APPLICANT: JONES, Tim
; APPLICANT: BAKER, Matthew
; APPLICANT: CARR, Francis, J.
; TITLE OF INVENTION: MODIFIED FACTOR VIII
; FILE REFERENCE: MER-133
; CURRENT APPLICATION NUMBER: US/10/511,559
; CURRENT FILING DATE: 2004-10-15
; PRIOR APPLICATION NUMBER: PCT/EP03/04063
; PRIOR FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: EP 02008712.8
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: EP 03006554.4
; PRIOR FILING DATE: 2003-03-24
; NUMBER OF SEQ ID NOS: 1147
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 127
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Potential Epitope of human Factor VIII
US-10-511-559-127
```

```
Query Match 22.6%; Score 26; DB 6; Length 13;
Best Local Similarity 50.0%; Pred. No. 1.6e+02;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

QY 4 HPTNTH 9

Db 6 HPVSLH 11

```
RESULT 61
US-10-511-559-128
; Sequence 128, Application US/10511559
; Publication No. US20050256304A1
; GENERAL INFORMATION:
; APPLICANT: JONES, Tim
; APPLICANT: BAKER, Matthew
; APPLICANT: CARR, Francis, J.
; TITLE OF INVENTION: MODIFIED FACTOR VIII
; FILE REFERENCE: MER-133
; CURRENT APPLICATION NUMBER: US/10/511,559
; CURRENT FILING DATE: 2004-10-15
; PRIOR APPLICATION NUMBER: PCT/EP03/04063
; PRIOR FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: EP 02008712.8
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: EP 03006554.4
; PRIOR FILING DATE: 2003-03-24
; NUMBER OF SEQ ID NOS: 1147
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 128
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Potential Epitope of human Factor VIII
US-10-511-559-128
```

```
Query Match 22.6%; Score 26; DB 6; Length 13;
Best Local Similarity 50.0%; Pred. No. 1.6e+02;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

QY 4 HPTNTH 9

Db 2 HPVSLH 7

```
RESULT 62
US-10-511-559-129
; Sequence 129, Application US/10511559
; Publication No. US20050256304A1
; GENERAL INFORMATION:
; APPLICANT: JONES, Tim
; APPLICANT: BAKER, Matthew
; APPLICANT: CARR, Francis, J.
; TITLE OF INVENTION: MODIFIED FACTOR VIII
; FILE REFERENCE: MER-133
; CURRENT APPLICATION NUMBER: US/10/511,559
; CURRENT FILING DATE: 2004-10-15
; PRIOR APPLICATION NUMBER: PCT/EP03/04063
; PRIOR FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: EP 02008712.8
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: EP 03006554.4
; PRIOR FILING DATE: 2003-03-24
; NUMBER OF SEQ ID NOS: 1147
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 129
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Potential Epitope of human Factor VIII
US-10-511-559-129
```

```
Query Match 22.6%; Score 26; DB 6; Length 13;
Best Local Similarity 50.0%; Pred. No. 1.6e+02;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

QY 4 HPTNTH 9

Db 1 HPVSLH 6

```
RESULT 63
US-11-116-144-64
; Sequence 64, Application US/11116144
; Publication No. US20050277181A1
; GENERAL INFORMATION:
; APPLICANT: BERTHELT, FRANCOIS XAVIER
; APPLICANT: CASADEVAL, FRANCESC VAYREDA
; APPLICANT: SANZ MARIA, MARIA CRUZ
; APPLICANT: GARCIA, TERESA ILOP
; APPLICANT: OLE, ANGELS MOR
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETECTING PATHOGEN
; FILE REFERENCE: INT-084
; CURRENT APPLICATION NUMBER: US/11/116,144
; CURRENT FILING DATE: 2005-04-27
; PRIOR APPLICATION NUMBER: PCT/ES04/000581
; PRIOR FILING DATE: 2004-12-23
; PRIOR APPLICATION NUMBER: EP 03380307.3
; PRIOR FILING DATE: 2003-12-23
; NUMBER OF SEQ ID NOS: 301
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 64
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Dengue virus 3
US-11-116-144-64
```

```
Query Match 22.6%; Score 26; DB 7; Length 13;
Best Local Similarity 33.3%; Pred. No. 1.6e+02;
Matches 4; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
```

QY 3 PHPTNIRKYLVC 14  
 Db 2 PHTEVEDIDC 13

# RESULT 64

US-10-929-988-189  
 ; Sequence 189, Application US/10929988  
 ; Publication No. US2005027588A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: CINTRIA, STEVEN E.  
 ; APPLICANT: BALU, PALANI  
 ; APPLICANT: DUFFIN, DAVID J.  
 ; APPLICANT: PIPLANI, SUNILA  
 ; APPLICANT: MERRILL, BARBARA MCEOWEN  
 ; APPLICANT: SCHATZ, PETER JOSEPH  
 ; TITLE OF INVENTION: COMPOUNDS HAVING AFFINITY FOR THE GRANULOCYTE-COLONY  
 ; TITLE OF INVENTION: STIMULATING FACTOR RECEPTOR (G-CSFR) AND ASSOCIATED  
 ; FILE REFERENCE: 0300-0014  
 ; CURRENT APPLICATION NUMBER: US/10/929,988  
 ; CURRENT FILING DATE: 2004-08-30  
 ; PRIOR APPLICATION NUMBER: US/09/620,091  
 ; PRIOR FILING DATE: 2000-07-20  
 ; NUMBER OF SEQ ID NOS: 491  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 189  
 ; LENGTH: 15  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 ; OTHER INFORMATION: peptide  
 ; US-10-929-988-189

Query Match 22.6%; Score 26; DB 6; Length 15;  
 Best Local Similarity 62.5%; Pred. No. 1.9e+02;  
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 13 VCESVNGG 20  
 Db 3 LCESVGVG 10

# RESULT 65

US-11-045-024-13137  
 ; Sequence 13137, Application US/11045024  
 ; Publication No. US20050271676A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Sette, Alessandro  
 ; APPLICANT: Sidney, John  
 ; APPLICANT: Southwood, Scott  
 ; APPLICANT: Livingston, Brian  
 ; APPLICANT: Chesnut, Robert  
 ; APPLICANT: Baker, Denise Marie  
 ; APPLICANT: Celis, Esben  
 ; APPLICANT: Kubo, Ralph  
 ; APPLICANT: Grey, Howard M.  
 ; APPLICANT: EpiImmune Inc.  
 ; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency  
 ; TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions  
 ; FILE REFERENCE: 2060.0040007  
 ; CURRENT APPLICATION NUMBER: US/11/045,024  
 ; CURRENT FILING DATE: 2005-01-28  
 ; PRIOR APPLICATION NUMBER: US 09/442,863  
 ; PRIOR FILING DATE: 1999-10-05  
 ; PRIOR APPLICATION NUMBER: US 08/027,146  
 ; PRIOR FILING DATE: 1993-03-05  
 ; PRIOR APPLICATION NUMBER: US 08/073,205  
 ; PRIOR FILING DATE: 1993-06-04  
 ; PRIOR APPLICATION NUMBER: US 08/103,396  
 ; PRIOR FILING DATE: 1993-08-06  
 ; PRIOR APPLICATION NUMBER: US 08/159,184

; PRIOR FILING DATE: 1993-11-29  
 ; PRIOR APPLICATION NUMBER: US 08/159,339  
 ; PRIOR FILING DATE: 1993-11-29  
 ; PRIOR APPLICATION NUMBER: US 08/205,713  
 ; PRIOR FILING DATE: 1994-03-04  
 ; PRIOR APPLICATION NUMBER: US 08/347,610  
 ; PRIOR FILING DATE: 1994-12-01  
 ; NUMBER OF SEQ ID NOS: 14528  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 13137  
 ; LENGTH: 15  
 ; TYPE: PRT  
 ; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS  
 ; US-11-045-024-13137

Query Match 22.6%; Score 26; DB 7; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 IPRP 5  
 Db 11 IPRP 14

# RESULT 66

US-10-623-155-247  
 ; Sequence 247, Application US/10623155  
 ; Publication No. US20050261166A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wang, Tongtong  
 ; APPLICANT: Beckham, David W.  
 ; APPLICANT: Retter, Marc W.  
 ; APPLICANT: Fanger, Gary R.  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
 ; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER  
 ; FILE REFERENCE: 210121.455C20  
 ; CURRENT APPLICATION NUMBER: US/10/623,155  
 ; CURRENT FILING DATE: 2003-07-17  
 ; NUMBER OF SEQ ID NOS: 560  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 247  
 ; LENGTH: 20  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-10-623-155-247

Query Match 22.6%; Score 26; DB 6; Length 20;  
 Best Local Similarity 57.1%; Pred. No. 2.5e+02;  
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 PHPTNIRH 9  
 Db 4 PHPMVLY 10

# RESULT 67

US-11-084-717-55  
 ; Sequence 55, Application US/11084717  
 ; Publication No. US20050260736A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: GEORGIU, GEORGE  
 ; APPLICANT: JEONG, KI-JUN  
 ; APPLICANT: HARVEY, BARRETT R.  
 ; APPLICANT: IVERSON, BRENT L.  
 ; TITLE OF INVENTION: SELECTION OF BACTERIAL INNER-MEMBRANE ANCHOR POLYPEPTIDES  
 ; FILE REFERENCE: UTSB:723US  
 ; CURRENT APPLICATION NUMBER: US/11/084,717  
 ; CURRENT FILING DATE: 2005-03-18  
 ; PRIOR APPLICATION NUMBER: 60/554,324  
 ; PRIOR FILING DATE: 2004-03-18  
 ; PRIOR APPLICATION NUMBER: 10/620,278  
 ; PRIOR FILING DATE: 2003-07-15  
 ; PRIOR APPLICATION NUMBER: 60/396,058

/ PRIOR FILING DATE: 2002-07-15  
/ NUMBER OF SEQ ID NOS: 61  
/ SOFTWARE: PatentIn Ver. 2.1  
/ SEQ ID NO: 55  
/ LENGTH: 6  
/ TYPE: PRT  
/ ORGANISM: Artificial Sequence  
/ FEATURE:  
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-11-084-717-55

Query Match 21.7% Score 25; DB 7; Length 6;  
Best Local Similarity 80.0%; Pred. No. 5.5e+04;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 14 CESUN 18  
|||:  
1 PTMLK 5

DB 1 PTMLK 5

RESULT 68  
US-11-010-748A-856  
/ Sequence 856, Application US/11010748A  
/ Publication No. US20050244421A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Merck Patent GmbH  
/ APPLICANT: STRITTMAYER, Wolfgang  
/ APPLICANT: MOLL, Heidrun  
/ APPLICANT: SCHARM, Burkhard  
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING IMMUNE RESPONSE  
/ FILE REFERENCE: MER-136  
/ CURRENT APPLICATION NUMBER: US/11/010,748A  
/ PRIOR FILING DATE: 2004-12-13  
/ PRIOR APPLICATION NUMBER: PCT/EP03/06251  
/ PRIOR FILING DATE: 2003-06-13  
/ PRIOR APPLICATION NUMBER: EP02013423.5  
/ PRIOR FILING DATE: 2002-06-13  
/ NUMBER OF SEQ ID NOS: 926  
/ SOFTWARE: PatentIn version 3.1  
/ SEQ ID NO: 856  
/ LENGTH: 9  
/ TYPE: PRT  
/ ORGANISM: Artificial Sequence  
/ FEATURE:  
/ OTHER INFORMATION: HLA-binding peptide of Seq. No. 855  
US-11-010-748A-856

Query Match 21.7% Score 25; DB 7; Length 9;  
Best Local Similarity 66.7%; Pred. No. 5.5e+04;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 PTMLK 10  
|||:  
3 PTMLK 8

DB 3 PTMLK 8

RESULT 69  
US-11-010-748A-860  
/ Sequence 860, Application US/11010748A  
/ Publication No. US20050244421A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Merck Patent GmbH  
/ APPLICANT: STRITTMAYER, Wolfgang  
/ APPLICANT: MOLL, Heidrun  
/ APPLICANT: SCHARM, Burkhard  
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING IMMUNE RESPONSE  
/ FILE REFERENCE: MER-136  
/ CURRENT APPLICATION NUMBER: US/11/010,748A  
/ PRIOR FILING DATE: 2004-12-13  
/ PRIOR APPLICATION NUMBER: PCT/EP03/06251  
/ PRIOR FILING DATE: 2003-06-13  
/ PRIOR APPLICATION NUMBER: EP02013423.5

/ PRIOR FILING DATE: 2002-06-13  
/ NUMBER OF SEQ ID NOS: 926  
/ SOFTWARE: PatentIn version 3.1  
/ SEQ ID NO: 860  
/ LENGTH: 9  
/ TYPE: PRT  
/ ORGANISM: Artificial Sequence  
/ FEATURE:  
/ OTHER INFORMATION: HLA-binding peptide of Seq. No. 855  
US-11-010-748A-860

Query Match 21.7% Score 25; DB 7; Length 9;  
Best Local Similarity 66.7%; Pred. No. 5.5e+04;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 PTMLK 10  
|||:  
1 PTMLK 6

DB 1 PTMLK 6

RESULT 70  
US-11-010-748A-861  
/ Sequence 861, Application US/11010748A  
/ Publication No. US20050244421A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Merck Patent GmbH  
/ APPLICANT: STRITTMAYER, Wolfgang  
/ APPLICANT: MOLL, Heidrun  
/ APPLICANT: SCHARM, Burkhard  
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING IMMUNE RESPONSE  
/ FILE REFERENCE: MER-136  
/ CURRENT APPLICATION NUMBER: US/11/010,748A  
/ PRIOR FILING DATE: 2004-12-13  
/ PRIOR APPLICATION NUMBER: PCT/EP03/06251  
/ PRIOR FILING DATE: 2003-06-13  
/ PRIOR APPLICATION NUMBER: EP02013423.5  
/ PRIOR FILING DATE: 2002-06-13  
/ NUMBER OF SEQ ID NOS: 926  
/ SOFTWARE: PatentIn version 3.1  
/ SEQ ID NO: 861  
/ LENGTH: 9  
/ TYPE: PRT  
/ ORGANISM: Artificial Sequence  
/ FEATURE:  
/ OTHER INFORMATION: HLA-binding peptide of Seq. No. 855  
US-11-010-748A-861

Query Match 21.7% Score 25; DB 7; Length 9;  
Best Local Similarity 66.7%; Pred. No. 5.5e+04;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 PTMLK 10  
|||:  
1 PTMLK 6

DB 1 PTMLK 6

RESULT 71  
US-11-010-748A-864  
/ Sequence 864, Application US/11010748A  
/ Publication No. US20050244421A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Merck Patent GmbH  
/ APPLICANT: STRITTMAYER, Wolfgang  
/ APPLICANT: MOLL, Heidrun  
/ APPLICANT: SCHARM, Burkhard  
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING IMMUNE RESPONSE  
/ FILE REFERENCE: MER-136  
/ CURRENT APPLICATION NUMBER: US/11/010,748A  
/ PRIOR FILING DATE: 2004-12-13  
/ PRIOR APPLICATION NUMBER: PCT/EP03/06251  
/ PRIOR FILING DATE: 2003-06-13  
/ PRIOR APPLICATION NUMBER: EP02013423.5

/ NUMBER OF SEQ ID NOS: 926  
/ SOFTWARE: PatentIn version 3.1  
/ SEQ ID NO 864  
/ LENGTH: 9  
/ TYPE: PRT  
/ ORGANISM: Artificial Sequence  
/ FEATURE:  
/ OTHER INFORMATION: HLA-binding peptide of Seq. No. 855  
US-11-010-748A-864

Query Match 21.7%; Score 25; DB 7; Length 9;  
Best Local Similarity 66.7%; Pred. No. 5.5e+04;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 PTMHRK 10  
||: ||  
Db 4 PTMLRK 9

RESULT 72  
US-11-010-748A-866  
/ Sequence 866, Application US/11010748A  
/ Publication No. US20050244421A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Merck Patent GmbH  
/ APPLICANT: STRITTMATTER, Wolfgang  
/ APPLICANT: MOLL, Heidrun  
/ APPLICANT: SCHAM, Burkhard

/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING IMMUNE RESPONSE

/ FILE REFERENCE: MER-136

/ CURRENT APPLICATION NUMBER: US/11/010,748A

/ CURRENT FILING DATE: 2004-12-13

/ PRIOR APPLICATION NUMBER: PCT/EP03/06251

/ PRIOR FILING DATE: 2003-06-13

/ PRIOR APPLICATION NUMBER: EP02013423.5

/ PRIOR FILING DATE: 2002-06-13

/ NUMBER OF SEQ ID NOS: 926

/ SOFTWARE: PatentIn version 3.1

/ SEQ ID NO 866

/ LENGTH: 9

/ TYPE: PRT

/ ORGANISM: Artificial Sequence

/ FEATURE:

/ OTHER INFORMATION: HLA-binding peptide of Seq. No. 855  
US-11-010-748A-866

Query Match 21.7%; Score 25; DB 7; Length 9;  
Best Local Similarity 66.7%; Pred. No. 5.5e+04;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 PTMHRK 10  
||: ||  
Db 4 PTMLRK 9

RESULT 73  
US-11-010-748A-868  
/ Sequence 868, Application US/11010748A  
/ Publication No. US20050244421A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Merck Patent GmbH  
/ APPLICANT: STRITTMATTER, Wolfgang  
/ APPLICANT: MOLL, Heidrun  
/ APPLICANT: SCHAM, Burkhard

/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING IMMUNE RESPONSE

/ FILE REFERENCE: MER-136

/ CURRENT APPLICATION NUMBER: US/11/010,748A

/ CURRENT FILING DATE: 2004-12-13

/ PRIOR APPLICATION NUMBER: PCT/EP03/06251

/ PRIOR FILING DATE: 2003-06-13

/ PRIOR APPLICATION NUMBER: EP02013423.5

/ PRIOR FILING DATE: 2002-06-13

/ NUMBER OF SEQ ID NOS: 926

/ SOFTWARE: PatentIn version 3.1  
/ SEQ ID NO 868  
/ LENGTH: 9  
/ TYPE: PRT  
/ ORGANISM: Artificial Sequence  
/ FEATURE:  
/ OTHER INFORMATION: HLA-binding peptide of Seq. No. 855  
US-11-010-748A-868

Query Match 21.7%; Score 25; DB 7; Length 9;  
Best Local Similarity 66.7%; Pred. No. 5.5e+04;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 PTMHRK 10  
||: ||  
Db 3 PTMLRK 8

RESULT 74  
US-11-010-748A-869

/ Sequence 869, Application US/11010748A

/ Publication No. US20050244421A1

/ GENERAL INFORMATION:  
/ APPLICANT: Merck Patent GmbH  
/ APPLICANT: STRITTMATTER, Wolfgang  
/ APPLICANT: MOLL, Heidrun  
/ APPLICANT: SCHAM, Burkhard

/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING IMMUNE RESPONSE

/ FILE REFERENCE: MER-136

/ CURRENT APPLICATION NUMBER: US/11/010,748A

/ CURRENT FILING DATE: 2004-12-13

/ PRIOR APPLICATION NUMBER: PCT/EP03/06251

/ PRIOR FILING DATE: 2003-06-13

/ PRIOR APPLICATION NUMBER: EP02013423.5

/ PRIOR FILING DATE: 2002-06-13

/ NUMBER OF SEQ ID NOS: 926

/ SOFTWARE: PatentIn version 3.1

/ SEQ ID NO 869

/ LENGTH: 9

/ TYPE: PRT

/ ORGANISM: Artificial Sequence

/ FEATURE:

/ OTHER INFORMATION: HLA-binding peptide of Seq. No. 855  
US-11-010-748A-869

Query Match 21.7%; Score 25; DB 7; Length 9;  
Best Local Similarity 66.7%; Pred. No. 5.5e+04;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 PTMHRK 10  
||: ||  
Db 2 PTMLRK 7

RESULT 75  
US-10-929-988-163

/ Sequence 163, Application US/10929988

/ Publication No. US2005027588A1

/ GENERAL INFORMATION:  
/ APPLICANT: CWRILA, STEVEN B.  
/ APPLICANT: BALU, PALANI  
/ APPLICANT: DUFFIN, DAVID J.  
/ APPLICANT: PIPLANI, SUNILA  
/ APPLICANT: MERRILL, BARBARA MCBOWEN

/ TITLE OF INVENTION: STIMULATING FACTOR RECEPTOR (G-CSFR) AND ASSOCIATED

/ TITLE OF INVENTION: USES

/ FILE REFERENCE: 0300-0014

/ CURRENT APPLICATION NUMBER: US/10/929,988

/ CURRENT FILING DATE: 2004-08-30

/ PRIOR APPLICATION NUMBER: US/09/620,091

/ PRIOR FILING DATE: 2000-07-20

/ NUMBER OF SEQ ID NOS: 491  
/ SOFTWARE: Patentin Ver. 2.1  
/ SEQ ID NO: 163  
/ LENGTH: 12  
/ TYPE: PRT  
/ ORGANISM: Artificial Sequence  
/ FEATURE:  
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-10-923-988-163

Query Match 21.7%; Score 25; DB 6; Length 12;  
Best Local Similarity 71.4%; Pred. No. 2.1e+02;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 14 CESVNG 20  
DB 1 CESVVG 7

RESULT 76

US-11-010-748A-855  
/ Sequence 855, Application US/11010748A  
/ Publication No. US20050244421A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Merck Patent GmbH  
/ APPLICANT: STRITTMAYER, Wolfgang  
/ APPLICANT: MOLL, Heidrun  
/ APPLICANT: SCHAM, Burkhard  
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING IMMUNE RESPONSE  
/ FILE REFERENCE: MER-136  
/ CURRENT APPLICATION NUMBER: US/11/010,748A  
/ PRIOR FILING DATE: 2004-12-13  
/ PRIOR APPLICATION NUMBER: PCT/EP03/06251  
/ PRIOR FILING DATE: 2003-06-13  
/ PRIOR APPLICATION NUMBER: EP02013423.5  
/ PRIOR FILING DATE: 2002-06-13  
/ NUMBER OF SEQ ID NOS: 926  
/ SOFTWARE: Patentin version 3.1  
/ SEQ ID NO: 855  
/ LENGTH: 17  
/ TYPE: PRT  
/ ORGANISM: Artificial Sequence  
/ FEATURE:  
/ OTHER INFORMATION: "Smcy" peptide fragment  
US-11-010-748A-855

Query Match 21.7%; Score 25; DB 7; Length 17;  
Best Local Similarity 66.7%; Pred. No. 3.1e+02;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 PNIHK 10  
DB 8 PTMLHK 13

RESULT 77

US-11-033-039-1223  
/ Sequence 1223, Application US/11033039  
/ Publication No. US20060002947A1  
/ GENERAL INFORMATION:  
/ APPLICANT: HUMPHREYS, ROBERT  
/ APPLICANT: XU, MINZHEN  
/ TITLE OF INVENTION: LI-KEY/ANTIGENIC EPIOTOP HYBRID PEPTIDE VACCINES  
/ FILE REFERENCE: REH-2017US01  
/ CURRENT APPLICATION NUMBER: US/11/033,039  
/ PRIOR FILING DATE: 2005-01-11  
/ PRIOR APPLICATION NUMBER: 10/245,871  
/ PRIOR FILING DATE: 2002-09-17  
/ PRIOR APPLICATION NUMBER: 10/197,000  
/ PRIOR FILING DATE: 2002-07-17  
/ PRIOR APPLICATION NUMBER: 09/396,813  
/ PRIOR FILING DATE: 1999-09-14

/ NUMBER OF SEQ ID NOS: 1452  
/ SOFTWARE: Patentin version 3.3  
/ SEQ ID NO: 1223  
/ LENGTH: 18  
/ TYPE: PRT  
/ ORGANISM: Artificial Sequence  
/ FEATURE:  
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
/ OTHER INFORMATION: hybrid peptide

Query Match 21.7%; Score 25; DB 7; Length 18;  
Best Local Similarity 57.1%; Pred. No. 3.2e+02;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 IPHPTNI 8  
DB 6 VHHPPNI 12

RESULT 78

US-10-485-788A-580  
/ Sequence 580, Application US/10485788A  
/ Publication No. US20050282743A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Lu, Peter S.  
/ APPLICANT: Rabinowitz, Joshua D.  
/ APPLICANT: Schweitzer, Johannes  
/ APPLICANT: Carrick, Deanna Marie  
/ APPLICANT: Arbor Vita Corporation  
/ TITLE OF INVENTION: Molecular Interactions in Cells  
/ FILE REFERENCE: 20054-003320US  
/ CURRENT APPLICATION NUMBER: US/10/485,788A  
/ PRIOR FILING DATE: 2004-02-03  
/ PRIOR APPLICATION NUMBER: US 60/309,841  
/ PRIOR FILING DATE: 2001-08-03  
/ PRIOR APPLICATION NUMBER: US 60/360,061  
/ PRIOR FILING DATE: 2002-02-25  
/ PRIOR APPLICATION NUMBER: WO PCT/US02/24655  
/ PRIOR FILING DATE: 2002-08-02  
/ NUMBER OF SEQ ID NOS: 841  
/ SOFTWARE: Patentin version 3.1  
/ SEQ ID NO: 580  
/ LENGTH: 20  
/ TYPE: PRT  
/ ORGANISM: Homo sapiens  
US-10-485-788A-580

Query Match 21.7%; Score 25; DB 6; Length 20;  
Best Local Similarity 80.0%; Pred. No. 3.6e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 HPTNI 8  
DB 1 HPTDI 5

RESULT 79

US-11-022-562-141  
/ Sequence 141, Application US/11022562  
/ Publication No. US20050249742A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Rupprecht, Ruth M.  
/ APPLICANT: Shisong, Jiang  
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING  
/ TITLE OF INVENTION: A CYTOTOXIC T LYMPHOCYTE IMMUNE RESPONSE  
/ FILE REFERENCE: DFN-043CN  
/ CURRENT APPLICATION NUMBER: US/11/022,562  
/ CURRENT FILING DATE: 2004-12-22



```

; PRIOR APPLICATION NUMBER: PCT/US03/20322
; PRIOR FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: 60/392718
; PRIOR FILING DATE: 2002-06-27
; NUMBER OF SEQ ID NOS: 340
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 141
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Simian Immunodeficiency Virus
US-11-022-562-141

Query Match          21.7%; Score 25; DB 7; Length 20;
Best Local Similarity 71.4%; Pred. No. 3.6e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      12 LVCESVN 18
Db      12 LVCEQGN 18

RESULT 80
US-11-022-562-142
; Sequence 142, Application US/11022562
; Publication No. US20050249742A1
; GENERAL INFORMATION:
; APPLICANT: Rudrecht, Ruth M.
; APPLICANT: Shisong, Jlang
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING
; TITLE OF INVENTION: A CYTOTOXIC T LYMPHOCYTE IMMUNE RESPONSE
; FILE REFERENCE: DEN-043CN
; CURRENT APPLICATION NUMBER: US/11/022,562
; PRIOR FILING DATE: 2004-12-22
; PRIOR APPLICATION NUMBER: PCT/US03/20322
; PRIOR FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: 60/392718
; PRIOR FILING DATE: 2002-06-27
; NUMBER OF SEQ ID NOS: 340
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 142
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Simian Immunodeficiency Virus
US-11-022-562-142

Query Match          21.7%; Score 25; DB 7; Length 20;
Best Local Similarity 71.4%; Pred. No. 3.6e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      12 LVCESVN 18
Db      2 LVCEQGN 8

RESULT 81
US-11-064-416-4
; Sequence 4, Application US/11064416
; Publication No. US20060008461A1
; GENERAL INFORMATION:
; APPLICANT: Oregon Health & Science University
; APPLICANT: Valtin, Milton B
; APPLICANT: Stowell, Michael HB
; APPLICANT: Gillicchio, Vincent S
; APPLICANT: Meredith, Michael J
; TITLE OF INVENTION: MICROPARTICLE-DRUG CONJUGATES FOR BIOLOGICAL TARGETING
; FILE REFERENCE: 899-71532
; CURRENT APPLICATION NUMBER: US/11/064,416
; PRIOR FILING DATE: 2005-02-22
; PRIOR APPLICATION NUMBER: 10/050,271
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 09/573,497
; PRIOR FILING DATE: 2000-05-16
; PRIOR APPLICATION NUMBER: 09/060,011
```

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; PRIOR FILING DATE: 1998-04-14
; PRIOR APPLICATION NUMBER: 08/691,891
; PRIOR FILING DATE: 1996-08-01
; PRIOR APPLICATION NUMBER: 08/441,770
; PRIOR FILING DATE: 1995-05-16
; PRIOR APPLICATION NUMBER: 08/246,941
; PRIOR FILING DATE: 1994-05-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: peptide linker
US-11-064-416-4

Query Match          20.9%; Score 24; DB 7; Length 8;
Best Local Similarity 100.0%; Pred. No. 5.5e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      11 YLVC 14
Db      5 YLVC 8

RESULT 82
US-11-064-416-5
; Sequence 5, Application US/11064416
; Publication No. US20060008461A1
; GENERAL INFORMATION:
; APPLICANT: Oregon Health & Science University
; APPLICANT: Valtin, Milton B
; APPLICANT: Stowell, Michael HB
; APPLICANT: Gillicchio, Vincent S
; APPLICANT: Meredith, Michael J
; TITLE OF INVENTION: MICROPARTICLE-DRUG CONJUGATES FOR BIOLOGICAL TARGETING
; FILE REFERENCE: 899-71532
; CURRENT APPLICATION NUMBER: US/11/064,416
; PRIOR FILING DATE: 2005-02-22
; PRIOR APPLICATION NUMBER: 10/050,271
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 09/573,497
; PRIOR FILING DATE: 2000-05-16
; PRIOR APPLICATION NUMBER: 09/060,011
; PRIOR FILING DATE: 1998-04-14
; PRIOR APPLICATION NUMBER: 08/691,891
; PRIOR FILING DATE: 1996-08-01
; PRIOR APPLICATION NUMBER: 08/441,770
; PRIOR FILING DATE: 1995-05-16
; PRIOR APPLICATION NUMBER: 08/246,941
; PRIOR FILING DATE: 1994-05-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: peptide linker
US-11-064-416-5

Query Match          20.9%; Score 24; DB 7; Length 8;
Best Local Similarity 100.0%; Pred. No. 5.5e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      11 YLVC 14
Db      4 YLVC 7

RESULT 83
US-10-966-483-14
```

```
/ Sequence 14, Application US/10966483
/ Publication No. US20050281783A1
/ GENERAL INFORMATION:
/ APPLICANT: Klnch, Michael S.
/ APPLICANT: Klemmer, Peter A.
/ APPLICANT: Bruckheimer, Elizabeth
/ APPLICANT: Dubensky, Jr. Thomas W.
/ APPLICANT: Cook, David N.
/ TITLE OF INVENTION: LISTERIA-BASED Epha2 VACCINES
/ FILE REFERENCE: 10271-146
/ CURRENT APPLICATION NUMBER: US/10/966,483
/ CURRENT FILING DATE: 2004-10-15
/ PRIOR APPLICATION NUMBER: US 60/511,919
/ PRIOR FILING DATE: 2003-10-15
/ PRIOR APPLICATION NUMBER: US 60/511,719
/ PRIOR FILING DATE: 2003-10-15
/ PRIOR APPLICATION NUMBER: US 60/532,666
/ PRIOR FILING DATE: 2003-12-24
/ PRIOR APPLICATION NUMBER: US 60/556,631
/ PRIOR FILING DATE: 2004-03-26
/ PRIOR APPLICATION NUMBER:
/ PRIOR FILING DATE: 2004-10-01
/ PRIOR APPLICATION NUMBER:
/ PRIOR FILING DATE: 2004-10-07
/ NUMBER OF SEQ ID NOS: 72
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 14
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-966-483-14

Query Match          20.9%; Score 24; DB 6; Length 9;
Best Local Similarity 44.4%; Pred. No. 5.5e+04;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      11 YVCSVNG 19
      |||
      1 YVCSVMSG 9

RESULT 84
US-10-614-599-26
/ Sequence 26, Application US/10614599
/ Publication No. US20050250178A1
/ GENERAL INFORMATION:
/ APPLICANT: ANDREW, DAVID P.
/ APPLICANT: LEWIN, DAVID A.
/ APPLICANT: PENNICA, DIANE
/ APPLICANT: RASTELLI, LUCA
/ APPLICANT: TALILON, BRUCE
/ TITLE OF INVENTION: WNT-REGULATED CYTOKINE-LIKE POLYPEPTIDE AND NUCLEIC
/ FILE REFERENCE: 0980080-0104
/ CURRENT APPLICATION NUMBER: US/10/614,599
/ CURRENT FILING DATE: 2003-07-07
/ PRIOR APPLICATION NUMBER: 09/715,747
/ PRIOR FILING DATE: 2000-11-17
/ PRIOR APPLICATION NUMBER: 09/715,418
/ PRIOR FILING DATE: 2000-11-16
/ PRIOR APPLICATION NUMBER: 60/166,177
/ PRIOR FILING DATE: 1999-11-18
/ NUMBER OF SEQ ID NOS: 48
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 26
/ LENGTH: 10
/ TYPE: PRT
/ ORGANISM: Unknown Organism
/ FEATURE:
/ OTHER INFORMATION: Description of Unknown Organism: Membrane attack
US-10-614-599-26
```

```
Query Match          20.9%; Score 24; DB 6; Length 10;
Best Local Similarity 57.1%; Pred. No. 2.6e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      7 NIKKLV 13
      |||
      3 NFHQYSV 9

RESULT 85
US-10-929-988-102
/ Sequence 102, Application US/10929988
/ Publication No. US20050277588A1
/ GENERAL INFORMATION:
/ APPLICANT: CMIRLA, STEVEN E.
/ APPLICANT: BALU, PALANI
/ APPLICANT: DUFFIN, DAVID J.
/ APPLICANT: PIPLANI, SONILA
/ APPLICANT: MERRILL, BARBARA MCBOWEN
/ APPLICANT: SCHATZ, PETER JOSEPH
/ TITLE OF INVENTION: COMPOUNDS HAVING AFFINITY FOR THE GRANULOCYTE-COLONY
/ TITLE OF INVENTION: STIMULATING FACTOR RECEPTOR (G-CSFR) AND ASSOCIATED
/ FILE REFERENCE: 0300-0014
/ CURRENT APPLICATION NUMBER: US/10/929,988
/ CURRENT FILING DATE: 2004-08-30
/ PRIOR APPLICATION NUMBER: US/09/620,091
/ PRIOR FILING DATE: 2000-07-20
/ NUMBER OF SEQ ID NOS: 491
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 102
/ LENGTH: 11
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-929-988-102

Query Match          20.9%; Score 24; DB 6; Length 11;
Best Local Similarity 57.1%; Pred. No. 2.8e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      14 CESVNGG 20
      |||
      1 CEQSNNG 7

RESULT 86
US-10-966-371-7
/ Sequence 7, Application US/10966371
/ Publication No. US20050250692A1
/ GENERAL INFORMATION:
/ APPLICANT: Huang, Jung San
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INHIBITING CELL PROLIFERATION
/ FILE REFERENCE: SLU 03-006 US
/ CURRENT APPLICATION NUMBER: US/10/966,371
/ CURRENT FILING DATE: 2004-10-15
/ PRIOR APPLICATION NUMBER: US 60/512,516
/ PRIOR FILING DATE: 2003-10-17
/ NUMBER OF SEQ ID NOS: 23
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 7
/ LENGTH: 12
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-966-371-7

Query Match          20.9%; Score 24; DB 6; Length 12;
Best Local Similarity 80.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 DIPHP 5
```

Db 7 DIEHP 11

## RESULT 87

US-11-180-997-5  
 / Sequence 5, Application US/11180997  
 / Publication No. US20050250150A1  
 / GENERAL INFORMATION:  
 / APPLICANT: Akzo Nobel Patent Department  
 / TITLE OF INVENTION: Lawsonia Intracellularis Vaccine  
 / FILE REFERENCE: 2000.605  
 / CURRENT APPLICATION NUMBER: US/11/180,997  
 / CURRENT FILING DATE: 2005-07-13  
 / NUMBER OF SEQ ID NOS: 32  
 / SOFTWARE: PatentIn version 3.2  
 / SEQ ID NO 5  
 / LENGTH: 12  
 / TYPE: PRT  
 / ORGANISM: Lawsonia Intracellularis  
 US-11-180-997-5

Query Match 20.9%; Score 24; DB 7; Length 12;  
 Best Local Similarity 50.0%; Pred. No. 3.1e+02;  
 Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 9 HKYLVCESVN 18  
 : : : : :  
 Db 3 YETVLMGVN 12

## RESULT 88

US-11-180-997-19  
 / Sequence 19, Application US/11180997  
 / Publication No. US20050250150A1  
 / GENERAL INFORMATION:  
 / APPLICANT: Akzo Nobel Patent Department  
 / TITLE OF INVENTION: Lawsonia Intracellularis Vaccine  
 / FILE REFERENCE: 2000.605  
 / CURRENT APPLICATION NUMBER: US/11/180,997  
 / CURRENT FILING DATE: 2005-07-13  
 / NUMBER OF SEQ ID NOS: 32  
 / SOFTWARE: PatentIn version 3.2  
 / SEQ ID NO 19  
 / LENGTH: 12  
 / TYPE: PRT  
 / ORGANISM: Lawsonia Intracellularis  
 US-11-180-997-19

Query Match 20.9%; Score 24; DB 7; Length 12;  
 Best Local Similarity 50.0%; Pred. No. 3.1e+02;  
 Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 9 HKYLVCESVN 18  
 : : : : :  
 Db 3 YETVLMGVN 12

## RESULT 89

US-10-939-890-44  
 / Sequence 44, Application US/10939890  
 / Publication No. US20050250700A1  
 / GENERAL INFORMATION:  
 / APPLICANT: Sato, Aaron K.  
 / APPLICANT: Sexton, Daniel J.  
 / APPLICANT: Dransfield, Daniel T.  
 / APPLICANT: Ledner, Robert C.  
 / APPLICANT: Arbogast, Christophe  
 / APPLICANT: Bussac, Philippe  
 / APPLICANT: Fan, Hong  
 / APPLICANT: Khurana, Sucha  
 / APPLICANT: Lindner, Karen B.  
 / APPLICANT: Marinelli, Edmund R.

APPLICANT: Nanjappan, Palaniappa  
 APPLICANT: Nunn, Adrian D.  
 APPLICANT: Pillai, Radhakrishna  
 APPLICANT: Pochon, Sibylle  
 APPLICANT: Ramalingam, Kondareddiar  
 APPLICANT: Shrivastava, Ajay  
 APPLICANT: Song, Bo  
 APPLICANT: Swenson, Rolf R.

APPLICANT: Von Wronski, Mathew A.  
 / TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES  
 / FILE REFERENCE: D0617.70014US00  
 / CURRENT APPLICATION NUMBER: US/10/939,890  
 / CURRENT FILING DATE: 2004-09-13  
 / PRIOR APPLICATION NUMBER: US 10/661,156  
 / PRIOR FILING DATE: 2003-09-11  
 / PRIOR APPLICATION NUMBER: US 10/382,082  
 / PRIOR FILING DATE: 2003-03-03  
 / PRIOR APPLICATION NUMBER: PCT/US03/06731  
 / PRIOR FILING DATE: 2003-03-03  
 / PRIOR APPLICATION NUMBER: US 60/440,411  
 / PRIOR FILING DATE: 2003-01-15  
 / PRIOR APPLICATION NUMBER: US 60/360,851  
 / PRIOR FILING DATE: 2002-03-01  
 / NUMBER OF SEQ ID NOS: 883  
 / SOFTWARE: FastSeq for Windows Version 4.0  
 / SEQ ID NO 44  
 / LENGTH: 14  
 / TYPE: PRT  
 / ORGANISM: Artificial Sequence  
 / FEATURE:  
 / OTHER INFORMATION: Library Isolate  
 US-10-939-890-44

Query Match 20.9%; Score 24; DB 6; Length 14;  
 Best Local Similarity 33.3%; Pred. No. 3.6e+02;  
 Matches 3; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 11 YLVCESVNG 19  
 : : : : :  
 Db 1 WIGQNSITG 9

## RESULT 90

US-11-033-039-1428  
 / Sequence 1428, Application US/11033039  
 / Publication No. US20060002947A1  
 / GENERAL INFORMATION:  
 / APPLICANT: HUMPHREYS, ROBERT  
 / APPLICANT: XU, MINZHEN  
 / TITLE OF INVENTION: LI-KEY/ANTIGENIC EPTOPE HYBRID PEPTIDE VACCINES  
 / FILE REFERENCE: REH-2017US01  
 / CURRENT APPLICATION NUMBER: US/11/033,039  
 / CURRENT FILING DATE: 2005-01-11  
 / PRIOR APPLICATION NUMBER: 10/245,871  
 / PRIOR FILING DATE: 2002-09-17  
 / PRIOR APPLICATION NUMBER: 10/197,000  
 / PRIOR FILING DATE: 2002-07-17  
 / PRIOR APPLICATION NUMBER: 09/396,813  
 / PRIOR FILING DATE: 1999-09-14  
 / NUMBER OF SEQ ID NOS: 1452  
 / SOFTWARE: PatentIn version 3.3  
 / SEQ ID NO 1428  
 / LENGTH: 16  
 / TYPE: PRT  
 / ORGANISM: Artificial Sequence  
 / FEATURE:  
 / OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 US-11-033-039-1428

Query Match 20.9%; Score 24; DB 7; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 4.2e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 YLVC 14  
|||  
Db 5 YLVC 8

RESULT 91  
US-11-033-039-1427  
; Sequence 1427, Application US/11033039  
; Publication No. US20060002947A1  
; GENERAL INFORMATION:  
; APPLICANT: HUMPHREYS, ROBERT  
; APPLICANT: XU, MINZHEN  
; TITLE OF INVENTION: LI-KEY/ANTIGENIC EPIOTOPE HYBRID PEPTIDE VACCINES  
; FILE REFERENCE: REH-2017US01  
; CURRENT APPLICATION NUMBER: US/11/033,039  
; CURRENT FILING DATE: 2005-01-11  
; PRIOR APPLICATION NUMBER: 10/245,871  
; PRIOR FILING DATE: 2002-09-17  
; PRIOR APPLICATION NUMBER: 10/197,000  
; PRIOR FILING DATE: 2002-07-17  
; PRIOR FILING DATE: 1999-09-14  
; PRIOR APPLICATION NUMBER: 09/396,813  
; NUMBER OF SEQ ID NOS: 1452  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 1427  
; LENGTH: 17  
; TYPR: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: hybrid peptide  
; FEATURE:  
; NAME/KEY: MOD\_RES  
; LOCATION: (5)..(5)  
; OTHER INFORMATION: Ava  
US-11-033-039-1427

Query Match 20.9%; Score 24; DB 7; Length 17;  
Best Local Similarity 100.0%; Pred.No. 4.4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 YLVC 14  
|||  
Db 6 YLVC 9

RESULT 92  
US-11-041-893-132  
; Sequence 132, Application US/11041893  
; Publication No. US20060002941A1  
; GENERAL INFORMATION:  
; APPLICANT: Mahaitas, Gregory G.  
; TITLE OF INVENTION: COMPOSITIONS COMPRISING IMMUNE RESPONSE  
; FILE REFERENCE: 100123, 401  
; CURRENT APPLICATION NUMBER: US/11/041,893  
; CURRENT FILING DATE: 2005-01-24  
; PRIOR APPLICATION NUMBER: US 60/616,855  
; PRIOR FILING DATE: 2004-10-06  
; PRIOR APPLICATION NUMBER: US 60/538,713  
; PRIOR FILING DATE: 2004-01-23  
; NUMBER OF SEQ ID NOS: 295  
; SOFTWARE: PatSeq for Windows Version 4.0  
; SEQ ID NO 132  
; LENGTH: 17  
; TYPR: PRT  
; ORGANISM: Epstein Barr virus  
US-11-041-893-132

Query Match 20.9%; Score 24; DB 7; Length 17;  
Best Local Similarity 75.0%; Pred.No. 4.4e+02;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LPHP 5  
:|  
Db 12 LPHP 15

RESULT 93  
US-11-033-039-1426  
; Sequence 1426, Application US/11033039  
; Publication No. US20060002947A1  
; GENERAL INFORMATION:  
; APPLICANT: HUMPHREYS, ROBERT  
; APPLICANT: XU, MINZHEN  
; TITLE OF INVENTION: LI-KEY/ANTIGENIC EPIOTOPE HYBRID PEPTIDE VACCINES  
; FILE REFERENCE: REH-2017US01  
; CURRENT APPLICATION NUMBER: US/11/033,039  
; CURRENT FILING DATE: 2005-01-11  
; PRIOR APPLICATION NUMBER: 10/245,871  
; PRIOR FILING DATE: 2002-09-17  
; PRIOR APPLICATION NUMBER: 10/197,000  
; PRIOR FILING DATE: 2002-07-17  
; PRIOR FILING DATE: 1999-09-14  
; PRIOR APPLICATION NUMBER: 09/396,813  
; NUMBER OF SEQ ID NOS: 1452  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 1426  
; LENGTH: 18  
; TYPR: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: hybrid peptide  
; FEATURE:  
; NAME/KEY: MOD\_RES  
; LOCATION: (5)..(5)  
; OTHER INFORMATION: Ava  
US-11-033-039-1426

Query Match 20.9%; Score 24; DB 7; Length 18;  
Best Local Similarity 100.0%; Pred.No. 4.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 YLVC 14  
|||  
Db 7 YLVC 10

RESULT 94  
US-11-033-039-1425  
; Sequence 1425, Application US/11033039  
; Publication No. US20060002947A1  
; GENERAL INFORMATION:  
; APPLICANT: HUMPHREYS, ROBERT  
; APPLICANT: XU, MINZHEN  
; TITLE OF INVENTION: LI-KEY/ANTIGENIC EPIOTOPE HYBRID PEPTIDE VACCINES  
; FILE REFERENCE: REH-2017US01  
; CURRENT APPLICATION NUMBER: US/11/033,039  
; CURRENT FILING DATE: 2005-01-11  
; PRIOR APPLICATION NUMBER: 10/245,871  
; PRIOR FILING DATE: 2002-09-17  
; PRIOR APPLICATION NUMBER: 10/197,000  
; PRIOR FILING DATE: 2002-07-17  
; PRIOR APPLICATION NUMBER: 09/396,813  
; PRIOR FILING DATE: 1999-09-14  
; NUMBER OF SEQ ID NOS: 1452  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 1425  
; LENGTH: 19  
; TYPR: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: hybrid peptide

Query Match 20.9%; Score 24; DB 7; Length 19;  
Best Local Similarity 75.0%; Pred.No. 4.7e+02;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

FEATURE:  
NAME/KEY: MOD\_RES  
LOCATION: (5)-(5)  
OTHER INFORMATION: Ava  
US-11-033-039-1423

Query Match 20.9%; Score 24; DB 7; Length 19;  
Best Local Similarity 100.0%; Pred. No. 5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 YLVC 14  
DB 8 YLVC 11

RESULT 95  
US-10-623-155-514  
Sequence 514, Application US/10623155  
Publication No. US20050261166A1  
GENERAL INFORMATION:  
APPLICANT: Wang, Tonglong  
APPLICANT: Beckham, David W.  
APPLICANT: Reiter, Marc W.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER  
FILE REFERENCE: 210121.455C20  
CURRENT APPLICATION NUMBER: US/10/623.155  
CURRENT FILING DATE: 2003-07-17  
NUMBER OF SEQ ID NOS: 560  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 514  
LENGTH: 20  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-623-155-514

Query Match 20.9%; Score 24; DB 6; Length 20;  
Best Local Similarity 80.0%; Pred. No. 5.2e+02;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 14 CESVN 18  
DB 11 CEQVN 15

RESULT 96  
US-11-022-562-173  
Sequence 173, Application US/11022562  
Publication No. US20050249742A1  
GENERAL INFORMATION:  
APPLICANT: Rupprecht, Ruth M.  
APPLICANT: Shijsong, Jiansg  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING  
TITLE OF INVENTION: A CYTOTOXIC T LYMPHOCYTE IMMUNE RESPONSE  
FILE REFERENCE: DPN-043CN  
CURRENT APPLICATION NUMBER: US/11/022.562  
CURRENT FILING DATE: 2004-12-22  
PRIOR APPLICATION NUMBER: PCT/US03/20322  
PRIOR FILING DATE: 2003-06-27  
PRIOR APPLICATION NUMBER: 60/392718  
PRIOR FILING DATE: 2002-06-27  
NUMBER OF SEQ ID NOS: 340  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 173  
LENGTH: 20  
TYPE: PRT  
ORGANISM: Simian Immunodeficiency Virus  
US-11-022-562-173

Query Match 20.9%; Score 24; DB 7; Length 20;  
Best Local Similarity 42.9%; Pred. No. 5.2e+02;  
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 5 PTNHCX 11  
DB 9 PTDVRY 15

RESULT 97  
US-11-033-039-1424  
Sequence 1424, Application US/11033039  
Publication No. US20060002947A1  
GENERAL INFORMATION:  
APPLICANT: HUMPHREYS, ROBERT  
APPLICANT: XU, MINZHEN  
TITLE OF INVENTION: LI-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES  
FILE REFERENCE: REH-2017US01  
CURRENT APPLICATION NUMBER: US/11/033.039  
CURRENT FILING DATE: 2005-01-11  
PRIOR APPLICATION NUMBER: 10/245.871  
PRIOR FILING DATE: 2002-09-17  
PRIOR APPLICATION NUMBER: 10/197.000  
PRIOR FILING DATE: 2002-07-17  
PRIOR APPLICATION NUMBER: 09/396.813  
PRIOR FILING DATE: 1999-09-14  
NUMBER OF SEQ ID NOS: 1452  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 1424  
LENGTH: 20  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
OTHER INFORMATION: hybrid peptide  
FEATURE:  
NAME/KEY: MOD\_RES  
LOCATION: (5)-(5)  
OTHER INFORMATION: Ava  
US-11-033-039-1424

Query Match 20.9%; Score 24; DB 7; Length 20;  
Best Local Similarity 100.0%; Pred. No. 5.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 YLVC 14  
DB 9 YLVC 12

RESULT 98  
US-11-226-701-28  
Sequence 28, Application US/11226701  
Publication No. US20060009632A1  
GENERAL INFORMATION:  
APPLICANT: Millennium Pharmaceuticals, Inc.  
APPLICANT: Kapeller-Libermann, Rosana  
APPLICANT: Robison, Keith E.  
APPLICANT: White, David  
APPLICANT: Williamson, Mark W.  
APPLICANT: Cook, William James  
APPLICANT: Meyers, Rachel E.  
APPLICANT: Macbeth, Kyle J.  
APPLICANT: Carroll, Joseph M.  
APPLICANT: Chun, Miyoung  
TITLE OF INVENTION: NOVEL 27875, 22025, 27420, 17906, 16319,  
TITLE OF INVENTION: 55092 AND 10218 MOLECULES AND USES THEREFOR  
FILE REFERENCE: MP103-0210NMIM  
CURRENT APPLICATION NUMBER: US/11/226.701  
CURRENT FILING DATE: 2005-09-14  
PRIOR APPLICATION NUMBER: US/10/386.414  
PRIOR FILING DATE: 2003-03-11  
PRIOR APPLICATION NUMBER: 09/426.282  
PRIOR FILING DATE: 1999-10-25  
PRIOR APPLICATION NUMBER: 09/668.266  
PRIOR FILING DATE: 2000-09-22

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; PRIOR APPLICATION NUMBER: 09/330,970
; PRIOR FILING DATE: 1999-06-11
; PRIOR APPLICATION NUMBER: 09/724,599
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 09/860,193
; PRIOR FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 09/571,689
; PRIOR FILING DATE: 2000-05-16
; PRIOR APPLICATION NUMBER: 10/283,023
; PRIOR FILING DATE: 2002-10-29
; PRIOR APPLICATION NUMBER: 60/335,044
; PRIOR FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: 10/010,943
; PRIOR FILING DATE: 2001-12-06
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Catalytic signature
US-11-226-701-28

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Query Match          20.0%; Score 23; DB 7; Length 7;
Best Local Similarity 60.0%; Pred. No. 5.5e+04;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 1 DHPHP 5
   |||
Db 2 DVDHP 6

```

```

RESULT 99
US-11-140-417-18
; Sequence 18, Application US/11140417
; Publication No. US20050266515A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Deborah A
; APPLICANT: Eddy, Edward M
; TITLE OF INVENTION: GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE-S (GAPDS), A GLYCOLYTIC
; TITLE OF INVENTION: ENZYME EXPRESSED ONLY IN MALE GERM CELLS, IS A TARGET FOR MALE
; FILE REFERENCE: 421/76/2 PCT/CIP
; CURRENT APPLICATION NUMBER: US/11/140,417
; CURRENT FILING DATE: 2005-05-27
; PRIOR APPLICATION NUMBER: US 60/429,638
; PRIOR FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: PCT/US2003/037800
; PRIOR FILING DATE: 2003-11-26
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 18
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-140-417-18

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```

Query Match          20.0%; Score 23; DB 7; Length 8;
Best Local Similarity 50.0%; Pred. No. 5.5e+04;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```

```

QY 6 TTHIKY 11
   |||
Db 2 TTVHSY 7

```

```

RESULT 100
US-11-108-135-8
; Sequence 8, Application US/11108135
; Publication No. US20050260213A1
; GENERAL INFORMATION:

```

```

; APPLICANT: Koenig, Scott
; APPLICANT: Veri, Maria Concetta
; APPLICANT: Thuillion, Nadine
; APPLICANT: Bonvini, Ezio
; APPLICANT: Stavenhagen, Jeffrey
; APPLICANT: Rankin, Christopher
; TITLE OF INVENTION: Fc-gamma-RIIB-specific antibodies and methods of use thereof
; FILE REFERENCE: 11183-014-999
; CURRENT APPLICATION NUMBER: US/11/108,135
; CURRENT FILING DATE: 2005-04-15
; PRIOR APPLICATION NUMBER: US 60/562,804
; PRIOR FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: US 60/582,044
; PRIOR FILING DATE: 2004-06-21
; PRIOR APPLICATION NUMBER: US 60/582,045
; PRIOR FILING DATE: 2004-06-21
; PRIOR APPLICATION NUMBER: US 60/654,713
; PRIOR FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: 286 Light chain variable region - CDRI
US-11-108-135-8

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Query Match          20.0%; Score 23; DB 7; Length 11;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

QY 6 TTHI 9
   |||
Db 8 TTHI 11

```

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Search completed: January 20, 2006, 19:46:29
Job time : 9.07692 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 20, 2006, 18:55:50 ; Search time 11.3462 Seconds  
(without alignments)  
169.602 Million cell updates/sec

Title: US-09-662-293-3

Perfect score: 115  
Sequence: 1 DHPPTNHHKYLVCBSVNGG 20

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 3886

Minimum DB seq length: 0  
Maximum DB seq length: 20

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database :

1: PIR 80: \*  
2: p1r1: \*  
3: p1r3: \*  
4: p1r4: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the target being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	38	33.0	15	2	A60929
2	38	33.0	15	2	B60929
3	27	23.5	11	2	S42587
4	27	23.5	18	2	H64711
5	26	22.6	18	2	S65454
6	25.5	22.2	16	2	S55307
7	25	21.7	19	2	PQ0548
8	25	21.7	20	2	D84716
9	24	20.9	9	2	A60108
10	24	20.9	9	2	S10920
11	24	20.9	17	2	S15778
12	24	20.9	18	2	S29264
13	24	20.9	18	2	PN0175
14	24	20.9	19	2	I50153
15	24	20.9	20	2	A45655
16	23	20.0	10	2	PH0925
17	23	20.0	10	2	C60787
18	23	20.0	13	2	S38736
19	23	20.0	13	2	A08416
20	23	20.0	16	2	PH1604
21	23	20.0	17	2	S15754
22	23	20.0	17	2	S63503
23	23	20.0	18	1	A58589
24	22.5	19.6	20	2	A48394
25	22	19.1	10	2	B59272
26	22	19.1	10	2	B37196
27	22	19.1	11	2	D60409
28	22	19.1	11	2	D60409
29	22	19.1	13	2	B47415

30	22	19.1	13	2	PH0788	T-cell receptor al
31	22	19.1	15	2	S60007	glial hyaluronate-
32	22	19.1	15	2	B56046	urinary tract ston
33	22	19.1	16	2	S00123	dihydrolipeamide S
34	22	19.1	16	2	A41170	photosystem II 6.1
35	22	19.1	16	2	A11488	taurocyamine kinase
36	22	19.1	17	2	S59512	probable integrin
37	22	19.1	18	2	B48839	T-cell receptor be
38	22	19.1	19	2	D44101	calmodulin, vasocac
39	22	19.1	20	2	A38566	GTP-binding protei
40	22	19.1	20	2	T50757	neuropeptide Grb-A
41	21	18.3	9	2	A57444	T-cell receptor be
42	21	18.3	11	2	PH0947	entactin/nidogen -
43	21	18.3	12	2	A54315	chondroitin sulfat
44	21	18.3	13	2	B47171	glanular kallikre
45	21	18.3	13	2	A54326	interferon alpha r
46	21	18.3	14	2	S41601	cystatin Cr-4a - m
47	21	18.3	15	2	PQ0232	pimeoyl-CoA synth
48	21	18.3	15	2	A56786	T-cell receptor be
49	21	18.3	15	2	PH0136	alpha-conotoxin Au
50	21	18.3	16	2	C59045	T-cell receptor be
51	21	18.3	17	2	C49255	hypothetical prote
52	21	18.3	17	2	S15064	photosystem I 5.6k
53	21	18.3	18	2	PQ0680	gluten - wheat
54	21	18.3	18	2	S20322	photosystem II chl
55	21	18.3	20	2	A24589	limbal antigen C
56	21	18.3	20	2	A60100	hypothetical prote
57	21	18.3	20	2	S18582	intracrySTALLINE C
58	21	18.3	20	2	C56894	pyrrolicystalline c
59	21	18.3	20	2	B56894	pyrrolicystalline c
60	21	18.3	20	2	S44465	pyrrolicystalline c
61	21	18.3	20	2	AB0120	insertion element
62	21	18.3	10	2	PH0944	T-cell receptor be
63	20	17.4	10	2	G60527	sperm-activating p
64	20	17.4	11	2	PA0028	protein OAJ00042 -
65	20	17.4	11	2	PH1375	T antigen variant
66	20	17.4	11	2	PH1376	T antigen variant
67	20	17.4	12	1	LFRCPE	pyr leader peptid
68	20	17.4	13	2	S47383	T-cell antigen rec
69	20	17.4	14	2	S48685	extension protein
70	20	17.4	15	2	S08209	hypothetical prote
71	20	17.4	15	2	PH1610	Ig H chain V-D-J r
72	20	17.4	15	2	PH0779	T-cell receptor al
73	20	17.4	15	2	PT0096	pyruvate dehydroge
74	20	17.4	17	2	PH1789	T-cell receptor al
75	20	17.4	18	2	SL0025	T-cell surface gly
76	20	17.4	19	2	S29167	guinaldine oxidore
77	20	17.4	19	2	PT0332	Ig heavy chain CRD
78	20	17.4	19	2	PH1352	Ig heavy chain DJ
79	20	17.4	19	2	D49404	T-cell receptor be
80	20	17.4	19	2	PQ0409	RNA-directed RNA p
81	20	17.4	20	2	PX0042	venomabin B (EC 3.4
82	20	17.4	20	2	S68028	iodochronone 5'-mo
83	20	17.4	20	2	B38382	15k protein B - ra
84	20	17.4	20	2	S03954	acidic fibroblast
85	19.5	17.0	14	2	A58963	alpha-conotoxin Cn
86	19.5	17.0	14	2	C32735	chrysoglobulin - pi
87	19.5	17.0	19	2	B32735	chrysoglobulin - sh
88	19.5	17.0	19	2	A34233	trehalase inhibito
89	19	16.5	9	2	S55696	phosphoenolpyruvat
90	19	16.5	9	2	B57444	neuropeptide Grb-A
91	19	16.5	10	2	S77980	cytochrome-c oxida
92	19	16.5	10	2	C60527	sperm-activating p
93	19	16.5	10	2	S6527	sperm-activating p
94	19	16.5	10	2	C60788	sperm-activating p
95	19	16.5	10	2	A60527	sperm-activating p
96	19	16.5	10	2	A60787	sperm-activating p
97	19	16.5	11	2	B49164	chromogranin-B - r
98	19	16.5	11	2	A26930	ermg leader peptid
99	19	16.5	13	2	S15755	actin 7 - soybean
100	19	16.5	13	2	PT0290	Ig heavy chain CRD

## ALIGNMENTS

## RESULT 1

A60929

dichloromethane dehalogenase (EC 4.5.1.3) - *Hyphomicrobium* sp. (ATCC 43129) (fragment)  
 C/Species: Hyphomicrobium sp.  
 C/Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 09-Jul-2004  
 C/Accession: A60929

R/Kohler-Staud, D.; Hartmann, S.; Gaelli, R.; Suter, F.; Leisinger, T.  
 J. Gen. Microbiol. 132, 2837-2843, 1986

A/Title: Evidence for identical dichloromethane dehalogenases in different methylotrophic  
 A/Reference number: A60929

A/Accession: A60929  
 A/Molecule type: protein

A/Residues: 1-15 <KOH>

A/Cross-references: UNIPROT:Q7M134; UNIPARC:UPI000017A8F8  
 C/Keywords: carbon-halide lyase

## Query Match

Best Local Similarity 33.0%; Score 38; DB 2; Length 15;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 PHPTNTH 9  
 |||||

DB 3 PNPTNTH 9

## RESULT 2

B60929

dichloromethane dehalogenase (EC 4.5.1.3) - *Pseudomonas* sp. (fragment)  
 C/Species: Pseudomonas sp.  
 C/Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 03-Jul-2004  
 C/Accession: B60929

R/Kohler-Staud, D.; Hartmann, S.; Gaelli, R.; Suter, F.; Leisinger, T.  
 J. Gen. Microbiol. 132, 2837-2843, 1986

A/Title: Evidence for identical dichloromethane dehalogenases in different methylotrophic  
 A/Reference number: A60929

A/Contents: DSM 1565

A/Accession: B60929

A/Molecule type: protein

A/Residues: 1-15 <KOH>

A/Cross-references: UNIPROT:Q7M126; UNIPARC:UPI000017A8F8  
 C/Keywords: carbon-halide lyase

## Query Match

Best Local Similarity 33.0%; Score 38; DB 2; Length 15;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 PHPTNTH 9  
 |||||

DB 3 PNPTNTH 9

## RESULT 3

S42587

celF protein - *Escherichia coli* (fragment)  
 C/Species: Escherichia coli  
 C/Date: 25-Dec-1994 #sequence\_revision 10-Nov-1995 #text\_change 10-Nov-1995  
 C/Accession: S42587

R/Guzzo, A.; Dubow, M. S.  
 Mol. Gen. Genet. 242, 455-460, 1994

A/Title: A luxAB transcriptional fusion to the cryptic celF gene of *Escherichia coli* dis-  
 A/Reference number: S42587; MUID:94166755; PMID:8121401

A/Accession: S42587

A/Molecule type: DNA

A/Residues: 1-11 <GUZ>

A/Cross-references: UNIPARC:UPI000017AA33  
 C/Genetics: celF  
 A/Genes: celF

Query Match 23.5%; Score 27; DB 2; Length 11;  
 Best Local Similarity 80.0%; Pred. No. 5.2e+02;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 PHPTN 7  
 |||||

DB 7 PHPRN 11

## RESULT 4

H64711

hypothetical protein HP1536 - *Helicobacter pylori* (strain 26695)  
 C/Species: Helicobacter pylori  
 C/Date: 09-Aug-1997 #sequence\_revision 09-Aug-1997 #text\_change 09-Jul-2004  
 C/Accession: H64711

R/Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.  
 Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khaliq, H.G.; Glodek, A.; McKen-  
 son, J.D.; Kelley, J.M.; Cotton, M.D.; Weldman, J.M.; Fujii, C.; Bowman, C.; Watney, L.  
 Nature 388, 539-547, 1997

A/Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpe, P.D.; Smith, H.O.; Fraser, C.  
 A/Title: The complete genome sequence of the gastric pathogen *Helicobacter pylori*.  
 A/Reference number: A64520; MUID:97394467; PMID:9252185

A/Accession: H64711  
 A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA  
 A/Residues: 1-18 <TOM>

A/Cross-references: UNIPROT:026062; UNIPARC:UPI00000C07C3; GB:AE000651; GB:AE000511; NID

## Query Match

Best Local Similarity 23.5%; Score 27; DB 2; Length 18;  
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 HPTNTHKL 12  
 |||||

DB 10 HPSRNPRTL 18

## RESULT 5

S65454

aspergillopepsin I (EC 3.4.23.18) - *Aspergillus niger* (fragments)  
 C/Species: Aspergillus niger  
 C/Date: 28-Oct-1996 #sequence\_revision 13-Mar-1997 #text\_change 17-Mar-1999  
 C/Accession: S65454

R/Inoue, H.; Hayashi, T.; Huang, X.P.; Lu, J.F.; Athauda, S.B.P.; Kong, K.H.; Yamagata,  
 Eur. J. Biochem. 237, 719-725, 1996

A/Title: Heterologous expression and site-directed mutagenesis studies on the activator  
 A/Reference number: S65454; MUID:96235238; PMID:8647118

A/Accession: S65454  
 A/Molecule type: protein

A/Residues: 1-5;6-10;11-18 <INO>  
 A/Cross-references: UNIPARC:UPI000017B3BC; UNIPARC:UPI000017B3BD; UNIPARC:UPI000017B3BE  
 C/Keywords: aspartic proteinase; hydrolase

Query Match 22.6%; Score 26; DB 2; Length 18;  
 Best Local Similarity 44.4%; Pred. No. 1.2e+03;  
 Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 PHPTNTHK 11  
 |||||

DB 2 PAPSLAKF 10

## RESULT 6

S55307

glutathione transferase 3-3 - rat (fragments)  
 C/Species: Rattus norvegicus (Norway rat)  
 C/Date: 27-Oct-1995 #sequence\_revision 03-Nov-1995 #text\_change 07-May-1999  
 C/Accession: S55307

R/Cooke, R.U.; Bjornestedt, R.; Douglas, K.T.; McKie, J.H.; King, M.D.; Coles, B.; Kett  
 Biochem. J. 302, 383-390, 1994

A/Title: Photoaffinity labelling of the active site of the rat glutathione transferases  
 A/Reference number: S55307; MUID:94379965; PMID:8092989

A/Accession: S55307  
 A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA  
 A/Residues: 1-18 <TOM>

A/Cross-references: UNIPROT:026062; UNIPARC:UPI00000C07C3; GB:AE000651; GB:AE000511; NID

Query Match 23.5%; Score 27; DB 2; Length 18;  
 Best Local Similarity 80.0%; Pred. No. 5.2e+02;



A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-16 <COO>  
A/Cross-references: UNIPARC:UPI000017C91E

Query Match 22.2%; Score 25.5; DB 2; Length 16;  
Best Local Similarity 42.9%; Pred. No. 1.3e+03;  
Matches 6; Conservative 2; Mismatches 3; Indels 3; Gaps 1;

QY 2 IHPPTN---HKYL 12  
DB 2 LTHPSQIMPEKYL 15

## RESULT 7

P00548  
capsid protein VP26 - human herpesvirus 1 (fragment)  
C/Species: human herpesvirus 1  
C/Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 09-Jul-2004  
C/Accession: P00548  
R/Davison, M.D.; Rixon, F.J.; Davison, A.J.  
J. Gen. Virol. 73, 2709-2713, 1992  
A/Title: Identification of genes encoding two capsid proteins (VP24 and VP26) of herpes  
A/Reference number: P00544; MUID:93019027; PMID:1328483  
A/Accession: P00548  
A/Molecule type: protein  
A/Residues: 1-19 <DAV>  
A/Cross-references: UNIPROT:Q7LZNS; UNIPARC:UPI000017A7C9  
A/Experimental source: strain 17  
C/Genetic:   
A/Gene: UL35  
C/Keywords: capsid protein

Query Match 21.7%; Score 25; DB 2; Length 19;  
Best Local Similarity 80.0%; Pred. No. 1.9e+03;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DHPH 5  
DB 11 DNPHP 15

## RESULT 8

D84716  
hypothetical protein Atcg31090 [imported] - Arabidopsis thaliana  
C/Species: Arabidopsis thaliana (mouse-ear cress)  
C/Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 09-Jul-2004  
C/Accession: D84716  
R/Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Bentol, M.I.; Town, C.D.; Fujii, C.Y.;  
M.; Koo, H.; Moffat, K.B.; Cronin, L.A.; Shen, M.; VanKen, S.B.; Umayam, L.; Tallon, L.;  
Neus, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.  
Nature 402, 761-768, 1999  
A/Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
A/Reference number: A84420; MUID:20083487; PMID:10617197  
A/Accession: D84716  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-20 <STO>  
A/Cross-references: UNIPROT:O82275; UNIPARC:UPI000017A6CB; GB:AE002093; MID:93746066; PI  
C/Genetic:   
A/Gene: Atcg31090  
A/Map position: 2

Query Match 21.7%; Score 25; DB 2; Length 20;  
Best Local Similarity 50.0%; Pred. No. 2e+03;  
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 12 LVCEVNG 19  
DB 7 LVCDCTSG 14

## RESULT 9

A60108  
exotoxin A - Streptococcus pyogenes (strain C203.S) (fragment)  
N/Alternate names: blactogen A; scarlet fever toxin  
C/Species: Streptococcus pyogenes  
C/Date: 10-Nov-1992 #sequence\_revision 10-Nov-1992 #text\_change 31-Dec-2004  
C/Accession: A60108  
R/Schlivert, P.M.; Gray, B.D.  
Infect. Immun. 57, 1865-1867, 1989  
A/Title: Group A streptococcal pyrogenic exotoxin (scarlet fever toxin) type A and blas  
A/Reference number: A60108; MUID:89254013; PMID:2498210  
A/Accession: A60108  
A/Molecule type: protein  
A/Residues: 1-9 <SCH>  
A/Cross-references: UNIPROT:Q54779; UNIPROT:P97163; UNIPROT:Q9R931; UNIPROT:Q57453; UNI  
C/Superfamily: enterotoxin B  
C/Keywords: exotoxin

Query Match 20.9%; Score 24; DB 2; Length 9;  
Best Local Similarity 42.9%; Pred. No. 2.8e+05;  
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 PHTNTH 9  
DB 3 PDPSQLH 9

## RESULT 10

S10920  
venom protein HR-3 - oriental hornet (fragment)  
C/Species: Vespa orientalis (oriental hornet)  
C/Date: 29-Jan-1993 #sequence\_revision 29-Jan-1993 #text\_change 09-Jul-2004  
C/Accession: S10920  
R/Tulchibayev, M.U.; Akhmedova, N.U.; Kazakov, I.; Korneev, A.S.; Gagel'gans, A.I.  
Biochemistry (N.Y.) 53, 183-190, 1988  
A/Title: Low-molecular-weight peptides of venom of the giant hornet Vespa orientalis. S  
A/Reference number: S06445  
A/Accession: S10920  
A/Molecule type: protein  
A/Residues: 1-9 <TUL>  
A/Cross-references: UNIPROT:Q7M471; UNIPARC:UPI000017BF07  
C/Keywords: venom

Query Match 20.9%; Score 24; DB 2; Length 9;  
Best Local Similarity 42.9%; Pred. No. 2.8e+05;  
Matches 3; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 7 NIKHYLV 13  
DB 2 SVHPELV 8

## RESULT 11

S15778  
insulin chain B - bovine (fragments)  
C/Species: Bos primigenius indicus x Bos primigenius taurus (cattle)  
C/Date: 19-Mar-1997 #sequence\_revision 16-Jul-1999 #text\_change 16-Jul-1999  
C/Accession: S15778; S15779  
R/Bergman, T.; Agerberch, B.; Joernvall, H.  
FEBS Lett. 283, 100-103, 1991  
A/Title: Direct analysis of peptides and amino acids from capillary electrophoresis.  
A/Reference number: S15778; MUID:91243852; PMID:2037061  
A/Accession: S15778  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-8 <FEB1>  
A/Cross-references: UNIPARC:UPI000015BC0B  
A/Accession: S15779  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 9-17 <FEB2>  
A/Cross-references: UNIPARC:UPI000015BC0B  
C/Superfamily: insulin  
C/Keywords: hormone; pancreas

Query Match 20.9%; Score 24; DB 2; Length 17;  
Best Local Similarity 100.0%; Pred. No. 2.4e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 YLVC 14  
| | | |  
DB 3 YLVC 6

## RESULT 12

S29264

ovoheremerythrin - duck leech (fragment)

N:Alternate names: 14K yolk protein

C:Species: Theromyzon tessulatsum (duck leech)

C&gt;Date: 19-Mar-1997 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004

C:Accession: S29264

R:Baert, J.L.; Britel, M.; Sautiere, P.; Malecha, J.

Eur. J. Biochem. 209, 563-569, 1992

A:Title: Ovoheremerythrin, a major 14-kDa yolk protein distinct from vitellogenin in leech

A:Reference number: S29264; MUID:93049299; PMID:1425663

A:Accession: S29264

A:Molecule type: protein

A:Residues: 1-18 &lt;BAE&gt;

A:Cross-references: UNIPROT:P80155; UNIPARC:UPI000012C58F; PIDN:AA823969.1; PID:9258980

C:Superfamily: hemerythrin

C:Keywords: egg yolk; oxygen carrier

Query Match 20.9%; Score 24; DB 2; Length 18;  
Best Local Similarity 80.0%; Pred. No. 2.5e+03;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DIPHP 5  
| | | |  
DB 2 DIPHP 6

## RESULT 13

PNO175

glutathione transferase (EC 2.5.1.18) 1 - Arabidopsis thaliana (fragment)

C:Species: Arabidopsis thaliana (mouse-ear cress)

C&gt;Date: 22-Dec-1995 #sequence\_revision 08-Feb-1996 #text\_change 23-Mar-2001

C:Accession: PNO175

R:Taugita, A.; Kamo, M.; Kawakami, M.; Ohki, Y.

submitted to JIPID, December 1995

A:Description: Two dimensional electrophoresis of plant proteins and standardization of

A:Reference number: PNO173

A:Accession: PNO175

A:Molecule type: protein

A:Residues: 1-18 &lt;TSU&gt;

A:Cross-references: UNIPARC:UPI000017AF59

A:Experimental source: leaf

C:Keywords: transferase

Query Match 20.9%; Score 24; DB 2; Length 18;  
Best Local Similarity 50.0%; Pred. No. 2.5e+03;  
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DIPHPNI 8  
| | | |  
DB 5 DEGHADI 12

## RESULT 14

I50153

alpha-actin - chicken (fragment)

C:Species: Gallus gallus (chicken)

C&gt;Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 05-Oct-2004

C:Accession: I50153

R:Chang, K. Biol. 4, 2498-2508, 1984

Mol. Cell. Biol. 4, 2498-2508, 1984

A:Title: Isolation and characterization of six different chicken actin genes.

A:Reference number: I50153; MUID:85085956; PMID:6513927

A:Accession: I50153

A&gt;Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-19 &lt;CHA&gt;

A:Cross-references: UNIPROT:Q9PSW6; UNIPARC:UPI0000FB20E; GB:K02258; NID:9211084; PIDN

C:Superfamily: Actin

Query Match 20.9%; Score 24; DB 2; Length 19;  
Best Local Similarity 50.0%; Pred. No. 2.7e+03;  
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 12 LVCSVNG 19  
| | | | |  
DB 10 LVCSVNG 17

## RESULT 15

A45655

Crotalus atrox serine proteinase (EC 3.4.21.-) - western diamondback rattlesnake (fragme

N:Alternate names: alpha-fibrinogenase; thrombin-like proteinase

C:Species: Crotalus atrox (western diamondback rattlesnake)

C&gt;Date: 17-Feb-1994 #sequence\_revision 17-Feb-1994 #text\_change 09-Jul-2004

C:Accession: A45655

R:Chlou, S.H.; Hung, C.C.; Lin, C.W.

Biochem. Int. 26, 105-112, 1992

A:Title: Isolation of a crotalase-like protease with alpha-fibrinogenase activity from t

A:Reference number: A45655; MUID:92313365; PMID:1616487

A:Accession: A45655

A:Molecule type: protein

A:Residues: 1-20 &lt;CHI&gt;

A:Cross-references: UNIPROT:Q9PS55; UNIPARC:UPI0000FB75C

A:Experimental source: venom

A:Note: sequence extracted from NCBI backbone (NCBI:P107297)

C:Superfamily: trypsin; trypsin homology

C:Keywords: hydrolase; serine proteinase; venom

Query Match 20.9%; Score 24; DB 2; Length 20;  
Best Local Similarity 57.1%; Pred. No. 2.8e+03;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 7 NIKKLV 13  
| | | | |  
DB 10 NEHRFLV 16

## RESULT 16

PH0925

T-cell receptor beta chain V-D-J region (isolate 11) - rat (fragment)

C:Species: Rattus norvegicus (Norway rat)

C&gt;Date: 09-Oct-1992 #sequence\_revision 09-Oct-1992 #text\_change 30-May-1997

C:Accession: PH0925

R:Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.

J. Exp. Med. 174, 1467-1476, 1991

A:Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergy

A:Reference number: PH0891; MUID:92078857; PMID:1836012

A:Accession: PH0925

A:Molecule type: mRNA

A:Residues: 1-10 &lt;GOL&gt;

A:Cross-references: UNIPARC:UPI000017C9F4

A:Experimental source: concaavalin A-activated lymphoblast

C:Keywords: T-cell receptor

Query Match 20.0%; Score 23; DB 2; Length 10;  
Best Local Similarity 57.1%; Pred. No. 2e+03;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 14 CESVNGG 20  
| | | | |  
DB 1 CASSDGG 7

## RESULT 17

C60787

sperm-activating peptide (Ser-3,10 speract) - sea urchin (*Hemicentrotus pulcherrimus*)  
 C/Species: *Hemicentrotus pulcherrimus*  
 C/Date: 03-Jun-1993 #sequence\_revision 03-Jun-1993 #text\_change 16-Aug-2004  
 C/Accession: C60787  
 R/Suzuki, N.; Kajitara, H.; Nomura, K.; Garbers, D.L.; Yoshino, K.; Kurita, M.; Tanaka, H.  
 Comp. Biochem. Physiol. B 89, 687-693, 1988  
 A/Title: Some more speract derivatives associated with eggs of sea urchins, *Pseudocentrotus*  
 A/Reference number: A60787; MUID:88242184; PMID:3378407  
 A/Molecule type: Protein  
 A/Residues: 1-10 <SU>  
 A/Cross-references: UNIPROT:Q7M4D0; UNIPARC:UPI000017A4DC  
 C/Comment: This oligopeptide from egg jelly is one of several from this species, all of  
 at shows some, but not absolute, species restriction.

Query Match 20.0%; Score 23; DB 2; Length 10;  
 Best Local Similarity 80.0%; Pred. No. 2e+03;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 16 SVNGG 20  
 DB 3 SLNGG 7

RESULT 18  
 S38736  
 Lipid transfer protein a1 - *Arabidopsis thaliana* (fragment)  
 C/Species: *Arabidopsis thaliana* (mouse-ear cress)  
 C/Date: 19-May-1994 #sequence\_revision 19-Jan-1996 #text\_change 19-Jan-1996  
 C/Accession: S38736  
 R/Segura, A.; Moreno, M.; Garcia-Olmedo, F.  
 FEBS Lett. 332, 243-246, 1993  
 A/Title: Purification and antipathogenic activity of lipid transfer proteins (LTPs) from  
 A/Reference number: S38736; MUID:94009709; PMID:8405465  
 A/Molecule type: Protein  
 A/Residues: 1-13 <SRG>  
 A/Cross-references: UNIPARC:UPI000017AFPC

Query Match 20.0%; Score 23; DB 2; Length 13;  
 Best Local Similarity 71.4%; Pred. No. 2.6e+03;  
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 12 LVCSVN 18  
 DB 2 LSCGSVN 8

RESULT 19  
 A08416  
 Lumbrikinase (EC 2.7.3.5) - earthworm (*Lumbricus terrestris*) (fragment)  
 C/Species: *Lumbricus terrestris* (common earthworm)  
 C/Date: 21-May-1988 #sequence\_revision 21-May-1988 #text\_change 09-Jul-2004  
 C/Accession: A08416  
 R/ter Terrosian, E.; Desvergne, G.; Pradel, L.A.; Kasab, R.; van Thool, N.  
 Eur. J. Biochem. 22, 585-592, 1971  
 A/Title: Comparative structural studies of the active site of ATP: guanidine phosphotran  
 A/Reference number: A08416; MUID:7206544; PMID:5128744  
 A/Accession: A08416  
 A/Molecule type: Protein  
 A/Residues: 1-15 <DBR>  
 A/Cross-references: UNIPROT:P11918; UNIPARC:UPI000012DEER  
 C/Keywords: phosphotransferase

Query Match 20.0%; Score 23; DB 2; Length 15;  
 Best Local Similarity 40.0%; Pred. No. 3e+03;  
 Matches 4; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 11 YLVCSVNGG 20  
 DB 3 YITCPGSNIG 12

RESULT 20

PH1604  
 Ig H chain V-D-J region (wild-type clone 327) - mouse (fragment)  
 C/Species: *Mus musculus* (house mouse)  
 C/Date: 02-Jun-1994 #sequence\_revision 02-Jun-1994 #text\_change 17-Mar-1999  
 C/Accession: PH1604  
 R/Lewinson, D.A.; Campos-Torres, J.; Leder, P.  
 J. Exp. Med. 178, 317-329, 1993  
 A/Title: Molecular characterization of transgene-induced immunodeficiency in B-less m/c  
 A/Reference number: PH1580; MUID:93301609; PMID:8315387  
 A/Accession: PH1604  
 A/Molecule type: DNA  
 A/Residues: 1-16 <LEV>  
 A/Cross-references: UNIPARC:UPI000017C6C0  
 A/Experimental source: bone marrow pre-B lymphocyte  
 C/Keywords: immunoglobulin

Query Match 20.0%; Score 23; DB 2; Length 16;  
 Best Local Similarity 44.4%; Pred. No. 3.2e+03;  
 Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 3 PHEPTINIKY 11  
 DB 4 PHEPTINIKY 12

RESULT 21  
 S15754  
 actin 6 - soybean (fragment)  
 C/Species: *Glycine max* (soybean)  
 C/Date: 04-Dec-1992 #sequence\_revision 04-Dec-1992 #text\_change 05-Oct-2004  
 C/Accession: S15754; S08049  
 R/Pearson, L.; Meagher, R.B.  
 Plant Mol. Biol. 14, 513-526, 1990  
 A/Title: Diverse soybean actin transcripts contain a large intron in the 5' untranslated  
 A/Reference number: S15754; MUID:91346640; PMID:2102831  
 A/Accession: S15754  
 A/Molecule type: DNA  
 A/Residues: 1-17 <PBA>  
 A/Cross-references: UNIPROT:P15986; UNIPARC:UPI0000125427; EMBL:X17119; MUID:918525; PID  
 C/Superfamily: Actin  
 C/Keywords: cytoskeleton

Query Match 20.0%; Score 23; DB 2; Length 17;  
 Best Local Similarity 50.0%; Pred. No. 3.4e+03;  
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 12 LVCSYNG 19  
 DB 10 LVCDNGTG 17

RESULT 22  
 S63503  
 83K protein - *Escherichia acidaminophilum* (fragment)  
 C/Species: *Escherichia acidaminophilum*  
 C/Date: 28-Oct-1996 #sequence\_revision 13-Mar-1997 #text\_change 17-Mar-1999  
 C/Accession: S63503  
 R/Meyer, M.; Granderath, K.; Andreessen, J.R.  
 Eur. J. Biochem. 234, 184-191, 1995  
 A/Title: Purification and characterization of protein (PB) of betaine reductase and its  
 A/Reference number: S63502; MUID:96096737; PMID:8529639  
 A/Accession: S63503  
 A/Status: preliminary  
 A/Molecule type: protein  
 A/Residues: 1-17 <MEY>  
 A/Cross-references: UNIPARC:UPI000017AD3D

Query Match 20.0%; Score 23; DB 2; Length 17;  
 Best Local Similarity 50.0%; Pred. No. 3.4e+03;  
 Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 7 NIKHYL 12  
:::|:|  
Db 2 DLHKFL 7

## RESULT 23

A58589  
alpha-conotoxin EI - cone shell (Conus ermineus)  
C:Species: Conus ermineus (ermine cone)  
C>Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004  
C:Accession: A58589  
R:Marinier, J.S.; Oliveira, B.M.; Gray, W.R.; Craig, A.G.; Groebe, D.R.; Abramson, S.N.;  
Biochemistry 34, 14519-14526, 1995  
A>Title: alpha-Conotoxin EI, a new nicotinic acetylcholine receptor antagonist with novel  
A:Reference number: A58589; PMID:96062516; PMID:7578057  
A:Accession: A58589  
A:Molecule type: protein  
A:Residues: 1-18 <MAR>  
A:Cross-references: UNIPROT:P50982; UNIPARC:UPI00001287C0  
A>Note: sequence confirmed by chemical synthesis  
C:Comment: This alpha-conotoxin, as an acetylcholine receptor inhibitor, is a postsynaptic  
C:Superfamily: alpha-conotoxin  
C:Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; hydroxyproline; pro  
F:3/Modified site: 4-hydroxyproline (Pro) #status experimental  
F:4-10,5-18/Disulfide bonds: #status experimental  
F:18/Modified site: amidated carboxyl end (Cys) #status experimental

Query Match 19.6%; Score 22.5; DB 1; Length 18;  
Best Local Similarity 41.7%; Pred. No. 4.3e+03;  
Matches 5; Conservative 2; Mismatches 4; Indels 1; Gaps 1;

QY 4 HPT-NIKHYLVC 14  
|||:|  
Db 7 HPTCNMSNPQIC 18

## RESULT 24

A48394  
major fat-globule membrane protein/MGF-E8 homolog - guinea pig (fragment)  
C:Species: Cavia porcellus (guinea pig)  
C>Date: 19-Nov-1993 #sequence\_revision 18-Nov-1994 #text\_change 31-Oct-1997  
C:Accession: A48394  
R:Mathier, I.H.; Banghart, L.R.; Lane, W.S.  
Biochem. Mol. Biol. Int. 29, 545-554, 1993  
A>Title: The major fat-globule membrane proteins, bovine components 15/16 and guinea-pig  
11-like sequences.  
A:Reference number: A48394; PMID:93250576; PMID:8485470  
A:Accession: A48394  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-20 <MAT>  
A:Cross-references: UNIPARC:UPI0000177APF  
A:Experimental source: milk  
A>Note: sequence extracted from NCBI backbone (NCBI:131440)  
C:Superfamily: milk fat globule protein; discoidin I amino-terminal homology; EGF homolog

Query Match 19.6%; Score 22.5; DB 2; Length 20;  
Best Local Similarity 50.0%; Pred. No. 4.8e+03;  
Matches 5; Conservative 2; Mismatches 0; Indels 3; Gaps 1;

QY 14 CES--VNGG 20  
|:|:|  
Db 6 CDSSTLNGG 15

## RESULT 25

B59272  
peptide-N4-(N-acetyl-beta-glucosaminyl)asparagine amidase (EC 3.5.1.52) A, small chain -  
N:Alternate names: peptide N-glycosidase  
C:Species: Prunus dulcis var. sativa (sweet almond)  
C>Date: 19-May-2000 #sequence\_revision 19-May-2000 #text\_change 09-Jul-2004  
C:Accession: B59272  
R:Altman, F.; Paschinger, K.; Dalik, T.; Vorauer, K.

Eur. J. Biochem. 252, 118-123, 1998  
A>Title: Characterisation of peptide-N4-(N-acetyl-beta-glucosaminyl)asparagine amidase A  
A:Reference number: B59272; PMID:98181894; PMID:9523720  
A:Accession: B59272  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-10 <ALT>  
A:Cross-references: UNIPROT:P81898; UNIPARC:UPI00000ABBC4  
C:Keywords: hydrolase

Query Match 19.1%; Score 22; DB 2; Length 10;  
Best Local Similarity 42.9%; Pred. No. 2.8e+03;  
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 PTNHYK 11  
||:|  
Db 2 PTPHDP 8

## RESULT 26

B37196  
bradykinin-potentiating peptide 2 - island jararaca  
C:Species: Bothrops insularis (island jararaca)  
C>Date: 14-Feb-1992 #sequence\_revision 01-Dec-1992 #text\_change 09-Jul-2004  
C:Accession: B37196  
R:Cintra, A.C.O.; Vieira, C.A.; Giglio, J.R.  
J. Protein Chem. 9, 221-227, 1990  
A>Title: Primary structure and biological activity of bradykinin potentiating peptides f  
A:Reference number: A37196; PMID:90351557; PMID:2386615  
A:Accession: B37196  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-10 <CIN>  
A:Cross-references: UNIPROT:P30422; UNIPARC:UPI0000126A8F  
C:Keywords: pyroglutamic acid  
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 19.1%; Score 22; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PHP 5  
|||  
Db 4 PHP 6

## RESULT 27

B60409  
kassinin-like peptide K-1 - frog (Pseudophryne guentheri)  
C:Species: Pseudophryne guentheri  
C>Date: 30-Jan-1993 #sequence\_revision 30-Jan-1993 #text\_change 18-Aug-2004  
C:Accession: B60409  
R:Simmaco, M.; Severini, C.; De Blase, D.; Barra, D.; Bossa, F.; Roberts, J.D.; Melchior  
Peptides 11, 299-304, 1990  
A>Title: Six novel tachykinin- and bombesin-related peptides from the skin of the Austro  
A:Reference number: A60409; PMID:90287814; PMID:2356157  
A:Accession: B60409  
A:Molecule type: protein  
A:Residues: 1-11 <SIM>  
A:Cross-references: UNIPROT:P42986; UNIPARC:UPI0000136PCD  
A>Note: this peptide was also found in a deamidated form  
C:Keywords: amidated carboxyl end; pyroglutamic acid  
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F:11/Modified site: amidated carboxyl end (Met) (partial) #status experimental

Query Match 19.1%; Score 22; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PHP 5  
|||  
Db 2 PHP 4

## RESULT 28

D60409

A:Species: Pseudophryne guentheri

C/Date: 30-Jan-1993 #sequence\_revision 30-Jan-1993 #text\_change 16-Aug-2004

C/Accession: D60409

R/Simanco, M.; Severini, C.; De Biase, D.; Barra, D.; Bosca, F.; Roberts, J.D.; Melchior

Peptides 11, 299-304, 1990

A/Title: Six novel tachykinin- and bombesin-related peptides from the skin of the Austre

A/Reference number: A60409; PMID:90287814; PMID:2356157

A/Accession: D60409

A/Molecule type: protein

A/Residues: 1-11 &lt;SIM&gt;

A/Cross-references: UNIPROT:P42988; UNIPARC:UPI0000136FD7

P/Modified site: amidated carboxyl end; pyroglutamic acid (Gln) #status experimental

P/1/Modified site: amidated carboxyl end (Met) #status experimental

## Query Match

Best Local Similarity 19.1%; Score 22; DB 2; Length 11;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PHP 5

Db 2 PHP 4

## RESULT 29

B47415

A:Species: 1-phosphate guanylyltransferase (EC 2.7.7.13) 43k alpha chain - pig (fragment)

N/Alternate names: GDP-mannose pyrophosphorylase 43k alpha chain

C/Species: Sus scrofa domestica (domestic pig)

C/Date: 25-Feb-1994 #sequence\_revision 12-Aug-1996 #text\_change 12-Aug-1996

C/Accession: B47415

R/Szumilo, T.; Drake, R.R.; York, J.L.; Elbein, A.D.

J. Biol. Chem. 268, 17943-17950, 1993

A/Title: GDP-mannose pyrophosphorylase. Purification to homogeneity, properties, and uti

A/Reference number: A47415; PMID:93352609; PMID:7688733

A/Accession: B47415

A/Molecule type: protein

A/Residues: 1-13 &lt;82U&gt;

A/Cross-references: UNIPARC:UPI000017C470

A/Experimental source: liver

C/Complex: The enzyme appears to be a heterodimer of alpha and beta chains.

C/Function: Generates GDP-mannose and pyrophosphate from mannose-1-phosphate and GTP

A/Note: also catalyzes synthesis of GDP-glucose from glucose-1-phosphate (EC 2.7.7.34 ac

C/Keywords: blocked amino end; nucleotidyltransferase

## Query Match

Best Local Similarity 19.1%; Score 22; DB 2; Length 13;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PHP 5

Db 8 PHP 10

## RESULT 30

PH0788

A:Species: T-cell receptor alpha chain (E22 V-alpha-8.F3.4) - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997

C/Accession: PH0788

R/Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.

J. Exp. Med. 174, 1371-1383, 1991

A/Title: T cell receptor gene in a series of class I major histocompatibility complex-2

A/Reference number: PH0746; PMID:9207846; PMID:1836010

A/Accession: PH0788

A/Molecule type: mRNA

A/Residues: 1-13 &lt;CNS&gt;

A/Cross-references: UNIPARC:UPI000017C76A; EMBL:X60893

A/Experimental source: T lymphocyte

C/Keywords: T-cell receptor

## Query Match

Best Local Similarity 19.1%; Score 22; DB 2; Length 13;

Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 14 CBSVNG 20

Db 1 CALVNSG 7

## RESULT 31

S60007

A:Species: Glial hyaluronate-binding protein - human (fragments)

C/Species: Homo sapiens (man)

C/Date: 23-Aug-1996 #sequence\_revision 13-Mar-1997 #text\_change 07-May-1999

C/Accession: S60007

R/Perides, G.; Asher, R.A.; Lark, M.W.; Lane, W.S.; Robinson, R.A.; Bignami, A.

Biochem. J. 312, 377-384, 1995

A/Title: Glial hyaluronate-binding protein: a product of metalloproteinase digestion of

A/Reference number: S60007; PMID:96103171; PMID:8526845

A/Accession: S60007

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-15 &lt;PER&gt;

A/Cross-references: UNIPARC:UPI000017C138

## Query Match

Best Local Similarity 19.1%; Score 22; DB 2; Length 15;

Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 14 CBSVNG 19

Db 7 CLDVNG 12

## RESULT 32

B56046

A:Species: urinary tract stone matrix protein 2, 21K - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 12-Apr-1995 #sequence\_revision 12-Apr-1995 #text\_change 12-Apr-1995

C/Accession: B56046

R/Binette, J.P.; Binette, M.B.; Gawinowicz, M.A.; Kendrick, N.

submitted to the Protein Sequence Database, February 1995

A/Description: Isolation, characterization and sequence of stone proteins.

A/Reference number: A56046

A/Accession: B56046

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-15 &lt;BIN&gt;

A/Cross-references: UNIPARC:UPI000017C408

## Query Match

Best Local Similarity 19.1%; Score 22; DB 2; Length 15;

Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 11 YLVCSVNG 20

Db 1 YVLQGVAPG 10

## RESULT 33

S00123

A:Species: dehydroepiandrosterone S-nuccinyltransferase (EC 2.3.1.61) - bovine (fragment)

C/Species: Bos primigenius taurus (cattle)

C/Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 09-Jul-2004

C/Accession: S00123

R/Bradford, A.P.; Altken, A.; Beg, F.; Cook, K.G.; Yeaman, S.J.

FEBS Lett. 222, 211-214, 1987

A/Title: Amino acid sequence surrounding the lipoid acid cofactor of bovine kidney 2-oxo

A/Reference number: S00123; MUID:88005143; PMID:3115829  
A/Accession: S00123  
A/Molecule type: protein  
A/Residues: 1-16 <BR>  
A/Cross-references: UNIPROT:P11179, UNIPARC:UPI0000130BDF  
C/Superfamily: dihydrolipoamide acetyltransferase; lipoyl/biotin-binding homology  
C/Keywords: acyltransferase; coenzyme A; lipoamide; mitochondrion; oxidoreductase; trica  
P:1-16/Domain: lipoyl/biotin-binding homology (fragment) <LPB>  
P:5/Binding site: lipoamide (lys) (covalent) #status experimental

Query Match 19.1%; Score 22; DB 2; Length 16;  
Best Local Similarity 50.0%; Pred. No. 4.5e+03;  
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 IHPPTN 7  
DB 10 VPSPAN 15

RESULT 34  
A41170  
photocystem II 6.1k protein - Chlamydomonas reinhardtii (fragment)  
C/Species: Chlamydomonas reinhardtii  
C/Date: 05-Jun-1992 #sequence\_revision 05-Jun-1992 #text\_change 09-Jul-2004  
C/Accession: A41170  
R/de Vltty, C.; Diner, B.A.; Popot, J.L.  
J. Biol. Chem. 266, 16614-16621, 1991  
A/Title: Photosystem II particles from Chlamydomonas reinhardtii. Purification, molecule  
A/Reference number: A41170; MUID:91358452; PMID:1885590  
A/Accession: A41170  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-16 <DEV>  
A/Cross-references: UNIPROT:Q7M14; UNIPARC:UPI000017AF05

Query Match 19.1%; Score 22; DB 2; Length 16;  
Best Local Similarity 62.5%; Pred. No. 4.5e+03;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 12 LVCEVNG 19  
DB 1 LVDERNNG 8

RESULT 35  
A11488  
taurocyamine kinase (EC 2.7.3.4) - lugworm (fragment)  
C/Species: Arenicola marina (lugworm, rock worm)  
C/Date: 05-Jun-1987 #sequence\_revision 05-Jun-1987 #text\_change 09-Jul-2004  
C/Accession: A11488  
R/Brevet, A.; Zeitoun, Y.; Pradel, L.A.  
Biochim. Biophys. Acta 393, 1-9, 1975  
A/Title: Comparative structural studies of the active site of ATP-guanidine phosphotrans  
A/Reference number: A11488; MUID:75184095; PMID:166684  
A/Accession: A11488  
A/Molecule type: protein  
A/Residues: 1-16 <BRE>  
A/Cross-references: UNIPROT:P11917; UNIPARC:UPI000012E121  
C/Keywords: phosphotransferase

Query Match 19.1%; Score 22; DB 2; Length 16;  
Best Local Similarity 100.0%; Pred. No. 4.5e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PTNI 8  
DB 8 PTNI 11

RESULT 36  
S59512  
probable integrin alpha3 beta1 - mouse (fragment)  
C/Species: Mus musculus (house mouse)

C/Date: 19-Mar-1997 #sequence\_revision 25-Apr-1997 #text\_change 09-Jul-2004  
C/Accession: S59512  
R/McCormick, J.I.; Johnstone, R.M.  
Biochem. J. 311, 743-751, 1995  
A/Title: Identification of the integrin alpha(3)beta(1) as a component of a partially pu  
A/Reference number: S59512; MUID:96067588; PMID:7487928  
A/Accession: S59512  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-17 <MC>  
A/Cross-references: UNIPROT:Q7MOD8; UNIPARC:UPI00000353C9

Query Match 19.1%; Score 22; DB 2; Length 17;  
Best Local Similarity 55.6%; Pred. No. 4.8e+03;  
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 12 LVCEVNG 20  
DB 9 VVKEAVNPG 17

RESULT 37  
B48839  
T-cell receptor beta chain V-N-J region - mouse (fragment)  
C/Species: Mus musculus (house mouse)  
C/Date: 07-Apr-1994 #sequence\_revision 18-Nov-1994 #text\_change 30-May-1997  
C/Accession: B48839  
R/Katz, J.D.; Wang, B.; Hawkins, K.; Benoist, C.; Mathis, D.  
Cell 74, 1089-1100, 1993  
A/Title: Following a diabetogenic T cell from genesis through pathogenesis.  
A/Reference number: A48839; MUID:94006520; PMID:8402882  
A/Accession: B48839  
A/Status: preliminary; not compared with conceptual translation  
A/Molecule type: nucleic acid  
A/Residues: 1-18 <RAT>  
A/Cross-references: UNIPARC:UPI000017C857  
A/Experimental source: NOD, transgenic, diabetogenic T cell clone BDC2.5  
A/Note: sequence extracted from NCBI backbone (NCBIP:138472)  
C/Keywords: T-cell receptor

Query Match 19.1%; Score 22; DB 2; Length 18;  
Best Local Similarity 57.1%; Pred. No. 5.1e+03;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 14 CESVNG 20  
DB 1 CASSQGG 7

RESULT 38  
D44101  
calmodulin, vasopactive intestinal peptide-binding protein, VIP binding protein, p18 - gu  
C/Species: Cavia porcellus (guinea pig)  
C/Date: 27-Apr-1993 #sequence\_revision 18-Nov-1994 #text\_change 07-Feb-1997  
C/Accession: D44101  
R/Stallwood, D.; Bruggen, C.H.; Baggenstoss, B.A.; Stemmer, P.M.; Shitraga, H.; Landers,  
J. Biol. Chem. 267, 19617-19621, 1992  
A/Title: Identity of a membrane-bound vasopactive intestinal peptide-binding protein with  
A/Reference number: A44101; MUID:92406918; PMID:1527080  
A/Accession: D44101  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-19 <STA>  
A/Cross-references: UNIPARC:UPI000017CA29  
A/Experimental source: lung membranes  
A/Note: sequence extracted from NCBI Backbone (NCBIP:114113)  
C/Keywords: intestine

Query Match 19.1%; Score 22; DB 2; Length 19;  
Best Local Similarity 38.5%; Pred. No. 5.4e+03;  
Matches 5; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 6 TIIHKYLVCEVNV 18

Db 4 TNLGEXLTDEBVD 16

## RESULT 39

A38566

GTP-binding protein G25K - bovine (fragmente)

C/Species: Bos primigenius taurus (cattle)

C/Date: 31-Jan-1992 #sequence\_revision 31-Jan-1992 #text\_change 16-Jul-1999

C/Accession: A38566

R/Yamane, H.K.; Farnsworth, C.C.; Xie, H.; Evans, T.; Howald, W.N.; Gelb, M.H.; Glomset, Proc. Natl. Acad. Sci. U.S.A. 88, 286-290, 1991

A/Title: Membrane-binding domain of the small G protein G25K contains an S-(all-trans-g

A/Reference number: A38566; MUID:91095446; PMID:1858776

A/Accession: A38566

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-20 &lt;YAM&gt;

A/Cross-references: UNIPARC:UPI000017643D

C/Keywords: GTP binding

F/8-11/Region: GTP-binding NKXD motif

Query Match 19.1%; Score 22; DB 2; Length 20;

Best Local Similarity 40.0%; Pred. No. 5.7e+03;

Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 DIPHTNIMK 10

Db 11 DLADPETERK 20

## RESULT 40

T50757

pufK protein [imported] - Rhodobacter sphaeroides

C/Species: Rhodobacter sphaeroides

C/Date: 21-Jul-2000 #sequence\_revision 21-Jul-2000 #text\_change 09-Jul-2004

C/Accession: T50757

R/Choudhary, M.; Kaplan, S.

Nucleic Acids Res. 28, 862-867, 2000

A/Title: DNA sequence analysis of the photosynthesis region of Rhodobacter sphaeroides 2

A/Reference number: Z25222; MUID:20115911; PMID:10648776

A/Residues: 1-20 &lt;CHO&gt;

A/Cross-references: UNIPROT:Q53121; UNIPARC:UPI00001329F3; EMBL:AF195122; PIRN:AAF24301.

A/Experimental source: strain 2.4.1

A/Genetics:

A/Gene: pufK

Query Match 19.1%; Score 22; DB 2; Length 20;

Best Local Similarity 21.1%; Pred. No. 5.7e+03;

Matches 4; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY 2 IPHPTNIHKLVESVNGG 20

Db 2 VPYRPNRHOHVAVLSRSGG 20

## RESULT 41

A57444

neuropeptide Grb-AST B1 - two-spotted cricket

C/Species: Gryllus bimaculatus (two-spotted cricket)

C/Date: 26-Jan-1996 #sequence\_revision 26-Jan-1996 #text\_change 09-Jul-2004

C/Accession: A57444

R/Lorenz, M.W.; Kellner, R.; Hoffmann, K.H.

J. Biol. Chem. 270, 21103-21108, 1995

A/Title: A family of neuropeptides that inhibit juvenile hormone biosynthesis in the cri

A/Reference number: A57444; MUID:95403341; PMID:7673141

A/Accession: A57444

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-9 <LOR>

A/Cross-references: UNIPROT:Q7M3N9; UNIPARC:UPI000017BE17

Query Match 18.3%; Score 21; DB 2; Length 9;

Best Local Similarity 50.0%; Pred. No. 2.8e+05;

Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 15 ESYVNG 20

Db 3 QDLNNG 8

## RESULT 42

PH0947

T-cell receptor beta chain V-D-J region (clone A2) - rat (fragment)

C/Species: Rattus norvegicus (Norway rat)

C/Date: 09-Oct-1992 #sequence\_revision 09-Oct-1992 #text\_change 30-May-1997

C/Accession: PH0947

R/Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.

J. Exp. Med. 174, 1467-1476, 1991

A/Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergy

A/Reference number: PH0891; MUID:92078857; PMID:1836012

A/Accession: PH0947

A/Molecule type: mRNA

A/Residues: 1-11 &lt;GOL&gt;

A/Cross-references: UNIPARC:UPI000017C9ED

A/Experimental source: myelin basic protein fragment-reactive T-cell, recovered from ex

C/Keywords: T-cell receptor

Query Match 18.3%; Score 21; DB 2; Length 11;

Best Local Similarity 57.1%; Pred. No. 4.4e+03;

Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 14 CBSVNGG 20

Db 1 CSMRRGG 7

## RESULT 43

A54315

enteractin/nidogen - bovine (fragment)

C/Species: Bos primigenius taurus (cattle)

C/Date: 13-Sep-1994 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004

C/Accession: A54315

R/Katcz, A.; Fish, A.J.; Kleppel, M.M.; Hagen, S.G.; Michael, A.F.; Butkowski, R.J.

Kidney Int. 40, 643-652, 1991

A/Title: Renal entactin (nidogen): isolation, characterization and tissue distribution.

A/Reference number: A54315; MUID:92079440; PMID:1745013

A/Accession: A54315

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-12 &lt;KAT&gt;

A/Cross-references: UNIPROT:Q9TRU9; UNIPARC:UPI0000088761

A/Experimental source: renal tubular basement membrane

A/Note: sequence extracted from NCBI backbone (NCBI:71053)

C/Superfamily: nidogen; EGF homology; LDL receptor VYTD-containing repeat homology; tny

Query Match 18.3%; Score 21; DB 2; Length 12;

Best Local Similarity 50.0%; Pred. No. 4.8e+03;

Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 12 LVCEVYNG 19

Db 2 IVTDSVRG 9

## RESULT 44

B47171

chondroitin sulfate proteoglycan PG-M core protein, splice form VI - chicken (fragment)

N/Alternate names: versican-like chondroitin sulfate proteoglycan

C/Species: Gallus gallus (chicken)

C/Date: 21-Sep-1993 #sequence\_revision 18-Nov-1994 #text\_change 28-Feb-1997

C/Accession: B47171

R/Shinomura, T.; Mishida, Y.; Ito, K.; Kimata, K.  
 J. Biol. Chem. 268, 14461-14469, 1993  
 A>Title: CDNA cloning of PG-M, a large chondroitin sulfate proteoglycan expressed during

A/Reference number: A47171; MUID:93300846; PMID:8314602  
 A/Accession: B47171  
 A/Status: preliminary  
 A/Molecule type: nucleic acid  
 A/Residues: 1-12 <SH1>  
 A/Cross-references: UNIPARC:UPI000017BPF2  
 A/Experimental source: CBF, embryo fibroblasts  
 A/Note: sequence extracted from NCBI backbone (NCBIN:134459, NCBI:134462)

Query Match 18.3%; Score 21; DB 2; Length 12;  
 Best Local Similarity 37.0%; Pred. No. 4.8e+03;  
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 HPTN 7  
 DB 8 HPVN 11

RESULT 45  
 A54326  
 glandular kallikrein-1 - human (fragment)  
 C/Species: Homo sapiens (man)  
 C/Date: 29-Aug-1994 #sequence\_revision 18-Nov-1994 #text\_change 23-Mar-1995  
 C/Accession: A54326  
 R/Riegman, P.H.; Vlietstra, R.J.; van der Korput, H.A.; Romijn, J.C.; Trapman, J.  
 Mol. Cell. Endocrinol. 76, 181-190, 1991  
 A>Title: Identification and androgen-regulated expression of two major human glandular K  
 A/Reference number: A54326; MUID:92324494; PMID:1726490  
 A/Accession: A54326  
 A/Status: preliminary; not compared with conceptual translation  
 A/Molecule type: nucleic acid  
 A/Residues: 1-13 <R1E>  
 A/Cross-references: UNIPARC:UPI0000035475  
 A/Experimental source: prostate  
 A/Note: sequence extracted from NCBI backbone (NCBI:108060)

Query Match 18.3%; Score 21; DB 2; Length 13;  
 Best Local Similarity 37.5%; Pred. No. 5.2e+03;  
 Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 IPHPTNH 9  
 DB 1 VSHPSQH 8

RESULT 46  
 S41601  
 Interferon alpha receptor 1 - human (fragments)  
 C/Species: Homo sapiens (man)  
 C/Date: 25-Dec-1994 #sequence\_revision 01-Dec-1995 #text\_change 30-May-1997  
 C/Accession: S41601  
 R/Abxmovich, C.; Ratovitski, E.; Lundgren, E.; Revel, M.  
 FEBS Lett. 338, 295-300, 1994  
 A>Title: Identification of mRNAs encoding two different soluble forms of the human inter  
 A/Reference number: S41601; MUID:94139943; PMID:8307198  
 A/Accession: S41601  
 A/Molecule type: mRNA  
 A/Residues: 1-14 <ABR>  
 A/Cross-references: UNIPARC:UPI000017C27A  
 C/Keywords: cytokine receptor

Query Match 18.3%; Score 21; DB 2; Length 14;  
 Best Local Similarity 66.7%; Pred. No. 5.6e+03;  
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 13 VCESVN 18  
 DB 3 VCESVN 8

RESULT 47  
 PQ0232  
 Cystatin CI-4a - maize (fragment)  
 N/Alternate names: cysteine proteinase inhibitor  
 C/Species: Zea mays (maize)  
 C/Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 09-Jul-2004  
 C/Accession: PQ0232  
 R/Abbe, M.; Arai, S.  
 Agric. Biol. Chem. 55, 2417-2418, 1991  
 A>Title: Some properties of a cysteine proteinase inhibitor from corn endosperm.  
 A/Reference number: PQ0232; MUID:92118331; PMID:1368742  
 A/Accession: PQ0232  
 A/Molecule type: protein  
 A/Residues: 1-15 <ABR>  
 A/Cross-references: UNIPROT:Q9S918, UNIPARC:UPI000009FDBE  
 C/Superfamily: cystatin, cystatin homology

Query Match 18.3%; Score 21; DB 2; Length 15;  
 Best Local Similarity 33.3%; Pred. No. 6.1e+03;  
 Matches 5; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 3 PPHNHHKLVCEV 17  
 DB 1 PHQELGMAVTEHV 15

RESULT 48  
 A56786  
 pmeIoyl-CoA synthase - Bacillus sphaericus (fragment)  
 C/Species: Bacillus sphaericus  
 C/Date: 18-Aug-1995 #sequence\_revision 18-Aug-1995 #text\_change 18-Aug-1995  
 C/Accession: A56786  
 R/Ploux, O.; Soularue, P.; Marquet, A.; Gloeckler, R.; Lemoine, Y.  
 Biochem. J. 287, 685-690, 1992  
 A>Title: Investigation of the first step of biotin biosynthesis in Bacillus sphaericus.  
 A/Reference number: A56786; MUID:93075017; PMID:1445232  
 A/Accession: A56786  
 A/Status: preliminary  
 A/Molecule type: protein  
 A/Residues: 1-15 <PLO>  
 A/Cross-references: UNIPARC:UPI000017ACAB  
 A/Experimental source: Bacillus sphaericus protein overexpressed in Escherichia coli  
 A/Note: sequence extracted from NCBI backbone (NCBI:117639)  
 C/Genetics:  
 A/Gene: bion  
 C/Keywords: biotin biosynthesis; homodimer

Query Match 18.3%; Score 21; DB 2; Length 15;  
 Best Local Similarity 50.0%; Pred. No. 6.1e+03;  
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 12 LVCEV 17  
 DB 2 LVCYSI 7

RESULT 49  
 PH0136  
 T-cell receptor beta chain V-D-J region MS18 - human (fragment)  
 C/Species: Homo sapiens (man)  
 C/Date: 23-Nov-1991 #sequence\_revision 23-Nov-1991 #text\_change 30-May-1997  
 C/Accession: PH0136  
 R/Martin, R.; Howell, M.D.; Jarquemade, D.; Flerlage, M.; Richert, J.; Brostoff, S.; Le  
 J. Exp. Med. 173, 19-24, 1991  
 A>Title: A myelin basic protein peptide is recognized by cytotoxic T cells in the contex  
 A/Reference number: PH0135; MUID:91086843; PMID:1702137  
 A/Accession: PH0136  
 A/Molecule type: mRNA  
 A/Residues: 1-15 <MAR>  
 A/Cross-references: UNIPARC:UPI000017C3AE  
 C/Keywords: T-cell receptor



Query Match 18.3% Score 21; DB 2; Length 15;  
 Best Local Similarity 44.4%; Pred. No. 6.1e+03;  
 Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 11 YLVCESVNG 19  
 DB 1 YLVCESVNG 9

## RESULT 50

CS9045

Alpha-conotoxin Aulic - cone shell (Conus aulicus)

C/Species: Conus aulicus (cone shell)

C/Date: 23-Jul-1999 #sequence\_rev1999 23-Jul-1999 #text\_change 09-Jul-2004

C/Accession: CS9045

R/Luo, S.; Kulak, J.M.; Cartier, G.B.; Jacobsen, R.B.; Yoshikami, D.; Oliveira, B.M.; McI

J. Neurosci. 18, 8571-8579, 1998

A/Title: Alpha-conotoxin Aulic selectively blocks alpha3beta4 nicotinic acetylcholine rec

A/Reference number: A59045; PMID:9903392; PMID:9786965

A/Accession: CS9045

A/Status: preliminary

A/Molecule type: protein

A/Residues: 116 &lt;LND&gt;

A/Cross-references: UNIPROT:P56641; UNIPARC:UPI00001287D0

C/Species: alpha-conotoxin

C/Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; postsynaptic neurot

P/1-16/Product: alpha-conotoxin Aulic #status experimental &lt;MT&gt;

P/2-8-16/Disulfide bonds: #status experimental

P/16/Modified site: amidated carboxyl end (Cys) #status experimental

Query Match 18.3% Score 21; DB 2; Length 16;  
 Best Local Similarity 40.0%; Pred. No. 6.5e+03;

Matches 4; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 11 YLVCESVNG 20  
 DB 5 YLVCESVNG 14

## RESULT 51

C49255

T-cell receptor beta chain V-D-J-C region (V beta 9, J beta 2.7) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 21-Jan-1994 #sequence\_rev1999 18-Nov-1994 #text\_change 30-May-1997

C/Accession: C49255

R/Rosenberg, W.M.; Moss, P.A.; Bell, J.I.

Eur. J. Immunol. 22, 541-549, 1992

A/Title: Variation in human T cell receptor V beta and J beta repertoire: analysis using

A/Reference number: A49039; PMID:92164737; PMID:1311263

A/Accession: C49255

A/Status: preliminary; not compared with conceptual translation

A/Molecule type: nucleic acid

A/Residues: 1-17 &lt;ROS&gt;

A/Cross-references: UNIPARC:UPI000017C3BB

A/Note: sequence extracted from NCBI backbone (NCBIP:90724)

C/Keywords: T-cell receptor

Query Match 18.3% Score 21; DB 2; Length 17;  
 Best Local Similarity 33.3%; Pred. No. 6.9e+03;  
 Matches 3; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 PHPTNHY 11  
 DB 7 PABSYEY 15

## RESULT 52

S15064

hypothetical protein A - Trypanosoma brucei (fragment)

C/Species: Trypanosoma brucei

C/Date: 31-Dec-1993 #sequence\_rev1999 31-Dec-1993 #text\_change 09-Jul-2004

C/Accession: S15064; S12677

R/Clayton, C.B.

submitted to the EMBL Data Library, April 1990  
 A/Reference number: S15063

A/Accession: S15064

A/Molecule type: DNA

A/Residues: 1-17 &lt;CLA&gt;

A/Cross-references: UNIPROT:P17961; UNIPARC:UPI000013A111; EMBL:X52586; NID:G10397; PID

R/Vijayasarathy, S.; Ernest, I.; Itzhaki, J.E.; Sherman, D.; Mowatt, M.R.; Michels, P.A.

Nucleic Acids Res. 18, 2967-2975, 1990

A/Title: The genes encoding fructose biphosphate aldolase in Trypanosoma brucei are in

A/Reference number: S12673; PMID:90272402; PMID:2349093

A/Accession: S12677

A/Molecule type: DNA

A/Residues: 1-9 &lt;VID&gt;

A/Cross-references: UNIPARC:UPI000017B597; EMBL:X52586

Query Match 18.3% Score 21; DB 2; Length 17;  
 Best Local Similarity 60.0%; Pred. No. 6.9e+03;  
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 IPHPT 6  
 DB 12 LPRPT 16

## RESULT 53

PQ0680

photosystem I 5.6K K chain - common tobacco (fragment)

C/Species: Nicotiana tabacum (common tobacco)

C/Date: 19-May-1994 #sequence\_rev1999 19-May-1994 #text\_change 09-Jul-2004

C/Accession: PQ0680

R/Obokata, J.; Miki, K.; Hayashida, N.; Nakamura, M.; Sugitara, M.

Plant Physiol. 102, 1259-1267, 1993

A/Title: Molecular heterogeneity of photosystem I. psad, psae, psaf, psah and psal are

A/Reference number: PQ0667; PMID:94105345; PMID:8278548

A/Accession: PQ0680

A/Molecule type: protein

A/Residues: 1-18 &lt;ORO&gt;

A/Cross-references: UNIPROT:Q9T2J5; UNIPARC:UPI0000097F66

C/Keywords: chloroplast; photosynthesis; photosystem I; thylakoid

Query Match 18.3% Score 21; DB 2; Length 18;  
 Best Local Similarity 57.1%; Pred. No. 7.3e+03;  
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 IPHPTI 8  
 DB 3 ICSPTVL 9

## RESULT 54

S20322

gluten - wheat

C/Species: Triticum aestivum (common wheat)

C/Date: 19-Mar-1997 #sequence\_rev1999 19-Mar-1997 #text\_change 09-Jul-2004

C/Accession: S20322

R/Fukudome, S.; Yoshikawa, M.

FEBS Lett. 296, 107-111, 1992

A/Title: Opioid peptides derived from wheat gluten: their isolation and characterization.

A/Reference number: S20322; PMID:92111773; PMID:1309704

A/Accession: S20322

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-18 &lt;FOK&gt;

A/Cross-references: UNIPROT:Q7MIG0; UNIPARC:UPI000017B139

Query Match 18.3% Score 21; DB 2; Length 18;  
 Best Local Similarity 37.5%; Pred. No. 7.3e+03;  
 Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 4 IPHPTIHY 11  
 DB 3 YPTGYVY 10

## RESULT 55

A24589

photosystem II chlorophyll a-binding protein psbB - barley chloroplast (fragment)

C/Species: chloroplast Hordeum vulgare (barley)

C/Date: 08-Aug-1987 #sequence\_revision 08-Aug-1987 #text\_change 09-Jul-2004

C/Accession: A24589

R/Hinz, U.G.

C/Reference number: A24589

A/Accession: A24589

A/Molecule type: protein

A/Residues: 1-20 &lt;HIN&gt;

A/Cross-references: UNIPROT:P10900; UNIPARC:UPI0000178147

C/Genetic3:

A/Status: preliminary

A/Genome: chloroplast

A/Reference number: A56894; MUID:92405551; PMID:1526140

A/Contents: Deshayes, red brachiopod shells

A/Accession: C56894

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-20 &lt;CUS&gt;

A/Cross-references: UNIPARC:UPI000017CACA

A/Note: sequence extracted from NCBI backbone (NCBIP:114884)

C/Keywords: chromoprotein

Query Match

Best Local Similarity 18.3%; Score 21; DB 2; Length 20;

Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 IPPTNIRK 10

DB 5 LPVATMISK 13

RESULT 59

B56894

intracrystalline chromoprotein 1 - Waltonia inconspicua (fragment)

C/Species: Waltonia inconspicua

C/Date: 05-Jan-1996 #sequence\_revision 05-Jan-1996 #text\_change 09-Jul-2004

C/Accession: B56894

R/Cusack, M.; Curry, G.; Clegg, H.; Abbott, G.

Comp. Biochem. Physiol. B 102, 93-95, 1992

A/Title: An intracrystalline chromoprotein from red brachiopod shells: implications for

A/Reference number: A56894; MUID:92405551; PMID:1526140

A/Contents: Sowerby, red brachiopod shells

A/Accession: B56894

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-20 &lt;CUS&gt;

A/Cross-references: UNIPROT:Q7M466; UNIPARC:UPI000017CACC

A/Note: sequence extracted from NCBI backbone (NCBIP:114883)

C/Keywords: chromoprotein

Query Match

Best Local Similarity 18.3%; Score 21; DB 2; Length 20;

Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 IPPTNIRK 10

DB 5 LPVATMISK 13

RESULT 60

S44465

pyrrocoricin - Pyrrhocoris apterus

C/Species: Pyrrhocoris apterus

C/Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 09-Jul-2004

C/Accession: S44465

R/Cocciandich, S.; Dupont, A.; Hegy, G.; Lanot, R.; Holdér, F.; Hetru, C.; Hoffmann, J.A.

Biochem. J. 300, 567-575, 1994

A/Title: Novel inducible antibacterial peptides from a hemipteran insect, the sep-suckli

A/Reference number: S44465; MUID:94271176; PMID:8002963

Query Match

Best Local Similarity 18.3%; Score 21; DB 2; Length 20;

Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 IPPTNIRK 10

DB 5 LPVATMISK 13

A/Accession: S44465  
 A/Molecule type: protein  
 A/Residues: 1-20 <COC>  
 A/Cross-references: UNIPROT:P37362; UNIPARC:UPI0000132B13  
 C/Function:  
 A/Description: antibacterial protein  
 A/Note: active against Gram-negative bacteria  
 C/Keywords: antibacterial; hemolymph; immune response

Query Match 18.3%; Score 21; DB 2; Length 20;  
 Best Local Similarity 60.0%; Pred. No. 8.2e+03;  
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 IPHPT 6  
 DB 7 LPRPT 11

## RESULT 61

AB0120  
 Insertion element protein (partial) [imported] - Yersinia pestis (strain CO92)  
 C/Species: Yersinia pestis  
 C/Date: 02-Nov-2001 #sequence\_revision 02-Nov-2001 #text\_change 09-Jul-2004  
 C/Accession: AB0120  
 R/Parhill, J.; Wren, B.W.; Thomson, N.R.; Tibball, R.W.; Holden, M.T.G.; Prentice, M.B.  
 demo-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;  
 11, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrall,  
 Nature 411, 523-527, 2001  
 A/Title: Genome sequence of Yersinia pestis, the causative agent of plague.  
 A/Reference number: AB0001; MUID:21470413; PMID:11586360  
 A/Accession: AB0120  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-20 <KOR>  
 A/Cross-references: UNIPROT:Q8ZHC1; UNIPARC:UPI00000CD77D; GB:AL590842; PIDN:CAC89824.1;  
 C/Genetics:  
 A/Genes: lnbB

Query Match 18.3%; Score 21; DB 2; Length 20;  
 Best Local Similarity 75.0%; Pred. No. 8.2e+03;  
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 12 LVCE 15  
 DB 3 LICE 6

## RESULT 62

PH0944  
 T-cell receptor beta chain V-D-J region (clone 15) - rat (fragment)  
 C/Species: Rattus norvegicus (Norway rat)  
 C/Date: 09-Oct-1992 #sequence\_revision 09-Oct-1992 #text\_change 30-May-1997  
 C/Accession: PH0944  
 R/Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenberg, A.A.; Wilson, D.B.  
 J. Exp. Med. 174, 1467-1476, 1991  
 A/Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergy  
 A/Reference number: PH0941; MUID:92078857; PMID:1836012  
 A/Accession: PH0944  
 A/Molecule type: mRNA  
 A/Residues: 1-10 <GOL>  
 A/Cross-references: UNIPARC:UPI000017C9E1  
 A/Experimental source: complete Freund's adjuvant-immunized lymph node  
 A/Note: the authors translated the codon GAC for residue 9 as Glu  
 C/Keywords: T-cell receptor

Query Match 17.4%; Score 20; DB 2; Length 10;  
 Best Local Similarity 57.1%; Pred. No. 5.7e+03;  
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 14 CSVNGG 20  
 DB 1 CASSPGG 7

## RESULT 63

G60527  
 sperm-activating peptide (Br-Phe-2, Asn-3 SAP-I) - sea urchin (Tripneustes gratilla)  
 N/Alternate names: speract homolog TG-2; TG-10  
 N/Contains: sperm-activating peptide (Asn-3 SAP-I)  
 C/Species: Tripneustes gratilla  
 C/Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 16-Aug-2004  
 C/Accession: G60527; B39572; A40051; B60527  
 R/Yoshino, K.I.; Kajitara, H.; Nomura, K.; Takao, T.; Shimonishi, Y.; Kurita, M.; Yamagu  
 Comp. Biochem. Physiol. B 94, 739-751, 1989  
 A/Title: A halogenated amino acid-containing sperm activating peptide and its related p  
 otus nudus, Echinosmetra mathaei and Heterocentrotus mammillatus.  
 A/Reference number: A60527  
 A/Accession: G60527  
 A/Molecule type: protein  
 A/Residues: 1-10 <YOS>  
 A/Cross-references: UNIPROT:Q7M3U0; UNIPARC:UPI000017A4E1

A/Note: this peptide was found both with both phenylalanine and bromophenylalanine  
 R/Yoshino, K.I.; Takao, T.; Suhara, M.; Kikita, T.; Hori, H.; Nomura, K.; Yamaguchi, M.; S  
 Biochemistry 30, 6203-6209, 1991  
 A/Title: Identification of a novel amino acid, o-bromo-L-phenylalanine, in egg-associated  
 A/Reference number: A39572; MUID:91283461; PMID:20596627  
 A/Accession: B39572

A/Molecule type: protein  
 A/Residues: 1-10 <Y02>  
 A/Cross-references: UNIPARC:UPI000017A4E1  
 C/Keywords: bromine  
 F/2/Modified site: 2'-bromophenylalanine or 4'-bromophenylalanine (Phe) (partial) #acti

Query Match 17.4%; Score 20; DB 2; Length 10;  
 Best Local Similarity 60.0%; Pred. No. 5.7e+03;  
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 16 SVNGG 20  
 DB 3 NLNGG 7

## RESULT 64

PA0028  
 protein OA300042 - Arabidopsis thaliana (fragment)  
 C/Species: Arabidopsis thaliana (mouse-ear cress)  
 C/Date: 30-Jun-1992 #sequence\_revision 06-Jan-1995 #text\_change 06-Jun-1997  
 C/Accession: PA0028  
 R/Kamo, M.; Kawakami, T.; Miyake, N.; Tsugita, A.  
 submitted to JIPID, July 1994  
 A/Description: Separation and characterization of Arabidopsis proteins by two-dimension.  
 A/Reference number: PA0001  
 A/Accession: PA0028  
 A/Molecule type: protein  
 A/Residues: 1-11 <KAM>  
 A/Cross-references: UNIPARC:UPI000017A9F9  
 A/Experimental source: seed  
 C/Keywords: seed

Query Match 17.4%; Score 20; DB 2; Length 11;  
 Best Local Similarity 42.9%; Pred. No. 6.3e+03;  
 Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DIPHPN 7  
 DB 4 EAPFPNN 10

## RESULT 65

PH1375  
 T antigen variant K-2 - mouse (fragment)  
 C/Species: Mus musculus (house mouse)  
 C/Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 11-May-2000  
 C/Accession: PH1375  
 R/Lill, N.L.; Judith Tevethia, M.; Hendrickson, W.G.; Tevethia, S.S.  
 J. Exp. Med. 176, 449-457, 1992

A/Title: Cytotoxic T lymphocytes (CTL) against a transforming gene product select for tr  
 A/Reference number: PH1373; MWID:92364547; PMID:1380062  
 A/Accession: PH1375  
 A/Status: preliminary  
 A/Molecule type: mRNA  
 A/Residues: 1-11 <LIL>  
 A/Cross-references: UNIPARC:UPI000017C758

Query Match 17.4%; Score 20; DB 2; Length 11;  
 Best Local Similarity 60.0%; Pred. No. 6.3e+03;  
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 14 CESVN 18  
 : : :  
 1 CKGVN 5

RESULT 66  
 PH1376  
 T antigen variant K-3 - mouse (fragment)  
 C/Species: Mus musculus (house mouse)  
 C/Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 11-May-2000  
 A/Accession: PH1376  
 R/Status: preliminary  
 R/Title: N.L.; Judith Tevethia, M.; Hendrickson, W.G.; Tevethia, S.S.  
 J. Exp. Med. 176, 449-457, 1992  
 A/Title: Cytotoxic T lymphocytes (CTL) against a transforming gene product select for tr  
 A/Reference number: PH1373; MWID:92364547; PMID:1380062  
 A/Accession: PH1376  
 A/Status: preliminary  
 A/Molecule type: mRNA  
 A/Residues: 1-11 <LIL>  
 A/Cross-references: UNIPARC:UPI000017C759

Query Match 17.4%; Score 20; DB 2; Length 11;  
 Best Local Similarity 60.0%; Pred. No. 6.3e+03;  
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 14 CESVN 18  
 : : :  
 1 CKGVN 5

RESULT 67  
 LPECPR  
 pyre leader peptide - Escherichia coli  
 C/Species: Escherichia coli  
 C/Date: 31-Mar-1990 #sequence\_revision 31-Mar-1990 #text\_change 09-Jul-2004  
 A/Accession: A30400; Q00495  
 R/Status: preliminary  
 R/Title: Bonekamp, P.; Jensen, K.F.  
 EMBO J. 3, 1783-1790, 1984  
 A/Title: Structure of the Escherichia coli pyre operon and control of pyre expression by  
 A/Reference number: A30400; MWID:85003588; PMID:6207018  
 A/Accession: A30400  
 A/Molecule type: DNA  
 A/Residues: 1-12 <POU1>  
 A/Cross-references: UNIPROT:P17776; UNIPARC:UPI000013C281  
 R/Status: preliminary  
 R/Title: Nucleotide sequence of the Escherichia coli pyre gene and of the DNA in front o  
 A/Reference number: A05110; MWID:83287414; PMID:6349999  
 A/Accession: A05110  
 A/Molecule type: DNA  
 A/Residues: 1-12 <POU2>  
 A/Cross-references: UNIPARC:UPI000013C281  
 C/Genetics:  
 A/Genes: pyre-LP  
 A/Map position: 82 min  
 C/Superfamily: pyre leader peptide

Query Match 17.4%; Score 20; DB 1; Length 12;  
 Best Local Similarity 42.9%; Pred. No. 6.3e+03;  
 Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 11 YLVCSV 17  
 : : :  
 5 PFVCKKV 11

RESULT 68  
 S47383  
 T-cell antigen receptor V $\alpha$  junction beta chain - human  
 C/Species: Homo sapiens (man)  
 C/Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 05-Nov-1999  
 A/Accession: S47383  
 R/Status: preliminary  
 R/Title: P.J.  
 submitted to the EMBL Data Library, August 1994  
 A/Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T c  
 A/Reference number: S47355  
 A/Accession: S47383  
 A/Status: preliminary  
 A/Molecule type: mRNA  
 A/Residues: 1-13 <LEH>  
 A/Cross-references: UNIPARC:UPI000011668D; EMBL:Z5709; NID:9527513; PIDN:CAA84778.1; PI  
 C/Keywords: T-cell receptor

Query Match 17.4%; Score 20; DB 2; Length 13;  
 Best Local Similarity 57.1%; Pred. No. 7.5e+03;  
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 14 CESVNGG 20  
 : : :  
 1 CASSWGG 7

RESULT 69  
 S48685  
 extension protein - Streptomyces sp.  
 C/Species: Streptomyces sp.  
 C/Date: 28-Oct-1995 #sequence\_revision 19-Apr-1996 #text\_change 09-Jul-2004  
 A/Accession: S48685  
 R/Status: preliminary  
 R/Title: The precursor of the Streptomyces R61 DP-peptidase containing a C-terminal exte  
 A/Reference number: S48685; MWID:94357278; PMID:8076692  
 A/Accession: S48685  
 A/Status: preliminary  
 A/Molecule type: protein  
 A/Residues: 1-14 <FAN>  
 A/Cross-references: UNIPROT:Q7MOK1; UNIPARC:UPI000017AB38  
 A/Note: the source is designated as Streptomyces R61

Query Match 17.4%; Score 20; DB 2; Length 14;  
 Best Local Similarity 60.0%; Pred. No. 8e+03;  
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DIFHP 5  
 : : :  
 7 DLPAP 11

RESULT 70  
 S08209  
 hypothetical protein 2 - garden pea  
 N/Alternate names: phytochrome  
 C/Species: Pisum sativum (garden pea)  
 C/Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 09-Sep-1997  
 A/Accession: S08209  
 R/Status: preliminary  
 R/Title: Nucleotide sequence and expression of the phytochrome gene in Pisum sativum: di  
 A/Reference number: S06856  
 A/Accession: S08209  
 A/Molecule type: DNA  
 A/Residues: 1-15 <SAT>  
 A/Cross-references: UNIPARC:UPI000011DF37; EMBL:X14077; NID:g20836; PID:g20838  
 C/Genetics:

A:Gene: phy

Query Match 17.4%; Score 20; DB 2; Length 15;

Best Local Similarity 44.4%; Pred. No. 8.6e+03;

Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 12 LVCSVNG 20

DB 1 MVCMSPTNG 9

RESULT 71

PH1610

Ig H chain V-D-J region (wild-type clone 337) - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 02-Jun-1994 #sequence\_revision 02-Jun-1994 #text\_change 17-Mar-1999

C/Accession: PH1610

R/Levinson, D.A.; Campos-Torres, J.; Leder, P.

J. Exp. Med. 178, 317-329, 1993

A/Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice

A/Reference number: PH1580; MUID:93301609; PMID:8315387

A/Accession: PH1610

A/Molecule type: DNA

A/Residues: 1-15 &lt;LEV&gt;

A/Cross-references: UNIPARC:UPI000017C6C4

A/Experimental source: bone marrow pre-B lymphocyte

C/Keywords: Immunoglobulin

Query Match

Best Local Similarity 17.0%; Score 20; DB 2; Length 15;

Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 14 CESVNG 19

DB 1 CARLNG 6

RESULT 72

PH0779

T-cell receptor alpha chain (B83) - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997

C/Accession: PH0779

R/Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Marjanecki, J.L.

J. Exp. Med. 174, 1371-1383, 1991

A/Title: T cell receptor genes in a series of class I major histocompatibility complex-II

allelic exclusion and antigen-specific repertoire.

A/Reference number: PH0746; MUID:92078846; PMID:1836010

A/Accession: PH0779

A/Molecule type: mRNA

A/Residues: 1-15 &lt;CNS&gt;

A/Cross-references: UNIPARC:UPI000017C75B; EMBL:X60877

A/Experimental source: T lymphocyte

C/Keywords: T-cell receptor

Query Match

Best Local Similarity 17.4%; Score 20; DB 2; Length 15;

Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 16 SVNG 20

DB 2 ALNG 6

RESULT 73

PT0096

pyruvate dehydrogenase (lipoamide) (EC 1.2.4.1) beta chain - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 21-Aug-1998 #sequence\_revision 21-Aug-1998 #text\_change 09-Jul-2004

C/Accession: PT0096

R/Kawakami, T.; Uchida, T.; Sakai, T.; Kamo, M.; Morinaga, T.; Tsugita, A.

submitted to JIPID, July 1998

A/Description: Proteome analysis of mouse brain.

A/Reference number: PT0091

A/Accession: PT0096

A/Molecule type: protein

A/Residues: 1-15 &lt;KAW&gt;

A/Cross-references: UNIPROT:Q9D051; UNIPARC:UPI000017C739

A/Experimental source: brain, striatum

C/Keywords: oxidoreductase

Query Match

Best Local Similarity 17.4%; Score 20; DB 2; Length 15;

Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 13 VCSVNG 20

DB 5 VRALNG 12

RESULT 74

PH1789

T cell receptor alpha chain V region (clone 2PBL V alpha 24-5) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 16-Jul-1999

C/Accession: PH1789

R/Porcelll, S.; Yockey, C.E.; Brenner, M.B.; Balk, S.P.

J. Exp. Med. 178, 1-16, 1993

A/Title: Analysis of T cell antigen receptor (TCR) expression by human peripheral blood

A/Reference number: PH1754; MUID:93301585; PMID:8391057

A/Accession: PH1789

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-17 &lt;POR&gt;

A/Cross-references: UNIPARC:UPI000017C378

Query Match

Best Local Similarity 17.4%; Score 20; DB 2; Length 17;

Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 11 YLVCSVNG 20

DB 1 YICVSPSG 10

RESULT 75

PL0025

T-cell surface glycoprotein Rta - rabbit (fragment)

N/Alternate names: thymocyte specific class I-like antigen, heavy chain

C/Species: Oryctolagus cuniculus (domestic rabbit)

C/Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 09-Jul-2004

C/Accession: PL0025

R/Wang, C.R.; Chen, G.H.; Newkirk, M.; Capra, J.D.; Mandy, W.J.

Mol. Immunol. 25, 945-952, 1988

A/Title: Biochemical properties of a novel rabbit thymocyte specific class I-like antigen

A/Reference number: PL0025; MUID:89096985; PMID:3264885

A/Accession: PL0025

A/Molecule type: protein

A/Residues: 1-18 &lt;WAN&gt;

A/Cross-references: UNIPROT:Q7M3P4; UNIPARC:UPI000017C5B9

A/Experimental source: thymus

C/Keywords: glycoprotein; surface antigen

Query Match

Best Local Similarity 17.4%; Score 20; DB 2; Length 18;

Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 PTNIH 9

DB 7 PTSYH 11

RESULT 76

S29167

guinaldine oxidoreductase (EC 1.5.99.-) gamma chain - Arthrobacter sp. (isolate Rue 61a)

C:Species: *Archrobacter* sp.  
 A:Variety: isolate Rue 61a  
 C:Date: 19-Mar-1997 #sequence\_revision 11-Jun-1999 #text\_change 11-Jun-1999  
 C:Accession: S29167  
 R:de Beyer, A.; Lingens, F.  
 Biol. Chem. Hoppe-Seyler 374, 101-110, 1993  
 A:Title: Microbial metabolism of glutathione and related compounds. XVI. Quinoline oxidoreductase.  
 A:Reference number: S29165; PMID:93228843; PMID:8471177  
 A:Accession: S29167  
 A:Molecule type: protein  
 A:Residues: 1-19 <BBY>  
 A:Cross-references: UNIPARC:UPI00000B1AAD  
 A:Experimental source: isolate Rue 61a  
 C:Complex: heterohexameric; two alpha, two beta and two gamma chains  
 C:Function:  
 A:Description: catalyzes the oxidation of quinoline to 1H-4-oxoquinoline  
 A:Pathway: quinoline degradation  
 C:Keywords: FAD; flavoprotein; heterohexameric; molybdopterin; oxidoreductase

Query Match      17.4%; Score 20; DB 2; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      16 SVNG 19  
 Db      7 SVNG 10

RESULT 77  
 PT0332  
 Ig heavy chain CDR3 region (clone J2-139) - human (fragment)  
 C:Species: *Homo sapiens* (man)  
 C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996  
 C:Accession: PT0332  
 R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.  
 J. Exp. Med. 173, 395-407, 1991  
 A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and J  
 A:Reference number: PT0222; PMID:91108337; PMID:1899102  
 A:Accession: PT0332  
 A:Molecule type: DNA  
 A:Residues: 1-19 <YAM>  
 A:Cross-references: UNIPARC:UPI000017C21A  
 A:Experimental source: B lymphocyte  
 C:Keywords: heterotetramer; immunoglobulin

Query Match      17.4%; Score 20; DB 2; Length 19;  
 Best Local Similarity 80.0%; Pred. No. 1.1e+04;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      16 SVNG 20  
 Db      15 SSNG 19

RESULT 78  
 PH1352  
 Ig heavy chain DJ region (clone C100-115) - human (fragment)  
 C:Species: *Homo sapiens* (man)  
 C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999  
 C:Accession: PH1352  
 R:Wasserman, R.; Gallil, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.  
 J. Exp. Med. 176, 1577-1581, 1992  
 A:Title: Predominance of fetal type DJH joining in young children with B precursor lymph  
 A:Reference number: PH1302; PMID:93094761; PMID:1460419  
 A:Accession: PH1352  
 A:Molecule type: DNA  
 A:Residues: 1-19 <MAS>  
 A:Cross-references: UNIPARC:UPI000017C221  
 A:Note: the authors translated the stop codon for residue 2 as X  
 C:Keywords: heterotetramer; immunoglobulin

Query Match      17.4%; Score 20; DB 2; Length 19;

Best Local Similarity 60.0%; Pred. No. 1.1e+04;  
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      2 IPHPT 6  
 Db      6 VPPPT 10

RESULT 79  
 D49404  
 T-cell receptor beta chain VDJ region - human (fragment)  
 C:Species: *Homo sapiens* (man)  
 C:Date: 07-Apr-1994 #sequence\_revision 18-Nov-1994 #text\_change 05-Nov-1999  
 C:Accession: D49404  
 R:Brooks, E.G.; Balk, S.P.; Aupetit, K.; Colonna, M.; Strominger, J.L.; Groh-Spies, V.  
 Proc. Natl. Acad. Sci. U.S.A. 90, 11787-11791, 1993  
 A:Title: Human T-cell receptor (TCR) alpha/beta + CD4-CD8- T cells express oligoclonal T  
 A:Reference number: D49404; PMID:94089717; PMID:7505446  
 A:Accession: D49404  
 A>Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-19 <BRO>  
 A:Cross-references: UNIPARC:UPI000017C3BE; GB:S67402; NID:9455872; PIDN:AA29277.1; PID  
 A:Experimental source: alpha/beta + CD4-CD8- T cells  
 A:Note: sequence extracted from NCBI backbone (NCBIN:141028, NCBI:141029)  
 C:Keywords: T-cell receptor

Query Match      17.4%; Score 20; DB 2; Length 19;  
 Best Local Similarity 30.0%; Pred. No. 1.1e+04;  
 Matches 3; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY      3 PPHPTNKKYL 12  
 Db      5 PPHPARYKYL 14

RESULT 80  
 P00409  
 RNA-directed RNA polymerase (EC 2.7.7.48) 2 - influenza A virus (strain A/Hobai/24/89 (I  
 N:Alternate names: P3 protein; PB2 protein  
 C:Species: *Influenza A virus*  
 C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 31-Dec-2004  
 C:Accession: P00409  
 R:Li, X.S.; Zhao, C.Y.; Gao, H.M.; Zhang, Y.Q.; Ishida, M.; Kanegae, Y.; Endo, A.; Nerov  
 J. Gen. Virol. 73, 1329-1337, 1992  
 A:Title: Origin and evolutionary characteristics of antigenic reassortant influenza A (I  
 A:Reference number: P00408; PMID:9230326; PMID:1607856  
 A:Accession: P00409  
 A:Molecule type: genomic RNA  
 A:Residues: 1-19 <LIA>  
 A:Cross-references: UNIPROT:Q67303; UNIPARC:UPI0000175782  
 C:Genetics:  
 A:Map position: segment 1  
 C:Keywords: nucleocidyltransferase

Query Match      17.4%; Score 20; DB 2; Length 19;  
 Best Local Similarity 40.0%; Pred. No. 1.1e+04;  
 Matches 4; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY      2 IPHPTNKKYL 11  
 Db      7 VDHMAIKKY 16

RESULT 81  
 PX0042  
 venombin B (EC 3.4.21.-) - himenobu (fragment)  
 N:Alternate names: beta-fibrinogenase; okinaxobin I  
 C:Species: *Trimerurus okinawensis* (himenobu)  
 C:Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 09-Jul-2004  
 C:Accession: PX0042  
 R:Iwaseki, A.; Shieh, T.C.; Shimohigashi, Y.; Waki, M.; Kihara, H.; Ohno, M.  
 J. Biochem. 108, 822-828, 1990

A/Title: Purification and characterization of a coagulant enzyme, okinaxobin I, from the  
A/Reference number: PX0042; MUID:91185341; PMID:1964457

A/Accession: PX0042

A/Molecule type: protein

A/Residues: 1-20 <I>MA>

A/Cross-references: UNIPROT:P20005; UNIPARC:UPI0000175C39

C/Superfamily: trypsin; trypsin homology

C/Keywords: hydrolase; serine proteinase; venom

Query Match

Best Local Similarity 17.4%; Score 20; DB 2; Length 20;  
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 7 NIKYLV 12

DB 10 NHRFL 15

RESULT 82

S68028

Iodothyronine 5'-monodeiodinase - rat (fragment)

C/Species: Rattus norvegicus (Norway rat)

C/Date: 15-Feb-1997 #sequence\_revision 13-Mar-1997 #text\_change 17-Mar-1999

C/Accession: S68028

R/Zhou, L.X.; Dahal, S.S.; Kupfer, D.; Morrell, S.; McKenzie, B.A.; Eccleston Jr., B.D.;

Arch. Biochem. Biophys. 322, 390-394, 1995

A/Title: Cytochrome P450 catalyzed covalent binding of methoxychlor to rat hepatic, microsomes

A/Reference number: S68028; MUID:96032659; PMID:7574712

A/Accession: S68028

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-20 <ZHO>

A/Cross-references: UNIPARC:UPI00001761A4

C/Superfamily: protein disulfide-isomerase; thioredoxin homology

Query Match

Best Local Similarity 17.4%; Score 20; DB 2; Length 20;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 9 HKYLV 13

DB 16 HNYVL 20

RESULT 83

B38382

15K protein B - rabbit (fragment)

C/Species: Oryctolagus cuniculus (domestic rabbit)

C/Date: 28-Jun-1991 #sequence\_revision 28-Jun-1991 #text\_change 02-Sep-2000

C/Accession: B38382

R/Ooi, C.E.; Weiser, J.J.; Levy, O.; Elisabeth, P.

J. Biol. Chem. 265, 15956-15962, 1990

A/Title: Isolation of two isoforms of a novel 15-kDa protein from rabbit polymorphonucle

A/Reference number: A38382; MUID:90368617; PMID:2203792

A/Accession: B38382

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-20 <OOI>

A/Cross-references: UNIPARC:UPI0000176378

C/Superfamily: cathelin; cystatin homology

Query Match

Best Local Similarity 17.4%; Score 20; DB 2; Length 20;  
Matches 4; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 2 IPHTNHYLVESV 17

DB 1 IPHRLRYEYVAQAL 16

RESULT 84

S03954

acidic fibroblast growth factor - pig (fragment)

N/Alternate names: alpha-endothelial cell growth factor

C/Species: Sus scrofa domestica (domestic pig)

C/Date: 28-Feb-1990 #sequence\_revision 28-Feb-1990 #text\_change 09-Jul-2004

C/Accession: S03954

R/Quinkler, W.; Maaberg, M.; Bernotat-Danielowski, S.; Luehe, N.; Sharma, H.S.; Schap

Bur, J. Biochem. 181, 67-73, 1989

A/Title: Isolation of heparin-binding growth factors from bovine, porcine and canine he

A/Reference number: S03953; MUID:89231704; PMID:2714282

A/Accession: S03954

A/Molecule type: protein

A/Residues: 1-20 <QUI>

A/Cross-references: UNIPROT:P20002; UNIPARC:UPI000017C453

C/Keywords: growth factor

Query Match

Best Local Similarity 17.4%; Score 20; DB 2; Length 20;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 16 SYNGG 20

DB 10 SSNGG 14

RESULT 85

A58963

alpha-conotoxin Cn1A - cone shell (Conus consors)

N/Contains: alpha-conotoxin Cn1B

C/Species: Conus consors

C/Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 09-Jul-2004

C/Accession: A58963

R/Favreau, P.; Krümm, I.; Le Gall, F.; Bobanleth, M.J.; Lamthanh, H.; Bouet, F.; Serre

Biochemistry 38, 6317-6326, 1999

A/Title: Biochemical characterization and nuclear magnetic resonance structure of novel

A/Reference number: A58963; MUID:99255390; PMID:10320362

A/Accession: A58963

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-14 <FAV>

A/Cross-references: UNIPROT:P56973; UNIPARC:UPI00001287B8

C/Superfamily: alpha-conotoxin

C/Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; postsynaptic neuro

F1-14/Product: alpha-conotoxin Cn1A #status experimental <MATA>

F3-14/Product: alpha-conotoxin Cn1B #status experimental <MATB>

F3-8, 4-14/Disulfide bonds: #status experimental

F14/Modified site: amidated carboxyl end (Cys) #status experimental

Query Match

Best Local Similarity 17.0%; Score 19.5; DB 2; Length 14;  
Matches 5; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY 4 HPTNHYLVLC 14

DB 5 HPA-CGKYSC 14

RESULT 86

C32735

thyroglobulin - pig (fragment)

C/Species: Sus scrofa domestica (domestic pig)

C/Date: 20-Jul-1990 #sequence\_revision 20-Jul-1990 #text\_change 09-Jul-2004

C/Accession: C32735

R/Rawitch, A.B.; Litwer, M.R.; Gregg, J.; Turner, C.D.; Rouse, J.B.; Hamilton, J.W.

Biochem. Biophys. Res. Commun. 118, 423-429, 1984

A/Title: The isolation of identical thyroxine containing amino acid sequences from bovin

A/Reference number: A32735; MUID:84153804; PMID:6704086

A/Accession: C32735

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-19 <RAW>

A/Cross-references: UNIPROT:Q7M2Z2; UNIPARC:UPI00001734C4

C/Superfamily: thyroglobulin; cholinesterase homology; thyroglobulin type I repeat homo

C/Keywords: dimer; glycoprotein; iodine; thyroid gland; thyroid hormone biosynthesis

F/5/Modified site: thyroxine (Tyr) #status predicted

Query Match 17.0%; Score 19.5; DB 2; Length 19;  
Best Local Similarity 37.5%; Pred. No. 1.3e+04;  
Matches 6; Conservative 1; Mismatches 2; Indels 7; Gaps 1;

QY 7 NIKHYLV-----CE 15  
||:|:|  
Db 1 NIFEYQVDAQPLRPCE 16

## RESULT 87

B32735

thyroglobulin - sheep (fragment)

C/Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C/Date: 20-Jul-1990 #sequence\_revision 20-Jul-1990 #text\_change 09-Jul-2004

C/Accession: B32735

R/Rawitch, A.B.; Litwer, M.R.; Grege, J.; Turner, C.D.; Rouse, J.B.; Hamilton, J.W.

Biochem. Biophys. Res. Commun. 118, 423-429, 1984

A/Title: The isolation of identical thyroxine containing amino acid sequences from bovin

A/Reference number: A32735; MUID:84153804; PMID:6704086

A/Accession: B32735

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-19 <RAW>

A/Cross-references: UNIPROT:Q7M2Z1; UNIPARC:UPI00001734C4

C/Suprafamily: thyroglobulin; cholinesterase homology; thyroglobulin type I repeat homol  
C/Keyword: dimer; glycoprotein; iodine; thyroid gland; thyroid hormone biosynthesis  
F/5/Modified site: thyroxine (Tyr) #status predicted

Query Match 17.0%; Score 19.5; DB 2; Length 19;  
Best Local Similarity 37.5%; Pred. No. 1.3e+04;

Matches 6; Conservative 1; Mismatches 2; Indels 7; Gaps 1;

QY 7 NIKHYLV-----CE 15  
||:|:|  
Db 1 NIFEYQVDAQPLRPCE 16

## RESULT 88

A34233

trehalase inhibitor - American cockroach (fragment)

C/Species: Periplaneta americana (American cockroach)

C/Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 09-Jul-2004

C/Accession: A34233

R/Hayakawa, Y.; Jahagirdar, A.P.; Yaguchi, M.; Downer, R.G.H.

J. Biol. Chem. 264, 16165-16169, 1989

A/Title: Purification and characterization of trehalase inhibitor from hemolymph of the

A/Reference number: A34233; MUID:89380218; PMID:2777784

A/Accession: A34233

A/Molecule type: protein

A/Residues: 1-19 <RAW>

A/Cross-references: UNIPROT:P19986; UNIPARC:UPI000012DA2D

Query Match 17.0%; Score 19.5; DB 2; Length 19;  
Best Local Similarity 50.0%; Pred. No. 1.3e+04;

Matches 6; Conservative 0; Mismatches 3; Indels 3; Gaps 1;

QY 2 IHPPTNIHKYLV 13  
||:|:|  
Db 2 IFTP--HVKV 10

## RESULT 89

S35696

phosphoenolpyruvate carboxykinase - Trypanosoma brucei

C/Species: Trypanosoma brucei

C/Date: 28-Oct-1995 #sequence\_revision 03-Nov-1995 #text\_change 09-Jul-2004

C/Accession: S35696

R/Hunt, M.; Koehler, P.

Biochim. Biophys. Acta 1249, 15-22, 1995

A/Title: Purification and characterization of phosphoenolpyruvate carboxykinase from Try  
A/Reference number: S35696; MUID:95284106; PMID:7766679

A/Accession: S35696

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-9 <HUN>

A/Cross-references: UNIPROT:Q7M3S5; UNIPARC:UPI000017B599

Query Match 16.5%; Score 19; DB 2; Length 9;  
Best Local Similarity 80.0%; Pred. No. 2.8e+05;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 IHKYL 12  
||:|:|  
Db 4 IHKYL 8

## RESULT 90

B57444

neuropeptide Grb-A2T B2 - two-spotted cricket

C/Species: Gryllus bimaculatus (two-spotted cricket)

C/Date: 26-Jan-1996 #sequence\_revision 26-Jan-1996 #text\_change 09-Jul-2004

C/Accession: B57444

R/Lorenz, M.W.; Kellner, R.; Hoffmann, K.H.

J. Biol. Chem. 270, 21103-21108, 1995

A/Title: A family of neuropeptides that inhibit juvenile hormone biosynthesis in the cri

A/Reference number: A57444; MUID:95403341; PMID:7673141

A/Accession: B57444

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-9 <LOR>

A/Cross-references: UNIPROT:Q7M3N8; UNIPARC:UPI000017B818

Query Match 16.5%; Score 19; DB 2; Length 9;  
Best Local Similarity 75.0%; Pred. No. 2.8e+05;

Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 17 VNGG 20  
||:|:|  
Db 5 LVNG 8

## RESULT 91

S77980

cytochrome-c oxidase (EC 1.9.3.1) chain IV - bigeye tuna (fragment)

C/Species: Thunnus obesus (bigeye tuna)

C/Date: 17-Sep-1997 #sequence\_revision 17-Sep-1997 #text\_change 09-Jul-2004

C/Accession: S77980

R/Arnold, S.; Lee, J.; Kim, M.; Song, E.; Linder, D.; Lottepeich, F.; Kadenbach, B.

submitted to the Protein Sequence Database, June 1997

A/Reference number: S77980

A/Accession: S77980

A/Molecule type: protein

A/Residues: 1-10 <ARN>

A/Cross-references: UNIPROT:P80971; UNIPARC:UPI000017BF70

A/Experimental source: heart; liver

A/Genome: nuclear

C/Function: oxidative phosphorylation; respiratory chain

A/Pathway: electron transfer; membrane-associated complex; mitochondrial inner membrane

Query Match 16.5%; Score 19; DB 2; Length 10;  
Best Local Similarity 50.0%; Pred. No. 8.1e+03;

Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 9 HKYLVCS 16  
||:|:|  
Db 3 HDHEVARS 10

## RESULT 92

I60527

sperm-activating peptide (SAP-I) - sea urchin (Strongylocentrotus nudus)

N/Alternate names: speract



C/Species: Strongylocentrotus nudus  
C/Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 16-Aug-2004  
C/Accession: I60527  
R/Yoshino, K. I.; Kajitani, H.; Nomura, K.; Takeao, T.; Shimonishi, Y.; Kurita, M.; Yamaguchi, Y.; Kato, T. Comp. Biochem. Physiol. B 94, 739-751, 1989  
A/Title: A halogenated amino acid-containing sperm activating peptide and its related peptides from the nudus, *Strongylocentrotus nudus* and *Heterocentrotus mammillatus*.  
A/Reference number: A60527  
A/Accession: I60527  
A/Molecule type: protein  
A/Residues: 1-10 <YOS>  
A/Cross-References: UNIPROT:Q7M4B5, UNIPARC:UPI000003545B

Query Match	16.5%	Score 19	DB 2	Length 10
Best Local Similarity	75.0%	Pred. No. 8.1e+03		
Matches 3	Conservative	1	Mismatches 0	Indels 0
			Gaps	0

```

RESULT 93
C60527
sperm-activating peptide (Ser-3, Ile-4, Gly-5 SAp-I) - sea urchin (Tripneustes gratilla)
N/Alternate names: speract homolog TG-4
N/Species: Tripneustes gratilla
C/Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-2004
J/Accession: C60527; D39572
R/Yoshino, K.I.; Kajitani, H.; Nomura, K.; Takao, T.; Shimonishi, Y.; Kurita, M.; Yamaguchi, S.; Bloch, R.; Kajiura, B. 94, 739-751, 1999
A/TITLE: A halogenated amino acid-containing sperm activating peptide and its related peptides from the sea urchin, Echinometra mathaei and Heterocentrotus mammillatus.
./Reference number: A60527

```

Query Match 16.5%; Score 19; DB 2; Length 10;  
Best Local Similarity 60.0%; Pred. No. 8.1e+03;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

RESULT 94
C60788
sperm-activating peptide (speract) - sea urchin (Pseudocentrotus depressus)
C/Species: Pseudocentrotus depressus
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-2004
C/Accession: C60788
R/Suzuki, N., Kajihara, H., Nomura, K., Garbers, D.L., Yoshino, K., Kurita, M., Tanaka, H.
Comp. Biochem. Physiol. B 89, 687-693, 1988
A/TITLE: Some more speract derivatives associated with eggs of sea urchins, Pseudocentrotus
A/Reference number: A60787, MUID:88242184, PMID:3378407
A/Accession: C60788
A/Molecule type: protein
A/Residues: 1-10 <SUZ>

```

AtCross-references: UNIPROT:Q7M4D3; UNIPARC:UPI000003545B  
CjComment: This oligopeptide from edg jelly is one of several  
at shows some, but not absolute, species restriction.

Query Match	16.5%	Score 19	DB 2	Length 10
Best Local Similarity	75.0%	Pred. No. 8.1e+03		
Matches 3, Conservative		1	Mismatches 0	Indels 0; Gaps 0

RESULT 95  
 A60527  
 sperm-activating peptide (Br-Phe-2 SAP-I) - sea urchin (*Triplaneustes gratillia*)  
 N/Alternate names: SAP-a; speract; TG-1; TG-9  
 C/Species: *Triplaneustes gratillia*  
 C/Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 05-Oct-2004  
 C/Accession: A60527; A39572; A60973; H60527; I39572  
 R/Yoshino, K.I.; Kajitani, H.; Nomura, K.; Takeao, T.; Shimomichi, Y.; Kurita, M.; Yamagu  
 Comp. Biochem. Physiol. B 94, 739-751, 1989  
 A>Title: A halogenated amino acid-containing sperm activating peptide and its related p  
 otus nudus, *Echinometra mathaei* and *Heterocentrotus mammillatus*.  
 ;Reference number: A60527

Query Match	16.5%	Score 19;	DB 2;	Length 10;
Best Local Similarity	75.0%;	Pred. No. 8	1e+03;	
Matches 3;	Conservative	1;	Mismatches	0;
			Indels	0;
			Gaps	0;

RESULT 96  
 A60787  
 sperm-activating peptide (speract) - sea urchin (*Hemicentrotus pulcherrimus*)  
 C/Species: *Hemicentrotus pulcherrimus*  
 C/Date: 03-Jun-1993 #sequence\_revision 03-Jun-1993 #text\_change 05-Oct-2004  
 C/Accession: A60787  
 R/Suzuki, N.; Kajitani, H.; Nomura, K.; Garbers, D.L.; Yoshino, K.; Kurita, M.; Tanaka, J  
 Comp. Biochem. Physiol. B 89, 687-693, 1988  
 A/TITLE: Some more speract derivatives associated with eggs of sea urchins, *Pseudocentrotus*  
 A/Reference number: A60787; PMID:88242184; PMID:3378407  
 A/Accession: A60787  
 A/Molecule type: protein  
 A/Residues: 1-10 <SUZ>  
 A/Cross-references: UNIPROT:Q25121; UNIPARC:UPI0000035458  
 C/Comment: This oligopeptide from egg jelly is one of several from this species, all of  
 it shows some, but not absolute, species restriction.

Query Match 16.5%; Score 19; DB 2; Length 10;  
Best Local Similarity 75.0%; Pred. No. 8.1e+03;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 17 VNGG 20  
: |||  
Db 4 LVNG 7

RESULT 97  
B49164

chromogranin-B - rat (fragment)  
C/Species: Rattus norvegicus (Norway rat)  
C/Date: 19-Dec-1993 #sequence\_revision 18-Nov-1994 #text\_change 31-Oct-1997  
C/Accession: B49164  
R/Reisen, E.; Wellinder, B.S.; Madsen, O.D.  
Endocrinology 129, 3147-3156, 1991  
A/Title: Chromogranin-B, a putative precursor of eight novel rat glucagonoma peptides th  
A/Reference number: A49164; MUID:92063871; PMID:1954895  
A/Accession: B49164  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-11 <NTE>  
A/Cross-references: UNIPARC:UPI00000E7128  
A/Note: sequence extracted from NCBI backbone (NCBIP:66370)  
C/Superfamily: chromogranin B precursor

Query Match 16.5%; Score 19; DB 2; Length 11;  
Best Local Similarity 66.7%; Pred. No. 8.9e+03;  
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 15 ESWNG 20  
: |||  
Db 4 EDVNG 9

RESULT 98  
A26930

ermg leader peptide 1 - Bacillus sphaericus  
C/Species: Bacillus sphaericus  
C/Date: 08-Mar-1989 #sequence\_revision 08-Mar-1989 #text\_change 05-Oct-2004  
C/Accession: A26930  
R/Monod, M.; Mohan, S.; Dubnau, D.  
J. Bacteriol. 169, 340-350, 1987  
A/Title: Cloning and analysis of ermG, a new macrolide-lincosamide-streptogramin B resis  
A/Reference number: A91840; MUID:87083389; PMID:3025178  
A/Accession: A26930  
A/Molecule type: DNA  
A/Residues: 1-11 <MON>  
A/Cross-references: UNIPROT:P26840; UNIPARC:UPI000016E856; GB:M15332; NID:9142881; PIDN:

Query Match 16.5%; Score 19; DB 2; Length 11;  
Best Local Similarity 27.3%; Pred. No. 8.9e+03;  
Matches 3; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 8 IHKYLCESVN 18  
: |||  
Db 1 MKYISGRDAIN 11

RESULT 99  
S15755

actin 7 - soybean (fragment)  
C/Species: Glycine max (soybean)  
C/Date: 20-Feb-1995 #sequence\_revision 29-May-1998 #text\_change 05-Oct-2004  
C/Accession: S15755  
R/Pearson, L.; Meagher, R.B.  
Plant Mol. Biol. 14, 513-526, 1990  
A/Title: Diverse soybean actin transcripts contain a large intron in the 5' untranslated  
A/Reference number: S15754; MUID:91346640; PMID:2102831  
A/Accession: S15755  
A/Status: preliminary

A/Molecule type: DNA  
A/Residues: 1-13 <PEA>  
A/Cross-references: UNIPROT:P15987; UNIPARC:UPI000012542C; EMBL:X17120; NID:918527; PIDN:  
C/Superfamily: Actin  
C/Keywords: cytoskeleton; structural protein

Query Match 16.5%; Score 19; DB 2; Length 13;  
Best Local Similarity 75.0%; Pred. No. 1.1e+04;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 12 LVCE 15  
: |||  
Db 10 LVCD 13

RESULT 100  
PT0290

Ig heavy chain CRD3 region (clone 4-115A) - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996  
C/Accession: PT0290  
R/Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.  
U. Exp. Med. 173, 395-407, 1991  
A/Title: Preferential utilization of specific immunoglobulin heavy chain diversity and J  
A/Reference number: PT0222; MUID:91108337; PMID:1899102  
A/Accession: PT0290  
A/Molecule type: DNA  
A/Residues: 1-13 <YAM>  
A/Cross-references: UNIPARC:UPI000017C1FE  
A/Experimental source: B lymphocyte  
C/Keywords: heterotetramer; immunoglobulin

Query Match 16.5%; Score 19; DB 2; Length 13;  
Best Local Similarity 60.0%; Pred. No. 1.1e+04;  
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 10 KYLC 14  
: |||  
Db 2 KYVC 6

Search completed: January 20, 2006, 19:12:11  
Job time : 12.3462 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 20, 2006, 18:54:54 ; Search time 66.5385 Seconds  
(without alignments)  
212.066 Million cell updates/sec

Title: US-09-662-293-3

Perfect score: 115

Sequence: 1 DIHPPTNHHKLVLCESVNGS 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 14590

Minimum DB seq length: 0

Maximum DB seq length: 20

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

1: uniprot\_05.80.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Query length	DB ID	Description
1	38	33.0	15	2	Q7M126 PSEBSP
2	38	33.0	15	2	Q7M134_PRRHIZ
3	37	32.2	13	2	Q00789_PDEBLA
4	37	32.2	13	2	Q76R60_9DEBLA
5	33	28.7	19	2	Q5C123_SCHJA
6	32	27.8	13	2	Q7S901_NEUCR
7	30	26.1	10	2	Q4X4H2_PLACH
8	30	26.1	18	2	Q16244_HUMAN
9	29	25.2	6	1	TWOF_SABU
10	29	25.2	19	2	Q5EX89_GLAMI
11	28	24.3	19	2	Q5EX77_GLAMI
12	28	24.3	19	2	Q5EX78_GLAMI
13	28	24.3	19	2	Q5EX88_GLAMI
14	28	24.3	19	2	Q5EX90_GLAMI
15	28	24.3	19	2	Q5EX91_GLAMI
16	28	24.3	19	2	Q5EX92_GLAMI
17	28	24.3	19	2	Q5EX94_GLAMI
18	28	24.3	19	2	Q5EX95_GLAMI
19	28	24.3	19	2	Q5EX96_GLAMI
20	28	24.3	19	2	Q5EX97_GLAMI
21	28	24.3	19	2	Q5EX98_GLAMI
22	28	24.3	19	2	Q5EX99_GLAMI
23	28	24.3	19	2	Q5EXA1_GLAMI
24	28	24.3	19	2	Q5EXA2_GLAMI
25	28	24.3	19	2	Q5EXA3_GLAMI
26	28	24.3	19	2	Q5EXA4_GLAMI
27	28	24.3	19	2	Q5EXA5_GLAMI
28	28	24.3	19	2	Q5EXA6_GLAMI
29	28	24.3	19	2	Q5EXA7_GLAMI
30	28	24.3	19	2	Q5EXA8_GLAMI
31	28	24.3	19	2	Q5EXA9_GLAMI

32	28	24.3	19	2	Q5EXB0_GLAMI	Q5exb0 saintpaulia
33	28	24.3	19	2	Q5EXB1_GLAMI	Q5exb1 saintpaulia
34	28	24.3	20	2	Q4YML1_PLABE	Q4ylm1 plasmidium
35	27	23.5	18	2	Q26062_HELPY	Q26062 helicobacte
36	27	23.5	19	2	Q4XJ38_PLACH	Q4xj38 plasmidium
37	27	23.5	19	2	Q4YK87_PLABE	Q4yk87 plasmidium
38	27	23.5	20	2	Q7RR59_PLAYO	Q7rr59 plasmidium
39	26	22.6	12	2	Q9UDR0_HUMAN	Q9udr0 homo sapien
40	26	22.6	17	2	Q4L0W0_BACTX	Q4l0w0 bacillus th
41	26	22.6	19	2	Q9XNQ7_BOONI	Q9xnq7 boophilus m
42	26	22.6	19	2	Q5EX86_GLAMI	Q5ex86 streptocarp
43	26	22.6	20	1	PHYLA_PHYOR	P94569 phyllomedu
44	26	22.6	20	2	Q7RS12_PLAYO	Q7rs12 plasmidium
45	26	22.6	20	2	Q5K4V0_BOVIN	Q5k4v0 bos taurus
46	26	22.6	20	2	Q90X94_CHICK	Q90x94 gallus gall
47	26	21.7	11	2	Q8MM58_GNEOP	Q8mm58 heliconi
48	25	21.7	12	2	Q8MUN4_GNEOP	Q8mun4 heliconi
49	25	21.7	12	2	Q8MUN9_GNEOP	Q8mun9 heliconi
50	25	21.7	13	2	Q8MM57_GNEOP	Q8mm57 heliconi
51	25	21.7	14	2	Q8MUN8_GNEOP	Q8mun8 heliconi
52	25	21.7	14	2	Q8MUP0_GNEOP	Q8mup0 homo sapien
53	25	21.7	15	2	Q9BZNO_HUMAN	Q9bzn0
54	25	21.7	15	2	Q8MUP2_GNEOP	Q8mup2 heliconi
55	25	21.7	16	2	Q8MM83_GNEOP	Q8mm83 heliconi
56	25	21.7	16	2	Q8MM84_GNEOP	Q8mm84 heliconi
57	25	21.7	16	2	Q8MM85_GNEOP	Q8mm85 heliconi
58	25	21.7	16	2	Q8MUN3_GNEOP	Q8mun3 heliconi
59	25	21.7	16	2	Q8MUN5_GNEOP	Q8mun5 heliconi
60	25	21.7	16	2	Q5G554_BALMU	Q5g554 balaenopte
61	25	21.7	17	2	Q9TW64_DICDI	Q9tw64 dicystostei
62	25	21.7	18	1	PHYI2_PHYTH	P84567 phyllomedu
63	25	21.7	18	2	Q6VYB3_GNEOP	Q6vyb3 heliconi
64	25	21.7	18	2	Q6VYD9_GNEOP	Q6vyd9 heliconi
65	25	21.7	18	2	Q6VYE7_GNEOP	Q6vye7 heliconi
66	25	21.7	18	2	Q4YEL0_PLABE	Q4yel0 plasmidium
67	25	21.7	18	2	Q28069_BOVIN	Q28069 bos taurus
68	25	21.7	19	2	Q6VYD8_GNEOP	Q6vyd8 heliconi
69	25	21.7	19	2	Q6VYE1_GNEOP	Q6vye1 heliconi
70	25	21.7	19	2	Q7RG13_PLAYO	Q7rg13 plasmidium
71	25	21.7	19	2	Q7YK42_9FABA	Q7yk42 desmanthu
72	25	21.7	19	2	Q8CJ05_MESAU	Q8cj05 mesocricetu
73	25	21.7	19	2	Q7LZW5_HHVI	Q7lzw5 human herpe
74	25	21.7	20	1	APY3_PLECT	P83477 pleurotus c
75	25	21.7	20	1	APY3_PLECT	P83481 pleurotus c
76	25	21.7	20	2	Q64619_RAT	Q64619 rattus norv
77	25	21.7	20	2	Q9PRY1_TORCA	Q9pry1 torpedo cal
78	24.5	21.3	20	2	Q9R4Z4_PROMI	Q9r4z4 proteus mir
79	24	20.9	9	2	Q7M471_VESOR	Q7m471 vespa orien
80	24	20.9	15	2	Q9UC17_HUMAN	Q9uc17 homo sapien
81	24	20.9	17	2	Q6R9U9_HUMAN	Q6r9u9 homo sapien
82	24	20.9	17	2	Q6R9P0_TRAFR	Q6r9p0 trachypithe
83	24	20.9	17	2	Q6R9P1_TRAFR	Q6r9p1 trachypithe
84	24	20.9	17	2	Q6R9P2_PYGNE	Q6r9p2 pygathrix n
85	24	20.9	17	2	Q6R9P3_PYGNI	Q6r9p3 pygathrix b
86	24	20.9	17	2	Q6R9P4_MACCU	Q6r9p4 macaca mula
87	24	20.9	17	2	Q6R9Q1_PONPY	Q6r9q1 ponpo pygma
88	24	20.9	17	2	Q6R9Q5_PPRIM	Q6r9q5 gorilla gor
89	24	20.9	18	1	Q6R9R4_PANTR	Q6r9r4 pan troglod
90	24	20.9	18	1	HEMTO_THETS	P80155 theomyson
91	24	20.9	18	2	Q9ZVY5_9HYME	Q9zvy5 opus kraus
92	24	20.9	18	2	Q4X569_PLACH	Q4x569 plasmidium
93	24	20.9	19	2	Q5CS28_SCHJA	Q5cs28 schistosoma
94	24	20.9	19	2	Q9ZYW3_9HYME	Q9zyw3 gnathopodon
95	24	20.9	19	2	Q9ZYX2_9HYME	Q9zyx2 centistes s
96	24	20.9	19	2	Q4Y3P1_PLACH	Q4y3p1 plasmidium
97	24	20.9	19	2	Q6R9P5_HYLLB	Q6r9p5 hylobates l
98	24	20.9	19	2	Q6R9P6_9PRIM	Q6r9p6 bunopithec
99	24	20.9	19	2	Q6R9P7_MACCU	Q6r9p7 macaca mula
100	24	20.9	19	2	Q5EXA0_GLAMI	Q5exa0 streptocarp

#### ALIGNMENTS

```

RESULT 1
O7M126_PSESP PRELIMINARY; PRT; 15 AA.
AC O7M126;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Dichloromethane dehalogenase (EC 4.5.1.3) (Fragment).
OS Pseudomonas sp.
OC Bacteria; Proteobacteria.
OX NCBI_TaxID=306;
RN [1]
RP PROTEIN SEQUENCE.
RA Kohler-Staud D., Hartmann S., Gaelell R., Suter F., Leisinger T.;
RT "Evidence for identical dichloromethane dehalogenases in different
methylorophic bacteria."
RL J. Gen. Microbiol. 132:2837-2843 (1986).
DR PIR; B60929; B60929.
DR GO; GO:0018834; F:dichloromethane dehalogenase activity; IEA.
FT NON_TER 15
SQ SEQUENCE 15 AA; 1667 MW; 05B170EF8B3721D9 CRC64;

Query Match 33.0%; Score 38; DB 2; Length 15;
Best Local Similarity 85.7%; Pred. No. 68;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 PHPNTNH 9
DB 3 PHPNTNH 9

RESULT 2
O7M134_9RHIZ PRELIMINARY; PRT; 15 AA.
AC O7M134;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Dichloromethane dehalogenase (EC 4.5.1.3) (Fragment).
OS Hyphomicrobium sp.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Hyphomicrobiaceae; Hyphomicrobium.
OX NCBI_TaxID=82;
RN [1]
RP PROTEIN SEQUENCE.
RA Kohler-Staud D., Hartmann S., Gaelell R., Suter F., Leisinger T.;
RT "Evidence for identical dichloromethane dehalogenases in different
methylorophic bacteria."
RL J. Gen. Microbiol. 132:2837-2843 (1986).
DR PIR; A60929; A60929.
DR GO; GO:0018834; F:dichloromethane dehalogenase activity; IEA.
FT NON_TER 15
SQ SEQUENCE 15 AA; 1667 MW; 05B170EF8B3721D9 CRC64;

Query Match 33.0%; Score 38; DB 2; Length 15;
Best Local Similarity 85.7%; Pred. No. 68;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 PHPNTNH 9
DB 3 PNPNTNH 9

```

```

OS Human T-lymphotropic virus 1.
OX Viruses; Retroid viruses; Retroviridae; Deltaretrovirus.
OX NCBI_TaxID=11908;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=87111460; PubMed=3027244;
RA Hiramatsu K., Nishida J., Naito A., Yoshikawa H.;
RT "Molecular cloning of the closed circular provirus of human T cell
leukaemia virus type I: A new open reading frame in the gag-pol
region."
RL J. Gen. Virol. 68:213-218 (1987).
DR EMBL; D10033; BAA00925.1; -; Genomic_DNA.
FT NON_TER 1
SQ SEQUENCE 13 AA; 1363 MW; 408035320911B443 CRC64;

Query Match 32.2%; Score 37; DB 2; Length 13;
Best Local Similarity 85.7%; Pred. No. 84;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DIPHPNTN 7
DB 1 DIPHPKN 7

RESULT 4
O76R60_9DELA PRELIMINARY; PRT; 13 AA.
AC O76R60;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Gag Protein (Fragment).
OS Human T-lymphotropic virus 1.
OX Viruses; Retroid viruses; Retroviridae; Deltaretrovirus.
OX NCBI_TaxID=11908;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=87111460; PubMed=3027244;
RA Hiramatsu K., Nishida J., Naito A., Yoshikawa H.;
RT "Molecular cloning of the closed circular provirus of human T cell
leukaemia virus type I: A new open reading frame in the gag-pol
region."
RL J. Gen. Virol. 68:213-218 (1987).
DR EMBL; X04800; CAA28492.1; -; Genomic_DNA.
FT NON_TER 1
SQ SEQUENCE 13 AA; 1363 MW; 408035320911B443 CRC64;

Query Match 32.2%; Score 37; DB 2; Length 13;
Best Local Similarity 85.7%; Pred. No. 84;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DIPHPNTN 7
DB 1 DIPHPKN 7

RESULT 5
O5C123_SCHUA PRELIMINARY; PRT; 19 AA.
AC O5C123;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Hypothetical protein.
OS Schistosoma japonicum (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
OC Schistosomatoidea; Schistosomatidae; Schistosoma.
OX NCBI_TaxID=6182;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Han Z.;
RT Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY810763; AAX26652.1; -; mRNA.

```

KW Hypothetical protein.  
SQ SEQUENCE 19 AA; 2259 MW; FE24492FB8464550 CRC64;

Query Match 28.7%; Score 33; DB 2; Length 19;  
Best Local Similarity 66.7%; Pred. No. 5.6e+02;  
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 PTNHHKLV 13  
| | | | |  
| | | | |  
Db 8 PMKIHNYLV 16

## RESULT 6

07S901\_NEUCR PRELIMINARY; PRT; 13 AA.

AC 07S901,  
DT 01-MAR-2004 (TrEMBLrel. 26, Created)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)  
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Predicted protein.  
GN Name=NCU05297.1;  
OS Neurospora crassa.  
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.  
OX NCBI\_TaxID=5141;  
[1]

## NUCLEOTIDE SEQUENCE.

RA STRAIN-OR74A;  
RC Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,  
Jaffe D., Fitzhugh W., Ma L.-J., Smirnov S., Purcell S., Rahman B.,  
Bikins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,  
Qui D., Iankilev P., Pedersen D., Nelson M., Washburne M.,  
Seltrenikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,  
Kothe G.O., Jedd G., Mewes W., Scaben C., Marcotte B., Greenberg D.,  
Roy A., Foley K., Naylor J., Thoman N., Barrett R., Gierke S.,  
Kamel M., Kamysheva S., Mauceli E., Bielke C., Rudd S., Frishman D.,  
Kryofova S., Rasmussen C., Metzberg R.L., Perkins D.D., Kroken S.,  
Cogoni C., Macino G., Catchside D., Li W., Pratt R.J., Omani S.A.,  
Desouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R.,  
Yarden O., Plamann M., Selzer S., Dunlap J., Radford A., Atamayo R.,  
Paulsen I., Sachs L.A., Manhaupt G., Ebbole D.J., Prellag M.,  
RA Paulsen I., Sachs L.A., Lander B.S., Nussbaum C., Birren B.;  
RT "The Genome Sequence of the Filamentous Fungus Neurospora crassa."  
RT Nature 0:0-0 (2003).  
-1- CAUTION: The sequence shown here is derived from an  
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
preliminary data.  
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
CC CC  
DR EMBL/ABX01000220; EMBL/ABX01000220; EMBL/ABX01000220; EMBL/ABX01000220;  
SQ SEQUENCE 13 AA; 1543 MW; 091807018C8D404B CRC64;

Query Match 27.8%; Score 32; DB 2; Length 13;  
Best Local Similarity 36.4%; Pred. No. 5.4e+02;  
Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 8 IHKYLVCASN 18  
: | | | | | | | | | |  
Db 3 VHTYINCTALN 13

## RESULT 7

04X4H2\_PLACH PRELIMINARY; PRT; 10 AA.

AC 04X4H2,  
DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
DE Hypothetical protein (Fragment).  
GN ORFNames=PC400586.00.0;  
OS Plasmodium chabaudi.  
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
OX NCBI\_TaxID=5825;  
[1]  
RP NUCLEOTIDE SEQUENCE.

RA Hall N., Karras M., Raine J.D., Carlton J.M., Kool J.T.W.A.,  
RA Bertman M., Plorens L., Jansen C.S., Pain A., Christophides G.K.,  
RA James K., Rutherford K., Harris B., Harris D., Churcher C.,  
RA Quail M.A., Ormond D., Doggett J., Truman H.B., Mendoza J.,  
RA Bidwell S.L., Rajadream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,  
RA Jansz C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.;  
RT "A comprehensive survey of the Plasmodium life cycle by genomic,  
RT transcriptomic, and proteomic analyses."  
RT Science 307:82-86(2005).  
RL Science 307:82-86(2005).  
-1- CAUTION: The sequence shown here is derived from an  
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
preliminary data.  
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
CC CC  
DR EMBL/CAJ010050; CAH88321.1; -; Genomic\_DNA.  
KW Hypothetical protein.  
FT NON\_TER  
SQ SEQUENCE 10 AA; 1230 MW; 4C729FD7205059C3 CRC64;

Query Match 26.1%; Score 30; DB 2; Length 10;  
Best Local Similarity 30.0%; Pred. No. 8.5e+02;  
Matches 3; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 8 IHKYLVCESV 17  
: | | | | | | | | | |  
Db 1 MHKFIILQSI 10

## RESULT 8

Q16244\_HUMAN PRELIMINARY; PRT; 18 AA.

AC 016244;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DE 01-MAY-1999 (TrEMBLrel. 10, Last annotation update)  
DE SRS protein (Fragment).  
GN Name=SRS;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
[1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=95038775; PubMed=7951263;  
RA Yen P.H., Ferrero G.B., Chinault A.C., Mohandas T., Ballabio A.;  
RT "Characterization of the deletion breakpoints in a patient with  
RT steroid sulfatase deficiency."  
RT Hum. Mutat. 4:76-78(1994).  
DR EMBL/S74383; AAD14153.1; -; Genomic\_DNA.  
FT NON\_TER  
SQ SEQUENCE 18 AA; 1958 MW; 3B3072711330CCFA CRC64;

Query Match 26.1%; Score 30; DB 2; Length 18;  
Best Local Similarity 41.7%; Pred. No. 1.6e+03;  
Matches 5; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 3 PHEPTNHHKLVLC 14  
| | | | | | | | | |  
Db 7 PCRVNHSYOLC 18

## RESULT 9

TWOF\_SARBU STANDARD; PRT; 6 AA.

AC P41495;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Trypsin-modulating oostatic factor (TWOF).  
OS Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;  
OC Sarcophagidae; Sarcophaga; Neobellieria.  
OX NCBI\_TaxID=7385;

```
RN [1]
RP PROTEIN SEQUENCE, AND SYNTHESIS.
RC TISSUE-Ovary;
RX MEDLINE=94211930; PubMed=8159807; DOI=10.1016/0167-0115(94)90192-9;
RA Bylemans D., Borovsky D., Hunt D.F., Shabanowitz J., Grauwels L.,
de Loof A.;
RT "Sequencing and characterization of trypsin modulating oostatic factor
(TMof) from the ovaries of the grey fleshfly, Neobellieria
(Sarcophaga) bullata.";
RL Regul. Pept. 50:61-72(1994).
CC -1- FUNCTION: Has an oostatic activity. Inhibits trypsin biosynthesis
in the midgut which indirectly reduces the vitellogenin
concentration in the hemolymph resulting in inhibition of oocyte
development.
CC -1- DEVELOPMENTAL STAGE: Synthesized and released from follicular
epithelium after a blood meal.
CC -----
CC This Swiss-Prot entry is copyrighted. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.
CC -----
CC Direct protein sequencing; Hormone.
SQ SEQUENCE 6 AA; 695 MW; 61B72451B7642000 CRC64;

Query Match 25.2%; Score 29; DB 1; Length 6;
Best Local Similarity 66.7%; Pred. No. 2.2e+06;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 HPTNIN 9
DB 1 NPTNLA 6

RESULT 10
Q5EX89_9LAMI PRELIMINARY; PRT; 19 AA.
ID Q5EX89_9LAMI
AC Q5EX89_9LAMI
DT 10-MAY-2005 (TREMBLrel. 30, Created)
DT 10-MAY-2005 (TREMBLrel. 30, Last sequence update)
DE STM2 protein (Fragment).
OS Streptococcus venosus.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Gentianales; Gesneriaceae; Cytrandroideae; Didymocarpaceae;
OC Streptocarpus.
OC NCBI_TaxID=301922;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=B;
RX PubMed=15659624; DOI=10.1105/lpc.104.028936;
RA Harrison J., Moller M., Langdale J., Cronk Q., Hudson A.;
RT "The Role of KNOX Genes in the Evolution of Morphological Novelty in
Streptocarpus.";
RL Plant Cell 17:430-443(2005).
EMBL AY662115; AAW33769.1; -; Genomic_DNA.
DR InterPro; IPR001356; Homeobox.
DR ProDom; PD000010; Homeobox; 1.
FT NON_TER 1 1
FT NON_TER 19 19
SQ SEQUENCE 19 AA; 2057 MW; 1069FC9782AFD64A CRC64;

Query Match 25.2%; Score 29; DB 2; Length 19;
Best Local Similarity 35.7%; Pred. No. 2.5e+03;
Matches 5; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
```

```
RESULT 11
Q5EX77_9LAMI PRELIMINARY; PRT; 19 AA.
ID Q5EX77_9LAMI
AC Q5EX77_9LAMI
DT 10-MAY-2005 (TREMBLrel. 30, Created)
DT 10-MAY-2005 (TREMBLrel. 30, Last sequence update)
DE STM1 protein (Fragment).
OS Streptocarpus thyanotus.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Gentianales; Gesneriaceae; Cytrandroideae; Didymocarpaceae;
OC Streptocarpus.
OC NCBI_TaxID=167308;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC PubMed=15659624; DOI=10.1105/lpc.104.028936;
RA Harrison J., Moller M., Langdale J., Cronk Q., Hudson A.;
RT "The Role of KNOX Genes in the Evolution of Morphological Novelty in
Streptocarpus.";
RL Plant Cell 17:430-443(2005).
EMBL AY662127; AAW33745.1; -; Genomic_DNA.
DR InterPro; IPR001356; Homeobox.
DR ProDom; PD000010; Homeobox; 1.
FT NON_TER 1 1
FT NON_TER 19 19
SQ SEQUENCE 19 AA; 2034 MW; 1069FC9782A6314A CRC64;

Query Match 24.3%; Score 28; DB 2; Length 19;
Best Local Similarity 35.7%; Pred. No. 3.6e+03;
Matches 5; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 3 PHTNINHKYLVCS 16
DB 1 PYPSSEOKLALAS 14

RESULT 12
Q5EX78_9LAMI PRELIMINARY; PRT; 19 AA.
ID Q5EX78_9LAMI
AC Q5EX78_9LAMI
DT 10-MAY-2005 (TREMBLrel. 30, Created)
DT 10-MAY-2005 (TREMBLrel. 30, Last sequence update)
DE STM1 protein (Fragment).
OS Streptocarpus glandulosissimus.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Gentianales; Gesneriaceae; Cytrandroideae; Didymocarpaceae;
OC Streptocarpus.
OC NCBI_TaxID=167270;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC PubMed=15659624; DOI=10.1105/lpc.104.028936;
RA Harrison J., Moller M., Langdale J., Cronk Q., Hudson A.;
RT "The Role of KNOX Genes in the Evolution of Morphological Novelty in
Streptocarpus.";
RL Plant Cell 17:430-443(2005).
EMBL AY662126; AAW33744.1; -; Genomic_DNA.
DR InterPro; IPR001356; Homeobox.
DR ProDom; PD000010; Homeobox; 1.
FT NON_TER 1 1
FT NON_TER 19 19
SQ SEQUENCE 19 AA; 2034 MW; 1069FC9782A6314A CRC64;

Query Match 24.3%; Score 28; DB 2; Length 19;
Best Local Similarity 35.7%; Pred. No. 3.6e+03;
Matches 5; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
```

```
RESULT 13
Q5EX88_9LAMI PRELIMINARY; PRT; 19 AA.
AC Q5EX88;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DE STM2 protein (Fragment).
OS Streptocarpus beamingiargatensis.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Lamiales; Gesneriaceae; Cyrtandroideae; Didymocarpeae;
OC Streptocarpus.
OX NCBI_TaxID=167246;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15659624; DOI=10.1105/tpc.104.028936;
RA Harrison J., Moller M., Langdale J., Cronk Q., Hudson A.;
RT "The Role of KNOX Genes in the Evolution of Morphological Novelty in
Streptocarpus.";
RL Plant Cell 17:430-443(2005).
DR EMBL; AY662116; AAW33770.1; -; Genomic_DNA.
DR InterPro; IPR001356; Homeobox.
DR ProDom; PD000010; Homeobox; 1.
FT NON_TER 1 19
SQ SEQUENCE 19 AA; 2034 MW; 1069FC9782A6314A CRC64;

Query Match 24.3%; Score 28; DB 2; Length 19;
Best Local Similarity 35.7%; Pred. No. 3.6e+03;
Matches 5; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 3 PHPTINIKYLVCES 16
|:|:|:|:|
DB 1 PYPSESQKLALAS 14

RESULT 14
Q5EX90_9LAMI PRELIMINARY; PRT; 19 AA.
AC Q5EX90;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DE STM2 protein (Fragment).
OS Streptocarpus venosus.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Lamiales; Gesneriaceae; Cyrtandroideae; Didymocarpeae;
OC Streptocarpus.
OX NCBI_TaxID=301922;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15659624; DOI=10.1105/tpc.104.028936;
RA Harrison J., Moller M., Langdale J., Cronk Q., Hudson A.;
RT "The Role of KNOX Genes in the Evolution of Morphological Novelty in
Streptocarpus.";
RL Plant Cell 17:430-443(2005).
DR EMBL; AY662114; AAW33768.1; -; Genomic_DNA.
DR InterPro; IPR001356; Homeobox.
DR ProDom; PD000010; Homeobox; 1.
FT NON_TER 1 19
SQ SEQUENCE 19 AA; 2034 MW; 1069FC9782A6314A CRC64;

Query Match 24.3%; Score 28; DB 2; Length 19;
Best Local Similarity 35.7%; Pred. No. 3.6e+03;
Matches 5; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 3 PHPTINIKYLVCES 16
|:|:|:|:|
DB 1 PYPSESQKLALAS 14
```

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DB 1 PYPSESQKLALAS 14

RESULT 15
Q5EX91_9LAMI PRELIMINARY; PRT; 19 AA.
AC Q5EX91;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DE STM2 protein (Fragment).
OS Streptocarpus thompsonii.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Lamiales; Gesneriaceae; Cyrtandroideae; Didymocarpeae;
OC Streptocarpus.
OX NCBI_TaxID=167307;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15659624; DOI=10.1105/tpc.104.028936;
RA Harrison J., Moller M., Langdale J., Cronk Q., Hudson A.;
RT "The Role of KNOX Genes in the Evolution of Morphological Novelty in
Streptocarpus.";
RL Plant Cell 17:430-443(2005).
DR EMBL; AY662113; AAW33767.1; -; Genomic_DNA.
DR InterPro; IPR001356; Homeobox.
DR ProDom; PD000010; Homeobox; 1.
FT NON_TER 1 19
SQ SEQUENCE 19 AA; 2034 MW; 1069FC9782A6314A CRC64;

Query Match 24.3%; Score 28; DB 2; Length 19;
Best Local Similarity 35.7%; Pred. No. 3.6e+03;
Matches 5; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 3 PHPTINIKYLVCES 16
|:|:|:|:|
DB 1 PYPSESQKLALAS 14

RESULT 16
Q5EX92_9LAMI PRELIMINARY; PRT; 19 AA.
AC Q5EX92;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DE STM2 protein (Fragment).
OS Streptocarpus primulifolius.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Lamiales; Gesneriaceae; Cyrtandroideae; Didymocarpeae;
OC Streptocarpus.
OX NCBI_TaxID=64018;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15659624; DOI=10.1105/tpc.104.028936;
RA Harrison J., Moller M., Langdale J., Cronk Q., Hudson A.;
RT "The Role of KNOX Genes in the Evolution of Morphological Novelty in
Streptocarpus.";
RL Plant Cell 17:430-443(2005).
DR EMBL; AY662112; AAW33766.1; -; Genomic_DNA.
DR InterPro; IPR001356; Homeobox.
DR ProDom; PD000010; Homeobox; 1.
FT NON_TER 1 19
SQ SEQUENCE 19 AA; 2034 MW; 1069FC9782A6314A CRC64;

Query Match 24.3%; Score 28; DB 2; Length 19;
Best Local Similarity 35.7%; Pred. No. 3.6e+03;
Matches 5; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 3 PHPTINIKYLVCES 16
|:|:|:|:|
DB 1 PYPSESQKLALAS 14
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Db 1 PYPSESQKLALES 14

RESULT 17  
QSEX94\_9LAMI PRELIMINARY; PRT; 19 AA.

AC QSEX94; 10-MAY-2005 (TREMBLrel. 30, Created)  
DT 10-MAY-2005 (TREMBLrel. 30, Last sequence update)  
DE STM2 protein (Fragment).  
OS Streptococcus modestus.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;  
OC Lamiales; Gentianaceae; Cyrtandroidae; Didymocarpaceae;  
OC Streptocarpus.  
OX NCBI\_TaxId=167287;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=A, and B;  
RX PubMed=15659624; DOI=10.1105/ltpc.104.028936;  
RA Harrison J., Moller M., Langdale J., Cronk Q., Hudson A.;  
RT "The Role of KNOX Genes in the Evolution of Morphological Novelty in  
Streptocarpus.";  
RT Plant Cell 17:430-443(2005).  
RL EMBL; AY662111; AAW33765.1; -; Genomic\_DNA.  
DR EMBL; AY662110; AAW33764.1; -; Genomic\_DNA.  
DR InterPro; IPR001356; Homeobox.  
DR ProDom; PD000010; Homeobox; 1.  
FT NON\_TER 1 19  
SQ SEQUENCE 19 AA; 2034 MW; 1069FC9782A6314A CRC64;

Query Match 24.3%; Score 28; DB 2; Length 19;  
Best Local Similarity 35.7%; Pred. No. 3.6e+03;  
Matches 5; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 3 PPHPTNHHKYLVCES 16  
Db 1 PYPSESQKLALES 14

RESULT 18  
QSEX95\_9LAMI PRELIMINARY; PRT; 19 AA.  
AC QSEX95; 10-MAY-2005 (TREMBLrel. 30, Created)  
DT 10-MAY-2005 (TREMBLrel. 30, Last sequence update)  
DE STM2 protein (STM1 protein) (Fragment).  
OS Streptocarpus hirticaepa.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;  
OC Lamiales; Gentianaceae; Cyrtandroidae; Didymocarpaceae;  
OC Streptocarpus.  
OX NCBI\_TaxId=167276;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX PubMed=15659624; DOI=10.1105/ltpc.104.028936;  
RA Harrison J., Moller M., Langdale J., Cronk Q., Hudson A.;  
RT "The Role of KNOX Genes in the Evolution of Morphological Novelty in  
Streptocarpus.";  
RT Plant Cell 17:430-443(2005).  
RL EMBL; AY662109; AAW33763.1; -; Genomic\_DNA.  
DR EMBL; AY662122; AAW33740.1; -; Genomic\_DNA.  
DR InterPro; IPR001356; Homeobox.  
DR ProDom; PD000010; Homeobox; 1.  
FT NON\_TER 1 19  
SQ SEQUENCE 19 AA; 2034 MW; 1069FC9782A6314A CRC64;

Query Match 24.3%; Score 28; DB 2; Length 19;

Best Local Similarity 35.7%; Pred. No. 3.6e+03;  
Matches 5; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 3 PPHPTNHHKYLVCES 16  
Db 1 PYPSESQKLALES 14

RESULT 19  
QSEX96\_9LAMI PRELIMINARY; PRT; 19 AA.  
AC QSEX96; 10-MAY-2005 (TREMBLrel. 30, Created)  
DT 10-MAY-2005 (TREMBLrel. 30, Last sequence update)  
DE STM2 protein (STM1 protein) (Fragment).  
OS Streptocarpus burundianus.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;  
OC Lamiales; Gentianaceae; Cyrtandroidae; Didymocarpaceae;  
OC Streptocarpus.  
OX NCBI\_TaxId=167253;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX PubMed=15659624; DOI=10.1105/ltpc.104.028936;  
RA Harrison J., Moller M., Langdale J., Cronk Q., Hudson A.;  
RT "The Role of KNOX Genes in the Evolution of Morphological Novelty in  
Streptocarpus.";  
RT Plant Cell 17:430-443(2005).  
RL EMBL; AY662108; AAW33762.1; -; Genomic\_DNA.  
DR EMBL; AY662123; AAW33741.1; -; Genomic\_DNA.  
DR InterPro; IPR001356; Homeobox.  
DR ProDom; PD000010; Homeobox; 1.  
FT NON\_TER 1 19  
SQ SEQUENCE 19 AA; 2034 MW; 1069FC9782A6314A CRC64;

Query Match 24.3%; Score 28; DB 2; Length 19;  
Best Local Similarity 35.7%; Pred. No. 3.6e+03;  
Matches 5; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 3 PPHPTNHHKYLVCES 16  
Db 1 PYPSESQKLALES 14

RESULT 20  
QSEX97\_9LAMI PRELIMINARY; PRT; 19 AA.  
AC QSEX97; 10-MAY-2005 (TREMBLrel. 30, Created)  
DT 10-MAY-2005 (TREMBLrel. 30, Last sequence update)  
DE STM2 protein (Fragment).  
OS Streptocarpus witell.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;  
OC Lamiales; Gentianaceae; Cyrtandroidae; Didymocarpaceae;  
OC Streptocarpus.  
OX NCBI\_TaxId=167311;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX PubMed=15659624; DOI=10.1105/ltpc.104.028936;  
RA Harrison J., Moller M., Langdale J., Cronk Q., Hudson A.;  
RT "The Role of KNOX Genes in the Evolution of Morphological Novelty in  
Streptocarpus.";  
RT Plant Cell 17:430-443(2005).  
RL EMBL; AY662107; AAW33761.1; -; Genomic\_DNA.  
DR InterPro; IPR001356; Homeobox.  
DR ProDom; PD000010; Homeobox; 1.  
FT NON\_TER 1 19  
SQ SEQUENCE 19 AA; 2034 MW; 1069FC9782A6314A CRC64;



Query Match 24.3%; Score 28; DB 2; Length 19;  
Best Local Similarity 35.7%; Pred. No. 3.6e+03;  
Matches 5; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 3 PHPTNIHKYLVCS 16  
|:|:|:|:  
Db 1 PYPSESQKLAALS 14

## RESULT 21

QSEX99\_9LAMI PRELIMINARY; PRT; 19 AA.  
ID QSEX98\_9LAMI PRELIMINARY; PRT; 19 AA.  
AC QSEX98;  
DT 10-MAY-2005 (TREMBlrel. 30, Created)  
DT 10-MAY-2005 (TREMBlrel. 30, Last sequence update)  
DE 10-MAY-2005 (TREMBlrel. 30, Last annotation update)  
OS Streptococcus rexi1.  
OC Bacteria; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;  
OC Lamiales; Gentianales; Gentianaceae; Didymocarpaceae;  
OC Streptocarpus.  
OC NCBI\_TaxID=121488;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX PubMed=15659624; DOI=10.1105/tpc.104.028936;  
RA Harrison J., Moller M., Langdale J., Cronk O., Hudson A.;  
RT "The Role of KNOX Genes in the Evolution of Morphological Novelty in  
RT Streptocarpus."  
RL Plant Cell 17:430-443(2005).  
DR EMBL; AY662106; AAW33760.1; -; Genomic\_DNA.  
DR InterPro; IPR001356; Homeobox.  
DR ProDom; PD000010; Homeobox; 1.  
FT NON\_TER 1 1  
FT NON\_TER 19 19  
SQ SEQUENCE 19 AA; 2034 MW; 1069FC9782A6314A CRC64;

Query Match 24.3%; Score 28; DB 2; Length 19;  
Best Local Similarity 35.7%; Pred. No. 3.6e+03;  
Matches 5; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 3 PHPTNIHKYLVCS 16  
|:|:|:|:  
Db 1 PYPSESQKLAALS 14

## RESULT 22

QSEX99\_9LAMI PRELIMINARY; PRT; 19 AA.  
ID QSEX99\_9LAMI PRELIMINARY; PRT; 19 AA.  
AC QSEX99;  
DT 10-MAY-2005 (TREMBlrel. 30, Created)  
DT 10-MAY-2005 (TREMBlrel. 30, Last sequence update)  
DE 10-MAY-2005 (TREMBlrel. 30, Last annotation update)  
OS Streptocarpus wendlandii.  
OC Bacteria; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;  
OC Lamiales; Gentianales; Gentianaceae; Didymocarpaceae;  
OC Streptocarpus.  
OC NCBI\_TaxID=167310;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX PubMed=15659624; DOI=10.1105/tpc.104.028936;  
RA Harrison J., Moller M., Langdale J., Cronk O., Hudson A.;  
RT "The Role of KNOX Genes in the Evolution of Morphological Novelty in  
RT Streptocarpus."  
RL Plant Cell 17:430-443(2005).  
DR EMBL; AY662105; AAW33759.1; -; Genomic\_DNA.  
DR InterPro; IPR001356; Homeobox.  
DR ProDom; PD000010; Homeobox; 1.  
FT NON\_TER 1 1  
FT NON\_TER 19 19

SQ SEQUENCE 19 AA; 2034 MW; 1069FC9782A6314A CRC64;

Query Match 24.3%; Score 28; DB 2; Length 19;  
Best Local Similarity 35.7%; Pred. No. 3.6e+03;  
Matches 5; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 3 PHPTNIHKYLVCS 16  
|:|:|:|:  
Db 1 PYPSESQKLAALS 14

## RESULT 23

QSEXA1\_9LAMI PRELIMINARY; PRT; 19 AA.  
ID QSEXA1\_9LAMI PRELIMINARY; PRT; 19 AA.  
AC QSEXA1;  
DT 10-MAY-2005 (TREMBlrel. 30, Created)  
DT 10-MAY-2005 (TREMBlrel. 30, Last sequence update)  
DE 10-MAY-2005 (TREMBlrel. 30, Last annotation update)  
OS Streptocarpus dunali.  
OC Bacteria; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;  
OC Lamiales; Gentianales; Gentianaceae; Didymocarpaceae;  
OC Streptocarpus.  
OC NCBI\_TaxID=121487;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX PubMed=15659624; DOI=10.1105/tpc.104.028936;  
RA Harrison J., Moller M., Langdale J., Cronk O., Hudson A.;  
RT "The Role of KNOX Genes in the Evolution of Morphological Novelty in  
RT Streptocarpus."  
RL Plant Cell 17:430-443(2005).  
DR EMBL; AY662103; AAW33757.1; -; Genomic\_DNA.  
DR InterPro; IPR001356; Homeobox.  
DR ProDom; PD000010; Homeobox; 1.  
FT NON\_TER 1 1  
FT NON\_TER 19 19  
SQ SEQUENCE 19 AA; 2034 MW; 1069FC9782A6314A CRC64;

Query Match 24.3%; Score 28; DB 2; Length 19;  
Best Local Similarity 35.7%; Pred. No. 3.6e+03;  
Matches 5; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 3 PHPTNIHKYLVCS 16  
|:~:~:~:~:  
Db 1 PYPSESQKLAALS 14

## RESULT 24

QSEXA2\_9LAMI PRELIMINARY; PRT; 19 AA.  
ID QSEXA2\_9LAMI PRELIMINARY; PRT; 19 AA.  
AC QSEXA2;  
DT 10-MAY-2005 (TREMBlrel. 30, Created)  
DT 10-MAY-2005 (TREMBlrel. 30, Last sequence update)  
DE 10-MAY-2005 (TREMBlrel. 30, Last annotation update)  
OS Streptocarpus schliebentii.  
OC Bacteria; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;  
OC Lamiales; Gentianales; Gentianaceae; Didymocarpaceae;  
OC Streptocarpus.  
OC NCBI\_TaxID=167302;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX PubMed=15659624; DOI=10.1105/tpc.104.028936;  
RA Harrison J., Moller M., Langdale J., Cronk O., Hudson A.;  
RT "The Role of KNOX Genes in the Evolution of Morphological Novelty in  
RT Streptocarpus."  
RL Plant Cell 17:430-443(2005).  
DR EMBL; AY662102; AAW33756.1; -; Genomic\_DNA.  
DR EMBL; AY662124; AAW33742.1; -; Genomic\_DNA.  
DR InterPro; IPR001356; Homeobox.  
DR ProDom; PD000010; Homeobox; 1.

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FT  NON TER      1      1
FT  NON TER      19     19
SQ  SEQUENCE      19 AA; 2034 MW; 1069FC9782A6314A CRC64;

Query Match
Best Local Similarity 24.3%; Score 28; DB 2; Length 19;
Matches 5; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY  3 PHPTNHKYLVCES 16
    |||:|:|:|
Db  1 PYPSESQKLALAES 14

RESULT 25
QSEXA3_9LAMI PRELIMINARY; PRT; 19 AA.
ID  QSEXA3_9LAMI PRELIMINARY; PRT; 19 AA.
AC  QSEXA3;
DT  10-MAY-2005 (TrEMBLrel. 30, Created)
DT  10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DE  STM2 protein (Fragment).
OS  Streptococcus thermophilus.
OC  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC  Lamiales; Gentianales; Cytrandroideae; Didymocarpaceae;
OC  Streptocarpaceae.
OX  NCBI_TaxID=167279;
RN  [1]
RP  NUCLEOTIDE SEQUENCE.
RX  PubMed=15659624; DOI=10.1105/tpc.104.028936;
RA  Harrison J., Moller M., Langdale J., Cronk Q., Hudson A.;
RT  "The Role of KNOX Genes in the Evolution of Morphological Novelty in
RT  Streptocarpus.";
RL  Plant Cell 17:430-443(2005).
DR  EMBL; AY662101; AAW3375.1; -; Genomic_DNA.
DR  InterPro; IPR001356; Homeobox.
DR  ProDom; PD000010; Homeobox; 1.
FT  NON TER      1      1
FT  NON TER      19     19
SQ  SEQUENCE      19 AA; 2034 MW; 1069FC9782A6314A CRC64;

Query Match
Best Local Similarity 24.3%; Score 28; DB 2; Length 19;
Matches 5; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY  3 PHPTNHKYLVCES 16
    |||:|:|:|
Db  1 PYPSESQKLALAES 14

RESULT 26
QSEXA4_9LAMI PRELIMINARY; PRT; 19 AA.
ID  QSEXA4_9LAMI PRELIMINARY; PRT; 19 AA.
AC  QSEXA4;
DT  10-MAY-2005 (TrEMBLrel. 30, Created)
DT  10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DE  STM2 protein (STM1 protein) (Fragment).
OS  Streptocarpus ibitiensis.
OC  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC  Lamiales; Gentianales; Cytrandroideae; Didymocarpaceae;
OC  Streptocarpaceae.
OX  NCBI_TaxID=167278;
RN  [1]
RP  NUCLEOTIDE SEQUENCE.
RC  STRAIN=A, and B;
RX  PubMed=15659624; DOI=10.1105/tpc.104.028936;
RA  Harrison J., Moller M., Langdale J., Cronk Q., Hudson A.;
RT  "The Role of KNOX Genes in the Evolution of Morphological Novelty in
RT  Streptocarpus.";
RL  Plant Cell 17:430-443(2005).
DR  EMBL; AY662100; AAW33754.1; -; Genomic_DNA.
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DR  EMBL; AY662120; AAW33738.1; -; Genomic_DNA.
DR  EMBL; AY662121; AAW33739.1; -; Genomic_DNA.
DR  InterPro; IPR001356; Homeobox.
DR  ProDom; PD000010; Homeobox; 1.
FT  NON TER      1      1
FT  NON TER      19     19
SQ  SEQUENCE      19 AA; 2034 MW; 1069FC9782A6314A CRC64;

Query Match
Best Local Similarity 24.3%; Score 28; DB 2; Length 19;
Matches 5; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY  3 PHPTNHKYLVCES 16
    |||:|:|:|
Db  1 PYPSESQKLALAES 14

RESULT 27
QSEXA5_9LAMI PRELIMINARY; PRT; 19 AA.
ID  QSEXA5_9LAMI PRELIMINARY; PRT; 19 AA.
AC  QSEXA5;
DT  10-MAY-2005 (TrEMBLrel. 30, Created)
DT  10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DE  STM2 protein (STM1 protein) (Fragment).
OS  Streptocarpus papuanae.
OC  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC  Lamiales; Gentianales; Cytrandroideae; Didymocarpaceae;
OC  Streptocarpaceae.
OX  NCBI_TaxID=167293;
RN  [1]
RP  NUCLEOTIDE SEQUENCE.
RX  PubMed=15659624; DOI=10.1105/tpc.104.028936;
RA  Harrison J., Moller M., Langdale J., Cronk Q., Hudson A.;
RT  "The Role of KNOX Genes in the Evolution of Morphological Novelty in
RT  Streptocarpus.";
RL  Plant Cell 17:430-443(2005).
DR  EMBL; AY662099; AAW33753.1; -; Genomic_DNA.
DR  EMBL; AY662119; AAW33737.1; -; Genomic_DNA.
DR  InterPro; IPR001356; Homeobox.
DR  ProDom; PD000010; Homeobox; 1.
FT  NON TER      1      1
FT  NON TER      19     19
SQ  SEQUENCE      19 AA; 2034 MW; 1069FC9782A6314A CRC64;

Query Match
Best Local Similarity 24.3%; Score 28; DB 2; Length 19;
Matches 5; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY  3 PHPTNHKYLVCES 16
    |||:|:~|:|
Db  1 PYPSESQKLALAES 14

RESULT 28
QSEXA6_9LAMI PRELIMINARY; PRT; 19 AA.
ID  QSEXA6_9LAMI PRELIMINARY; PRT; 19 AA.
AC  QSEXA6;
DT  10-MAY-2005 (TrEMBLrel. 30, Created)
DT  10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DE  STM2 protein (Fragment).
OS  Streptocarpus saxorum.
OC  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC  Lamiales; Gentianales; Cytrandroideae; Didymocarpaceae;
OC  Streptocarpaceae.
OX  NCBI_TaxID=48776;
RN  [1]
RP  NUCLEOTIDE SEQUENCE.
RX  PubMed=15659624; DOI=10.1105/tpc.104.028936;
RA  Harrison J., Moller M., Langdale J., Cronk Q., Hudson A.;
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RT "The Role of KNOX Genes in the Evolution of Morphological Novelty in
RT Streptocarpus."
RT Plant Cell 17:430-443(2005).
DR EMBL: AY662098; AAW33752.1; -, Genomic_DNA.
DR InterPro: IPR001356; Homeobox.
DR Prodom: PD000010; Homeobox; 1.
FT NON_TER 1
FT NON_TER 19
SQ SEQUENCE 19 AA; 2034 MW; 1069FC9782A6314A CRC64;

Query Match
Best Local Similarity 35.7%; Score 28; DB 2; Length 19;
Matches 5; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 3 PHPTNIHKYLVCS 16
Db 1 PYPSSQKLALES 14

RESULT 29
QSEXA7_9LAMI PRELIMINARY; PRT; 19 AA.
AC QSEXA7;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DE STM2 protein (STM1 protein) (Fragment).
OS Streptocarpus pallidiflorus.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Lamiales; Gesneriaceae; Cytrandroideae; Didymocarpeae;
OC Streptocarpus.
OC NCBI_TaxID=67292;
RN NUCLEOTIDE SEQUENCE.
RP PubMed=15659624; DOI=10.1105/tpc.104.028936;
RA Harrison J., Moller M., Langdale J., Cronk O., Hudson A.;
RT "The Role of KNOX Genes in the Evolution of Morphological Novelty in
RT Streptocarpus."
RT Plant Cell 17:430-443(2005).
DR EMBL: AY662097; AAW33751.1; -, Genomic_DNA.
DR InterPro: IPR001356; Homeobox.
DR Prodom: PD000010; Homeobox; 1.
FT NON_TER 1
FT NON_TER 19
SQ SEQUENCE 19 AA; 2034 MW; 1069FC9782A6314A CRC64;

Query Match
Best Local Similarity 35.7%; Score 28; DB 2; Length 19;
Matches 5; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 3 PHPTNIHKYLVCS 16
Db 1 PYPSSQKLALES 14

RESULT 30
QSEXA8_9LAMI PRELIMINARY; PRT; 19 AA.
AC QSEXA8;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DE STM2 protein (Fragment).
OS Streptocarpus stomandrus.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Lamiales; Gesneriaceae; Cytrandroideae; Didymocarpeae;
OC Streptocarpus.
OC NCBI_TaxID=167305;
RN NUCLEOTIDE SEQUENCE.

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RC STRAIN=A;
RX PubMed=15659624; DOI=10.1105/tpc.104.028936;
RA Harrison J., Moller M., Langdale J., Cronk O., Hudson A.;
RT "The Role of KNOX Genes in the Evolution of Morphological Novelty in
RT Streptocarpus."
RT Plant Cell 17:430-443(2005).
DR EMBL: AY662096; AAW33750.1; -, Genomic_DNA.
DR InterPro: IPR001356; Homeobox.
DR Prodom: PD000010; Homeobox; 1.
FT NON_TER 1
FT NON_TER 19
SQ SEQUENCE 19 AA; 2034 MW; 1069FC9782A6314A CRC64;

Query Match
Best Local Similarity 35.7%; Score 28; DB 2; Length 19;
Matches 5; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 3 PHPTNIHKYLVCS 16
Db 1 PYPSSQKLALES 14

RESULT 31
QSEXA9_9LAMI PRELIMINARY; PRT; 19 AA.
AC QSEXA9;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DE STM2 protein (Fragment).
OS Saintpaulia velutina.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Lamiales; Gesneriaceae; Cytrandroideae; Didymocarpeae;
OC Saintpaulia.
OC NCBI_TaxID=86150;
RN NUCLEOTIDE SEQUENCE.
RP PubMed=15659624; DOI=10.1105/tpc.104.028936;
RA Harrison J., Moller M., Langdale J., Cronk O., Hudson A.;
RT "The Role of KNOX Genes in the Evolution of Morphological Novelty in
RT Streptocarpus."
RT Plant Cell 17:430-443(2005).
DR EMBL: AY662095; AAW33749.1; -, Genomic_DNA.
DR InterPro: IPR001356; Homeobox.
DR Prodom: PD000010; Homeobox; 1.
FT NON_TER 1
FT NON_TER 19
SQ SEQUENCE 19 AA; 2034 MW; 1069FC9782A6314A CRC64;

Query Match
Best Local Similarity 35.7%; Score 28; DB 2; Length 19;
Matches 5; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 3 PHPTNIHKYLVCS 16
Db 1 PYPSSQKLALES 14

RESULT 32
QSEXB0_9LAMI PRELIMINARY; PRT; 19 AA.
AC QSEXB0;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DE STM2 protein (Fragment).
OS Saintpaulia ionantha.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Lamiales; Gesneriaceae; Cytrandroideae; Didymocarpeae;
OC Saintpaulia.

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OX NCB1_Taxid=85262;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15659624; DOI=10.1105/tpc.104.028936;
RA Harrison J., Moller M., Langdale J., Cronk Q., Hudson A.;
RT "The Role of KNOX Genes in the Evolution of Morphological Novelty in
  Streptocarpus.";
RT Plant Cell 17:430-443(2005).
DR EMBL; AY662094; AAM33748.1; -; Genomic_DNA.
DR InterPro; IPR001356; Homeobox.
DR Prodom; PD000010; Homeobox; 1.
FT NON_TER
FT NON_TER
SQ SEQUENCE 19 AA; 2034 MW; 1069FC9782A6314A CRC64;

Query Match
Best Local Similarity 24.3%; Score 28; DB 2; Length 19;
Matches 5; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 3 PHPTNHYKLVCS 16
|:|:|:|:|
Db 1 PYPSESQKLAABS 14

RESULT 33
O5EXB1_9LAMI PRELIMINARY; PRT; 19 AA.
ID O5EXB1_9LAMI
AC O5EXB1_9LAMI
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DE STM2 protein (Fragment).
OS Sainpaulia longensis.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Gentianaceae; Cyrtandroidae; Didymocarpaceae;
OC Sainpaulia.
OX NCB1_Taxid=86149;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=B, and A;
RX PubMed=15659624; DOI=10.1105/tpc.104.028936;
RA Harrison J., Moller M., Langdale J., Cronk Q., Hudson A.;
RT "The Role of KNOX Genes in the Evolution of Morphological Novelty in
  Streptocarpus.";
RT Plant Cell 17:430-443(2005).
DR EMBL; AY662093; AAM33747.1; -; Genomic_DNA.
DR EMBL; AY662092; AAM33746.1; -; Genomic_DNA.
DR InterPro; IPR001356; Homeobox.
DR Prodom; PD000010; Homeobox; 1.
FT NON_TER
FT NON_TER
SQ SEQUENCE 19 AA; 2034 MW; 1069FC9782A6314A CRC64;

Query Match
Best Local Similarity 24.3%; Score 28; DB 2; Length 19;
Matches 5; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 3 PHPTNHYKLVCS 16
|:|:|:|:|
Db 1 PYPSESQKLAABS 14

RESULT 34
Q4YMN1_PLAAB PRELIMINARY; PRT; 20 AA.
ID Q4YMN1_PLAAB
AC Q4YMN1_PLAAB
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein (Fragment).
ORFNames=PB400077.00.0;
OS Plasmodium berghel.

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OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCB1_Taxid=5821;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Hall N., Karris M., Raine J.D., Carlton J.M., Kool J.T.W.A.,
RA Berrieman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
RA Bidwell S.L., Rajandream M.A., Carnuel D.J., Yates J.R., Kafatos F.C.,
RA James C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.;
RT "A comprehensive survey of the Plasmodium life cycle by genomic,
  transcriptomic, and proteomic analyses.";
RT Science 307:82-86(2005).
CC -! CAUTION: The sequence shown here is derived from an
  EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
  preliminary data.
CC EMBL; CA101003517; CA100729.1; -; Genomic_DNA.
DR Hypothetical protein.
FT NON_TER
FT NON_TER
SQ SEQUENCE 20 AA; 2221 MW; CB1EB3142E99E869 CRC64;

Query Match
Best Local Similarity 24.3%; Score 28; DB 2; Length 20;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 10 KYLVCS 15
|:|:|:|:|
Db 12 KYLVCD 17

RESULT 35
O26062_HELPY PRELIMINARY; PRT; 18 AA.
ID O26062_HELPY
AC O26062_HELPY
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein HP1536.
OS OrderedclucNames=HP1536;
OS Helicobacter pylori (Campylobacter pylori).
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
OC Helicobacteraceae; Helicobacter.
OX NCB1_Taxid=210;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=26695 / ATCC 700392;
RX MEDLINE=97394467; PubMed=9252185; DOI=10.1038/41483;
RA Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,
RA Fleischmann R.D., Ketchum K.A., Klein H.-P., Gill S.R.,
RA Dougherty B.A., Nelson K.E., Quackenbush J., Zhou L., Kirkness B.F.,
RA Peterson S.N., Loftus B.J., Richardson D.L., Dodson R.J., Khalak H.G.,
RA Glodek A., McKenney K., Fitzgerald L.M., Lee N., Adams M.D.,
RA Hickey E.K., Berg D.B., Gocayne J.D., Uterback T.R., Peterson J.D.,
RA Kelley J.M., Cotton M.D., Weidman J.F., Fujii C., Bowman C.,
RA Wathey L., Wallin B., Hayes W.S., Borodovsky M., Karp P.D.,
RA Smith H.O., Fraser C.M., Venter J.C.;
RT "The complete genome sequence of the gastric pathogen Helicobacter
  pylori.";
RT Nature 388:539-547(1997).
DR EMBL; AB000651; AAD08578.1; -; Genomic_DNA.
DR PIR; H64711; H64711.
DR TIGR; HP1536; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 18 AA; 2296 MW; AC0B5A3DPD9CD482 CRC64;

Query Match
Best Local Similarity 23.5%; Score 27; DB 2; Length 18;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 HPTNHYKLV 12
|:|:|:|:|
Db 10 HPSRNPXYL 18

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RESULT 36
Q4XJ38_PLACH PRELIMINARY; PRT; 19 AA.
ID Q4XJ38_PLACH PRELIMINARY; PRT; 19 AA.
AC Q4XJ38;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DE Hypothetical protein.
ORFNames=PC400757.00.0;
OS Plasmodium chabaudi.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5825;
[1]
RP NUCLEOTIDE SEQUENCE.
RA Hall N., Karrar M., Ratne J.D., Carlton J.M., Kool J.T.W.A.,
RA Bertman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
RA Quail M.A., Ormond D., Doggett J., Trueman H.B., Mendoza J.,
RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
RA Janse C.J., Barrett B., Turner C.M.R., Waters A.P., Sinden R.S.;
RA "A comprehensive survey of the Plasmodium life cycle by genomic,
RT transcriptomic, and proteomic analyses.";
RL Science 307:82-86(2005).
CC -1- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
preliminary data.
DR EMBL/CAJ01005589; CAH83076.1; -; Genomic_DNA.
KM Hypothetical protein.
SQ SEQUENCE 19 AA; 2375 MW; 339771F259128CNC CRC64;

Query Match 23.5%; Score 27; DB 2; Length 19;
Best Local Similarity 55.6%; Pred. No. 5.2e+03;
Matches 5; Conservative 2; Mismatches 0; Indels 2; Gaps 1;

QY 8 IHK-YLVC 14
DB 3 VHKCTYIVC 11

RESULT 37
Q4YK87_PLABE PRELIMINARY; PRT; 19 AA.
ID Q4YK87_PLABE PRELIMINARY; PRT; 19 AA.
AC Q4YK87;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DE Hypothetical protein (Fragment).
ORFNames=PA401730.00.0;
OS Plasmodium berghei.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5821;
[1]
RP NUCLEOTIDE SEQUENCE.
RA Hall N., Karrar M., Ratne J.D., Carlton J.M., Kool J.T.W.A.,
RA Bertman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
RA Quail M.A., Ormond D., Doggett J., Trueman H.B., Mendoza J.,
RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
RA Janse C.J., Barrett B., Turner C.M.R., Waters A.P., Sinden R.S.;
RA "A comprehensive survey of the Plasmodium life cycle by genomic,
RT transcriptomic, and proteomic analyses.";
RL Science 307:82-86(2005).
CC -1- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
preliminary data.
DR EMBL/CAJ01004271; CAI01575.1; -; Genomic_DNA.
KM Hypothetical protein.
SQ SEQUENCE 19 AA; 2230 MW; E9A5F910F35E0F35 CRC64;

Query Match 23.5%; Score 27; DB 2; Length 19;
Best Local Similarity 55.6%; Pred. No. 5.2e+03;
Matches 5; Conservative 2; Mismatches 0; Indels 2; Gaps 1;
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Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 IHPPTNKH 10
DB 8 LPPRNIPK 16

RESULT 38
Q7RR59_PLAYO PRELIMINARY; PRT; 20 AA.
ID Q7RR59_PLAYO PRELIMINARY; PRT; 20 AA.
AC Q7RR59;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DE Hypothetical protein (Fragment).
ORFNames=PY00877;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=73239;
[1]
RP NUCLEOTIDE SEQUENCE.
RA STRAIN=17XN1;
RX MEDLINE=22255706; PubMed=12368865; DOI=10.1038/nature01099;
RA Carlton J.M., Angiuoli S.V., Suh B.B., Kool J.T.W., Perce M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA Shallow S.J., van Aken S.B., Riedmiller S.B., Feldblyum T.V.,
RA Florens L., Yates J.R. III, Ratne J.D., Sinden R.E., Harris M.A.,
RA Cunningham D.A., Pfeiser P.R., Bergman L.W., Valdivia A.B.,
RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA Carucci D.J.;
RT "Genome sequence and comparative analysis of the model rodent malaria
parasite Plasmodium yoelii yoelii.";
RL Nature 419:512-519(2002).
CC -1- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
preliminary data.
DR EMBL/AAJL01000235; EAA19069.1; -; Genomic_DNA.
KM Hypothetical protein.
FT NON TER 20
SQ SEQUENCE 20 AA; 2509 MW; 85C3599786475AA6 CRC64;

Query Match 23.5%; Score 27; DB 2; Length 20;
Best Local Similarity 27.3%; Pred. No. 5.5e+03;
Matches 3; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 7 NIKYIVCSV 17
DB 8 NINYIIMONT 18

RESULT 39
Q9UMR0_HUMAN PRELIMINARY; PRT; 12 AA.
ID Q9UMR0_HUMAN PRELIMINARY; PRT; 12 AA.
AC Q9UMR0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Fructose-1,6-bisphosphatase (BC 3.1.3.11) (Fragment).
ORFNames=FBP2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae;
OC Homo.
NCBI_TaxID=9606;
[1]
RP NUCLEOTIDE SEQUENCE.
RA MEDLINE=20237676; PubMed=10773464; DOI=10.1016/S0378-1119(00)00079-2;
RA Tillmann H., Stein S., Liehr T., Bechtich K.;
RT "Structure and chromosomal localization of the human and mouse muscle
fructose-1,6-bisphosphatase genes.";
```

RL Gene 247:241-253(2000).  
 DR EMBL; AJ238483; CAB53359.1; -; Genomic DNA.  
 DR GO; GO:004132; F:fructose-bisphosphatase activity; IEA.  
 DR GO; GO:0016787; F:hydrolase activity; IEA.  
 KM Hydrolase.  
 FT NON\_TER 1 1  
 FT NON\_TER 12 12  
 SQ SEQUENCE 12 AA; 1382 MW; 4CEB259E57386403 CRC64;

Query Match 22.6%; Score 26; DB 2; Length 12;  
 Best Local Similarity 80.0%; Pred. No. 4.6e+03;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 10 KYLVC 14  
 ||:|  
 DB 8 KYVVC 12

RESULT 40  
 Q4LOW0 BACTK PRELIMINARY; PRT; 17 AA.

AC Q4LOW0;  
 DT 13-SEP-2005 (TREMBLrel. 31, Created)  
 DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)  
 DT 13-SEP-2005 (TREMBLrel. 31, Last annotation update)  
 DE Methyltransferase (Fragment).  
 OS Bacillus thuringiensis (subsp. kurstaki).  
 OC Bacteria; Firmicutes; Bacilliales; Bacillaceae; Bacillus;  
 OC Bacillus cereus group.  
 OK NCBI\_TaxID=29339;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=8010;  
 RA Huang T., Yu X., Guan X.;  
 RT "Differential expression of genes at different growth phases in  
 Bacillus thuringiensis strain 8010."  
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY646411; AAV65152.1; -; mRNA.  
 KM Methyltransferase; Transferase.  
 FT NON\_TER 1 1  
 FT NON\_TER 17 AA; 2201 MW; 49C3D8C675DB667F CRC64;  
 SQ SEQUENCE

Query Match 22.6%; Score 26; DB 2; Length 17;  
 Best Local Similarity 42.9%; Pred. No. 6.7e+03;  
 Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 9 HKYLCV 15  
 ||:|  
 DB 10 HRIPICE 16

RESULT 41  
 Q9XNO7\_BOOMI PRELIMINARY; PRT; 19 AA.

AC Q9XNO7;  
 DT 01-NOV-1999 (TREMBLrel. 12, Created)  
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)  
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)  
 DE Cytochrome b apoenzyme (Fragment).  
 GN Name=Cyb;  
 OS Boophilus microplus (Cattle tick).  
 OC Mitochondrion.  
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;  
 OC Parasitiformes; Ixodida; Ixodidae; Ixodidae; Boophilus.  
 OK NCBI\_TaxID=9941;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=N;  
 RX MEDLINE=99297341; PubMed=10368952;

RA Campbell N.J.H., Barker S.C.;  
 RT "The novel mitochondrial gene arrangement of the cattle tick,  
 Boophilus microplus: fivefold tandem repetition of a coding region";  
 Mol. Biol. Evol. 16:732-740(1999).

DR EMBL; AF110611; AAD28394.1; -; Genomic DNA.  
 DR GO; GO:0005739; C:mitochondrion; IEA.  
 KM Mitochondrion.  
 FT NON\_TER 19 19  
 FT NON\_TER 19 19  
 SQ SEQUENCE 19 AA; 2144 MW; 07A018D65CEBD8D0 CRC64;

Query Match 22.6%; Score 26; DB 2; Length 19;  
 Best Local Similarity 50.0%; Pred. No. 7.6e+03;  
 Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 DHPPTNI 8  
 ||:|  
 DB 10 NLPTPSNI 17

RESULT 42  
 Q5EX86\_9LAMI PRELIMINARY; PRT; 19 AA.

AC Q5EX86;  
 DT 10-MAY-2005 (TREMBLrel. 30, Created)  
 DT 10-MAY-2005 (TREMBLrel. 30, Last sequence update)  
 DT 10-MAY-2005 (TREMBLrel. 30, Last annotation update)  
 DE STM2 protein (Fragment).  
 OS Streptococcus sp. JH-2004.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;  
 OC Lamiales; Lamiales; Gesneriaceae; Cyrtandroidae; Didymocarpaceae;  
 OC Streptocarpus.  
 OK NCBI\_TaxID=301924;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX PubMed=15659624; DOI=10.1105/epc.104.028936;  
 RA Harrison J., Moller M., Langdale J., Cronk O., Hudson A.;  
 RT "The Role of KNOX Genes in the Evolution of Morphological Novelty in  
 Streptocarpus."  
 RT Plant Cell 17:430-443(2005).  
 RL EMBL; AY662118; AAW33772.1; -; Genomic DNA.  
 DR InterPro; IPR001356; Homeobox.  
 DR Prodom; PDD00010; Homeobox; 1.  
 FT NON\_TER 1 1  
 FT NON\_TER 19 19  
 FT NON\_TER 19 19  
 SQ SEQUENCE 19 AA; 2073 MW; 3D69FC9782A6315D CRC64;

Query Match 22.6%; Score 26; DB 2; Length 19;  
 Best Local Similarity 35.7%; Pred. No. 7.6e+03;  
 Matches 5; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 3 PPTNIHKYLCVS 16  
 ||:|  
 DB 1 PYPSESQKALXES 14

RESULT 43  
 PHYL4\_PHYOR STANDARD; PRT; 20 AA.

AC P84569;  
 DT 13-SEP-2005 (Rel. 48, Created)  
 DT 13-SEP-2005 (Rel. 48, Last sequence update)  
 DT 13-SEP-2005 (Rel. 48, Last annotation update)  
 DE Phylloleptin-4 (PS-4).  
 OS Phylloleptus oreades (Monkey frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Hylidae;  
 OC Phyllomedusinae; Phyllomedusa.  
 OK NCBI\_TaxID=239355;  
 RN [1]  
 RP PROTEIN SEQUENCE, FUNCTION, SUBCELLULAR LOCATION, TISSUE SPECIFICITY,  
 RP MASS SPECTROMETRY, AND AMIDATION.  
 RC TISSUE=Skin secretion;

RX PubMed=15752569; DOI=10.1016/j.peptides.2004.11.002;  
 RA Leite J.R.S.A., Silva L.P., Rodrigues M.I.S., Prates M.V., Brand G.D.,  
 R Lacerda B.M., Azevedo R.B., Bocca A.L., Albuquerque S., Bloch C. Jr.;  
 RT "Phylloleptins: a novel class of anti-bacterial and anti-protocozan

RT peptides from the *Phyllomedusa genus*."

RL Peptides 26:565-573(2005).

CC -1- FUNCTION: Has antiprotozoal activity against *T. cruzi*.

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- TISSUE SPECIFICITY: Expressed by the skin glands.

CC -1- MASS SPECTROMETRY: MW=2112.18; METHOD=WALDI; RANGE=1-20; NOTE=Ref.1.

CC -----

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CC -----

CC Antidation: Amphibian defense peptide; Antimicrobial;

KM Direct protein sequencing.

PT MOD RES 20 20 Glycine amide.

SQ SEQUENCE 20 AA; 2113 MW; C648DIC5CB91CFF CRC64;

QY Query Match 22.6%; Score 26; DB 1; Length 20; Best Local Similarity 46.7%; Pred. No. 8e+03; Mismatches 0; Indels 0; Gaps 0; Matches 7; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 2 IPRPTN1HKYLVCS 16  
| | | | |  
5 IPRH1NAVSTLVHHS 19

Db

RESULT 44

ID Q7RS12\_P1AYO PRELIMINARY; PRT; 20 AA.

AC Q7RS12;

DT 01-MAR-2004 (TrEMBLrel. 26, Created)

DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)

DE Hypothetical protein.

GN Name=PY00375;

OS Plasmodium yoelii yoelii.

OC Eukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium.

OX NCBI\_TaxID=73259;

RA

RN (1)

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=17XNL;

RX MEDLINE=2235706; PubMed=1236865; DOI=10.1038/nature01099;

RA Carlton J.M., Angluoli S.V., Sun B.B., Kooij T.W., Ferreira M., Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L., Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L., Shalloom S.J., Van Aken S.B., Riedmiller S.B., Feldblyum T.V., Cho J.K., Quackenbush J., Sedegah M., Shoabhi A., Cummings L.M., Florens L., Yates J.R. III, Raine J.D., Sinden R.E., Harris M.A., Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B., Van Lin L.H., Jense C.J., Waters A.P., Smith H.O., White O.R., Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J., Carucci D.J.;

RA "Genome sequence and comparative analysis of the model rodent malaria parasite *Plasmodium yoelii yoelii*."

RL Nature 419:512-519(2002).

CC -1- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is preliminary data.

CC EMBL: AABL0100104; EMBL: EMBL5337.1; -; Genomic\_DNA.

CC DR EMBL: AABL0100104; EMBL: EMBL5337.1; -; Genomic\_DNA.

CC Hypothetical protein.

KM SEQUENCE 20 AA; 2624 MW; 69E080147DF5DB06 CRC64;

SQ

QY Query Match 22.6%; Score 26; DB 2; Length 20; Best Local Similarity 36.4%; Pred. No. 8e+03; Mismatches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 7 NIHXYLCBSV 17  
| | | | |  
6 NIPRYLFMDTI 16

Db

RESULT 45

ID OSK4V0\_BOVIN PRELIMINARY; PRT; 20 AA.

AC OSK4V0;

DT 10-MAY-2005 (TrEMBLrel. 30, Created)

DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)

DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)

DE Zinc finger Y-chromosomal protein (Fragment).

GN Name=ZFY;

OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.

OX NCBI\_TaxID=9913;

RA

RN (1)

RP NUCLEOTIDE SEQUENCE.

RA Durselen G., Werner F.A.O., Bultkamp J., Thaller G., Kraemer W., Kollers S., Brem G., Pfisterhammer J., Lips U., Borchers H., Mosner J., Fries R.;

RA "Discovery of SNPs for digital DNA signatures in cattle."

RL Submitted (Aug-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL: AF507102; CAD45343.1; -; Genomic\_DNA.

DR GO: GO:0005634; C:nucleus; IEA.

DR GO: GO:0003676; F:nucleic acid binding; IEA.

DR GO: GO:0008270; F:zinc ion binding; IEA.

DR InterPro: IPR007087; Znf\_C2H2.

DR Pfam: PF00096; Zf\_C2H2; 1.

DR Prodom: PD000003; Znf\_C2H2; 1.

DR PROSITE: PSS0157; ZINC\_FINGER\_C2H2\_2; 1.

FT NON\_TER 1 1

FT SEQUENCE 20 AA; 2320 MW; 931EC10F3FDDBE2F CRC64;

QY Query Match 22.6%; Score 26; DB 2; Length 20; Best Local Similarity 33.3%; Pred. No. 8e+03; Mismatches 3; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 4 HPTN1HXYL 12  
| | | | |  
7 HPSLKKHM 15

Db

RESULT 46

ID Q90X94\_CHICK PRELIMINARY; PRT; 20 AA.

AC Q90X94;

DT 01-DEC-2001 (TrEMBLrel. 19, Created)

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)

DE Tyrosinase (Fragment).

GN Name=TYR;

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

OX NCBI\_TaxID=9031;

RA

RN (1)

RP NUCLEOTIDE SEQUENCE.

RA Deng X., Yang Y., Liu W.;

RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL: AF416913; AAL14559.1; -; Genomic\_DNA.

DR NON\_TER 1 1

DR NON\_TER 20 20

FT SEQUENCE 20 AA; 2198 MW; 13282PB31CD17AA CRC64;

SQ

QY Query Match 22.6%; Score 26; DB 2; Length 20; Best Local Similarity 100.0%; Pred. No. 8e+03; Mismatches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 HPTN 7  
| | | | |  
17 HPTN 20

Db

## RESULT 47

Q8MM58\_9NEOP PRELIMINARY; PRT; 11 AA.

AC Q8MM58; 01-OCT-2002 (TReMBLrel. 22, Created)  
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)  
DT 01-FEB-2005 (TReMBLrel. 29, Last annotation update)  
DE Mannose phosphate isomerase (Fragment).  
GN Name=Mpi;  
OS Heliconius cydno chioneus.  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;  
OC Papilionoidea; Nymphalidae; Heliconiinae; Heliconiini; Heliconius.  
OX NCBI\_TaxID=171915;  
RN [1]

## NUCLEOTIDE SEQUENCE.

RA Bull V., Beltran M., Bermingham E., Jiggins C., McMillan O.,  
RL Mallet J.,  
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF516222; AAM61908.1; -; Genomic DNA.  
DR EMBL; AF516223; AAM61909.1; -; Genomic DNA.  
DR GO; GO:0016853; F:isomerase activity; IEA.  
KW Isomerase.  
FT NON\_TER 1 1  
SQ SEQUENCE 11 AA; 1312 MW; 56A67DB31D1EAA3 CRC64;

Query Match 21.7%; Score 25; DB 2; Length 11;  
Best Local Similarity 66.7%; Pred. No. 6.1e+03;  
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 HPTNTH 9  
|||  
Db 1 HPTKDH 6

## RESULT 48

Q8MUN4\_9NEOP PRELIMINARY; PRT; 12 AA.

AC Q8MUN4; 01-OCT-2002 (TReMBLrel. 22, Created)  
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)  
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)  
DE Mannose phosphate isomerase (Fragment).  
GN Name=Mpi;  
OS Heliconius melpomene melpomene.  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;  
OC Papilionoidea; Nymphalidae; Heliconiinae; Heliconiini; Heliconius.  
OX NCBI\_TaxID=171917;  
RN [1]

## NUCLEOTIDE SEQUENCE.

RA Bull V., Beltran M., Bermingham E., Jiggins C., McMillan O.,  
RL Mallet J.,  
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF516254; AAM61940.1; -; Genomic DNA.  
DR GO; GO:0016853; F:isomerase activity; IEA.  
KW Isomerase.  
FT NON\_TER 1 1  
SQ SEQUENCE 12 AA; 1383 MW; 56A67DE318D1EAA3 CRC64;

Query Match 21.7%; Score 25; DB 2; Length 12;  
Best Local Similarity 66.7%; Pred. No. 6.7e+03;  
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 HPTNTH 9  
|||  
Db 2 HPTKDH 7

## RESULT 49

Q8MUN9\_9NEOP PRELIMINARY; PRT; 12 AA.

AC Q8MUN9; 01-OCT-2002 (TReMBLrel. 22, Created)  
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)  
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)  
DE Mannose phosphate isomerase (Fragment).  
GN Name=Mpi;  
OS Heliconius melpomene rosinia.  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;  
OC Papilionoidea; Nymphalidae; Heliconiinae; Heliconiini; Heliconius.  
OX NCBI\_TaxID=171916;  
RN [1]

## NUCLEOTIDE SEQUENCE.

RA Bull V., Beltran M., Bermingham E., Jiggins C., McMillan O.,  
RL Mallet J.,  
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF516231; AAM61917.1; -; Genomic DNA.  
DR GO; GO:0016853; F:isomerase activity; IEA.  
KW Isomerase.  
FT NON\_TER 1 1  
SQ SEQUENCE 12 AA; 1383 MW; 56A67DE318D1EAA3 CRC64;

Query Match 21.7%; Score 25; DB 2; Length 12;  
Best Local Similarity 66.7%; Pred. No. 6.7e+03;  
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 HPTNTH 9  
|||  
Db 2 HPTKDH 7

## RESULT 50

Q8MM57\_9NEOP PRELIMINARY; PRT; 13 AA.

AC Q8MM57; 01-OCT-2002 (TReMBLrel. 22, Created)  
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)  
DT 01-FEB-2005 (TReMBLrel. 29, Last annotation update)  
DE Mannose phosphate isomerase (Fragment).  
GN Name=Mpi;  
OS Heliconius melpomene rosinia.  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;  
OC Papilionoidea; Nymphalidae; Heliconiinae; Heliconiini; Heliconius.  
OX NCBI\_TaxID=171916;  
RN [1]

## NUCLEOTIDE SEQUENCE.

RA Bull V., Beltran M., Bermingham E., Jiggins C., McMillan O.,  
RL Mallet J.,  
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF516233; AAM61919.1; -; Genomic DNA.  
DR EMBL; AF516234; AAM61920.1; -; Genomic DNA.  
DR GO; GO:0016853; F:isomerase activity; IEA.  
KW Isomerase.  
FT NON\_TER 1 1  
SQ SEQUENCE 13 AA; 1512 MW; 56A67DE35C84EAA3 CRC64;

Query Match 21.7%; Score 25; DB 2; Length 13;  
Best Local Similarity 66.7%; Pred. No. 7.3e+03;  
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 HPTNTH 9  
|||  
Db 3 HPTKDH 8

## RESULT 51

Q8MUN8\_9NEOP PRELIMINARY; PRT; 14 AA.



AC OBMUN8;  
 DT 01-OCT-2002 (TReMBLrel. 22, Created)  
 DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)  
 DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)  
 DE Mannose phosphate isomerase (Fragment).  
 GN Name=Mpi;  
 OS Heliconius melpomene rosina.  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;  
 OC Papilionoidea; Nymphalidae; Heliconiinae; Heliconiini; Heliconius.  
 OX NCBI\_TaxId=171916;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Bull V., Beltzan M., Bermingham E., Jiggins C., McMillan O.,  
 Mallet J.,  
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF516232; AAM61918.1; -; Genomic DNA.  
 DR GO; GO:0016853; P:isomerase activity; IEA.  
 KW isomerase.  
 FT NON\_TER 1 1  
 FT NON\_TER 14 14  
 SQ SEQUENCE 14 AA; 1625 MW; 56A67DE35CDECTA3 CRC64;  
 Query Match 21.7%; Score 25; DB 2; Length 14;  
 Best Local Similarity 66.7%; Pred. No. 7.9e+03;  
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 HPTNTH 9  
 DB 4 HPTKDH 9

RESULT 52  
 OBMUP2\_9NEOP PRELIMINARY; PRT; 14 AA.  
 ID OBMUP2\_9NEOP PRELIMINARY; PRT; 14 AA.  
 AC OBMUP2;  
 DT 01-OCT-2002 (TReMBLrel. 22, Created)  
 DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)  
 DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)  
 DE Mannose phosphate isomerase (Fragment).  
 GN Name=Mpi;  
 OS Heliconius cydno chioneus.  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;  
 OC Papilionoidea; Nymphalidae; Heliconiinae; Heliconiini; Heliconius.  
 OX NCBI\_TaxId=171915;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Bull V., Beltzan M., Bermingham E., Jiggins C., McMillan O.,  
 Mallet J.,  
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF516221; AAM61907.1; -; Genomic DNA.  
 DR GO; GO:0016853; P:isomerase activity; IEA.  
 KW isomerase.  
 FT NON\_TER 1 1  
 FT NON\_TER 14 14  
 SQ SEQUENCE 14 AA; 1625 MW; 56A67DE35CDECTA3 CRC64;  
 Query Match 21.7%; Score 25; DB 2; Length 14;  
 Best Local Similarity 66.7%; Pred. No. 7.9e+03;  
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 HPTNTH 9  
 DB 4 HPTKDH 9

RESULT 53  
 OQBZNO\_HUMAN PRELIMINARY; PRT; 15 AA.  
 ID OQBZNO\_HUMAN PRELIMINARY; PRT; 15 AA.  
 AC OQBZNO;  
 DT 01-JUN-2001 (TReMBLrel. 17, Created)  
 DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)

DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)  
 DE CD36 (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Homo.  
 OX NCBI\_TaxId=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=1955;  
 RA Gelhaus A., Scheding A., Browne E., Burchard G.D., Horstmann R.D.;  
 RT "CD36 mutations in West Africa."  
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF306531; AAC60630.1; -; Genomic DNA.  
 FT NON\_TER 1 1  
 FT NON\_TER 15 15  
 SQ SEQUENCE 15 AA; 1770 MW; EF2226C56D1B8E47 CRC64;  
 Query Match 21.7%; Score 25; DB 2; Length 15;  
 Best Local Similarity 50.0%; Pred. No. 8.5e+03;  
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 14 CESVNG 19  
 DB 9 CDWING 14

RESULT 54  
 OBMUP2\_9NEOP PRELIMINARY; PRT; 15 AA.  
 ID OBMUP2\_9NEOP PRELIMINARY; PRT; 15 AA.  
 AC OBMUP2;  
 DT 01-OCT-2002 (TReMBLrel. 22, Created)  
 DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)  
 DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)  
 DE Mannose phosphate isomerase (Fragment).  
 GN Name=Mpi;  
 OS Heliconius cydno chioneus.  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;  
 OC Papilionoidea; Nymphalidae; Heliconiinae; Heliconiini; Heliconius.  
 OX NCBI\_TaxId=171915;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Bull V., Beltzan M., Bermingham E., Jiggins C., McMillan O.,  
 Mallet J.,  
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF516211; AAM61897.1; -; Genomic DNA.  
 DR GO; GO:0016853; P:isomerase activity; IEA.  
 KW isomerase.  
 FT NON\_TER 1 1  
 FT NON\_TER 15 15  
 SQ SEQUENCE 15 AA; 1712 MW; 56A67DE35CDEB17C CRC64;  
 Query Match 21.7%; Score 25; DB 2; Length 15;  
 Best Local Similarity 66.7%; Pred. No. 8.5e+03;  
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 HPTNTH 9  
 DB 5 HPTKDH 10

RESULT 55  
 OBMW83\_9NEOP PRELIMINARY; PRT; 16 AA.  
 ID OBMW83\_9NEOP PRELIMINARY; PRT; 16 AA.  
 AC OBMW83;  
 DT 01-OCT-2002 (TReMBLrel. 22, Created)  
 DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)  
 DT 01-FEB-2005 (TReMBLrel. 29, Last annotation update)  
 DE Mannose phosphate isomerase (Fragment).  
 GN Name=Mpi;  
 OS Heliconius melpomene rosina.  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;  
 OC Papilionoidea; Nymphalidae; Heliconiinae; Heliconiini; Heliconius.  
 OX NCBI\_TaxID=171916;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Bull V., Beltran M., Bermingham E., Jiggins C., McMillan O.,  
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF516224; AAM61910.1; -; Genomic DNA.  
 DR EMBL; AF516225; AAM61911.1; -; Genomic DNA.  
 DR EMBL; AF516226; AAM61912.1; -; Genomic DNA.  
 DR EMBL; AF516227; AAM61913.1; -; Genomic DNA.  
 DR EMBL; AF516228; AAM61914.1; -; Genomic DNA.  
 DR EMBL; AF516229; AAM61915.1; -; Genomic DNA.  
 DR EMBL; AF516230; AAM61916.1; -; Genomic DNA.  
 DR EMBL; AF516231; AAM61921.1; -; Genomic DNA.  
 DR EMBL; AF516236; AAM61922.1; -; Genomic DNA.  
 DR EMBL; AF516238; AAM61924.1; -; Genomic DNA.  
 DR EMBL; AF516239; AAM61925.1; -; Genomic DNA.  
 DR GO; GO:0016853; F:isomerase activity; IEA.  
 KW Isomerase.  
 FT NON\_TER 1 1  
 FT SEQUENCE 16 AA; 1825 MW; 1CE67DB35CDB8122 CRC64;  
 SQ  
 Query Match 21.7%; Score 25; DB 2; Length 16;  
 Best Local Similarity 66.7%; Pred. No. 9.1e+03;  
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 HPTNTH 9  
 ||||  
 Db 6 HPTKDH 11

RESULT 56  
 QBMM84\_9NEOP PRELIMINARY; PRT; 16 AA.  
 ID QBMM84\_9NEOP PRELIMINARY;  
 AC QBMM84;  
 DT 01-OCT-2002 (TReMBLrel. 22, Created)  
 DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)  
 DT 01-FEB-2003 (TReMBLrel. 29, Last annotation update)  
 DE Mammose phosphate isomerase (Fragment).  
 GN Name=Mpi;  
 OS Heliconius melipomene melipomene.  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;  
 OC Papilionoidea; Nymphalidae; Heliconiinae; Heliconiini; Heliconius.  
 OX NCBI\_TaxID=171917;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Bull V., Beltran M., Bermingham E., Jiggins C., McMillan O.,  
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF516240; AAM61926.1; -; Genomic DNA.  
 DR EMBL; AF516241; AAM61927.1; -; Genomic DNA.  
 DR EMBL; AF516242; AAM61928.1; -; Genomic DNA.  
 DR EMBL; AF516243; AAM61929.1; -; Genomic DNA.  
 DR EMBL; AF516244; AAM61930.1; -; Genomic DNA.  
 DR EMBL; AF516245; AAM61931.1; -; Genomic DNA.  
 DR EMBL; AF516246; AAM61932.1; -; Genomic DNA.  
 DR EMBL; AF516248; AAM61934.1; -; Genomic DNA.  
 DR EMBL; AF516249; AAM61935.1; -; Genomic DNA.  
 DR EMBL; AF516251; AAM61937.1; -; Genomic DNA.  
 DR EMBL; AF516253; AAM61939.1; -; Genomic DNA.  
 DR GO; GO:0016853; F:isomerase activity; IEA.  
 KW Isomerase.  
 FT NON\_TER 1 1  
 FT SEQUENCE 16 AA; 1825 MW; 1CE67DB35CDB8122 CRC64;  
 SQ  
 Query Match 21.7%; Score 25; DB 2; Length 16;  
 Best Local Similarity 66.7%; Pred. No. 9.1e+03;  
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 HPTNTH 9  
 ||||  
 Db 6 HPTKDH 11

RESULT 57  
 QBMM85\_9NEOP PRELIMINARY; PRT; 16 AA.  
 ID QBMM85\_9NEOP PRELIMINARY;  
 AC QBMM85;  
 DT 01-OCT-2002 (TReMBLrel. 22, Created)  
 DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)  
 DT 01-FEB-2003 (TReMBLrel. 29, Last annotation update)  
 DE Mammose phosphate isomerase (Fragment).  
 GN Name=Mpi;  
 OS Heliconius cytho chioneus.  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;  
 OC Papilionoidea; Nymphalidae; Heliconiinae; Heliconiini; Heliconius.  
 OX NCBI\_TaxID=171915;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Bull V., Beltran M., Bermingham E., Jiggins C., McMillan O.,  
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF516210; AAM61896.1; -; Genomic DNA.  
 DR EMBL; AF516212; AAM61898.1; -; Genomic DNA.  
 DR EMBL; AF516214; AAM61900.1; -; Genomic DNA.  
 DR EMBL; AF516215; AAM61901.1; -; Genomic DNA.  
 DR EMBL; AF516216; AAM61902.1; -; Genomic DNA.  
 DR EMBL; AF516217; AAM61903.1; -; Genomic DNA.  
 DR EMBL; AF516218; AAM61904.1; -; Genomic DNA.  
 DR EMBL; AF516219; AAM61905.1; -; Genomic DNA.  
 DR EMBL; AF516220; AAM61906.1; -; Genomic DNA.  
 DR GO; GO:0016853; F:isomerase activity; IEA.  
 KW Isomerase.  
 FT NON\_TER 1 1  
 FT SEQUENCE 16 AA; 1825 MW; 1CE67DB35CDB8122 CRC64;  
 SQ  
 Query Match 21.7%; Score 25; DB 2; Length 16;  
 Best Local Similarity 66.7%; Pred. No. 9.1e+03;  
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 HPTNTH 9  
 ||||  
 Db 6 HPTKDH 11

RESULT 58  
 QBMM83\_9NEOP PRELIMINARY; PRT; 16 AA.  
 ID QBMM83\_9NEOP PRELIMINARY;  
 AC QBMM83;  
 DT 01-OCT-2002 (TReMBLrel. 22, Created)  
 DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)  
 DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)  
 DE Mammose phosphate isomerase (Fragment).  
 GN Name=Mpi;  
 OS Heliconius numata.  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;  
 OC Papilionoidea; Nymphalidae; Heliconiinae; Heliconiini; Heliconius.  
 OX NCBI\_TaxID=33419;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Bull V., Beltran M., Bermingham E., Jiggins C., McMillan O.,  
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF516255; AAM61941.1; -; Genomic DNA.  
 DR GO; GO:0016853; F:isomerase activity; IEA.  
 KW Isomerase.  
 FT NON\_TER 1 1  
 FT SEQUENCE 16 AA; 1825 MW; 1CE67DB35CDB8122 CRC64;  
 SQ  
 Query Match 21.7%; Score 25; DB 2; Length 16;  
 Best Local Similarity 66.7%; Pred. No. 9.1e+03;  
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

SEQUENCE 16 AA; 1825 MW; 1CE67DE35CDE8122 CRC64;

Query Match 21.7%; Score 25; DB 2; Length 16;

Best Local Similarity 66.7%; Pred. No. 9.1e+03;

Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 HPTNTH 9  
| | | |  
Db 6 HPTKDH 11

#### RESULT 59

OBMUN5\_9NEOP

ID OBMUN5\_9NEOP PRELIMINARY; PRT; 16 AA.

AC OBMUN5\_9NEOP PRELIMINARY; PRT; 16 AA.

DT 01-OCT-2002 (TREMBlrel. 22, Created)

DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)

DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)

DE Mammose phosphate isomerase (Fragment).

NCBI\_TaxId=171917;

OS Heliconius melpomene melpomene.

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;

OC Papilionoidea; Nymphalidae; Heliconiinae; Heliconiini; Heliconus.

NCBI\_TaxId=171917;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RA Bull V., Beltrán M., Bermingham E., Jiggins C., McMillan O.,

RA Mallet J.,

RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF516252; AAM61938.1; -; Genomic DNA.

DR GO; GO:0016853; P:isomerase activity; TEA.

KM isomerase.

FT NON\_TER 1 16

FT NON\_TER 16 16

SQ SEQUENCE 16 AA; 1811 MW; 1CE67DE35C62222 CRC64;

Query Match 21.7%; Score 25; DB 2; Length 16;

Best Local Similarity 66.7%; Pred. No. 9.1e+03;

Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 HPTNTH 9  
| | | |  
Db 6 HPTKDH 11

#### RESULT 60

O5G554\_BALMU

ID O5G554\_BALMU PRELIMINARY; PRT; 16 AA.

AC O5G554\_BALMU PRELIMINARY; PRT; 16 AA.

DT 10-MAY-2005 (TREMBlrel. 30, Created)

DT 10-MAY-2005 (TREMBlrel. 30, Last sequence update)

DT 10-MAY-2005 (TREMBlrel. 30, Last annotation update)

DE DNA polymerase beta (Fragment).

GN Name=POLB;

OS Balenoptera musculus (Blue whale).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Cetacea;

OC Mysticeti; Balenopteridae; Balenoptera.

NCBI\_TaxId=9771;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RA Conway C.A., May B.P.,

RT "Global Population Structure of Blue Whales Balenoptera musculus ssp

Based on Nuclear Genetic Variation."

RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.

DR EMBL; AY651160; AAM65802.1; -; Genomic DNA.

FT NON\_TER 1 16

FT NON\_TER 16 16

SQ SEQUENCE 16 AA; 1732 MW; 06B7C60F1ACB84B0 CRC64;

Query Match 21.7%; Score 25; DB 2; Length 16;

Best Local Similarity 66.7%; Pred. No. 9.1e+03;

Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 15 ESYVNG 20  
| | | | |  
Db 3 ETLNGG 8

#### RESULT 61

O9TW4\_DICDI

ID O9TW4\_DICDI PRELIMINARY; PRT; 17 AA.

AC O9TW4\_DICDI PRELIMINARY; PRT; 17 AA.

DT 01-MAY-2000 (TREMBlrel. 13, Created)

DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)

DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)

DE V-ATPase 110 kDa subunit (Fragment).

OS Dictyostelium discoideum (Slime mold).

OC Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.

NCBI\_TaxId=44689;

RN [1]

RP PROTEIN SEQUENCE.

RX MEDLINE=96019266; PubMed=7593293;

RA Adesai C., Chapel A., Vincon M., Rabilloud T., Klein G., Satre M.,

RA Garin J.,

RT "Identification of major proteins associated with Dictyostelium

discoideum endocytic vesicles."

RL J. Cell Sci. 108:3331-3337(1995).

SQ SEQUENCE 17 AA; 2075 MW; 89F1B1A959D61BB CRC64;

Query Match 21.7%; Score 25; DB 2; Length 17;

Best Local Similarity 42.9%; Pred. No. 9.7e+03;

Matches 6; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 2 IHPHTNTHKYVCE 15  
| | | | |  
Db 3 IYHTXNLFOYDVG 16

#### RESULT 62

PHY12\_PHYHY

ID PHY12\_PHYHY STANDARD; PRT; 18 AA.

AC P84567;

DT 13-SEP-2005 (Rel. 48, Created)

DT 13-SEP-2005 (Rel. 48, Last sequence update)

DT 13-SEP-2005 (Rel. 48, Last annotation update)

DE Phyllosepitin-2 (PS-2).

OS Phyllomedusa hypochondrialis (Orange-legged leaf frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hyliidae;

OC Phyllomedusinae; Phyllomedusa.

NCBI\_TaxId=317381;

RN [1]

RP PROTEIN SEQUENCE, FUNCTION, SUBCELLULAR LOCATION, TISSUE SPECIFICITY,

RP MASS SPECTROMETRY, AND AMIDATION.

RC TISSUE-Skin secretion.

RX PubMed=15752569; DOI=10.1016/j.peptides.2004.11.002;

RA Leite J.R.S.A., Silva L.P., Rodrigues M.T.S., Prates M.V., Brand G.D.,

RA Lacava B.M., Azevedo R.B., Bocca A.L., Albuquerque S., Bloch C. Jr.,

RT "Phyllosepitins: a novel class of anti-bacterial and anti-protozoan

peptides from the Phyllomedusa genus."

RL Peptides 26:565-573(2005).

-1- FUNCTION: Has antimicrobial activity. No hemolytic activity.

-1- SUBCELLULAR LOCATION: Secreted.

-1- TISSUE SPECIFICITY: Expressed by the skin glands.

-1- MASS SPECTROMETRY: MW=2115.26; METHOD=MALDI; RANGE=1-18;

NOTE=Ref.1.

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CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use as long as its content is in no way modified and this statement is not  
CC removed.

-----  
CC Amidation; Amphibian defense peptide; Antimicrobial;

```

KW Direct protein sequencing.
FT MOD_RES 18 18 Phenylalanine amide.
SQ SEQUENCE 18 AA; 2003 MW; 0B100A4F91CF9C9 CRC64;

Query Match
Best Local Similarity 21.7%; Score 25; DB 1; Length 18;
Pred. No. 1e+04;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 IPHPTNHHKIV 13
DB 4 IPHAINAVSTLV 15

RESULT 63
Q6VYB3_9NEOP
ID Q6VYB3_9NEOP PRELIMINARY; PRT; 18 AA.
AC Q6VYB3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Mannose phosphate isomerase (Fragment).
GN Name=Mpi;
OS Heliconius erato notabilis.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Dictyota;
OC Papilionoidea; Nymphalidae; Heliconiinae; Heliconiini; Heliconius.
OX NCBI_TaxID=246613;
[1]
RN NUCLEOTIDE SEQUENCE.
RX PubMed=15210977; DOI=10.1073/pnas.0306243101;
RA Planagan N.S., Tobler A., Davison A., Pybus O.G., Kapan D.D.,
RA Planas S., Linares M., Heckel D., McMillan W.O.;
RT "Historical demography of Mullerian mimicry in the neotropical
RT Heliconius butterflies."
RL Proc. Natl. Acad. Sci. U.S.A. 101:9704-9709(2004).
DR EMBL; AY319914; AA084670.1; -; Genomic DNA.
DK GO; GO:0016853; F:isomerase activity; IEA.
KW Isomerase.
FT NON_TER 1 1
FT NON_TER 18 18
SQ SEQUENCE 18 AA; 2039 MW; AA942CE67DE35CDB CRC64;

Query Match
Best Local Similarity 21.7%; Score 25; DB 2; Length 18;
Pred. No. 1e+04;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 HPTNTH 9
DB 6 HPTKNH 11

RESULT 64
Q6VYD9_9NEOP
ID Q6VYD9_9NEOP PRELIMINARY; PRT; 18 AA.
AC Q6VYD9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Mannose phosphate isomerase (Fragment).
GN Name=Mpi;
OS Heliconius erato notabilis.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Dictyota;
OC Papilionoidea; Nymphalidae; Heliconiinae; Heliconiini; Heliconius.
OX NCBI_TaxID=64530;
[1]
RN NUCLEOTIDE SEQUENCE.
RX PubMed=15210977; DOI=10.1073/pnas.0306243101;
RA Planagan N.S., Tobler A., Davison A., Pybus O.G., Kapan D.D.,
RA Planas S., Linares M., Heckel D., McMillan W.O.;
RT "Historical demography of Mullerian mimicry in the neotropical
RT Heliconius butterflies."
RL Proc. Natl. Acad. Sci. U.S.A. 101:9704-9709(2004).
DR EMBL; AY319914; AA084670.1; -; Genomic DNA.
DK GO; GO:0016853; F:isomerase activity; IEA.
KW Isomerase.
FT NON_TER 1 1
FT NON_TER 18 18
SQ SEQUENCE 18 AA; 2039 MW; AA942CE67DE35CDB CRC64;

Query Match
Best Local Similarity 21.7%; Score 25; DB 2; Length 18;
Pred. No. 1e+04;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 HPTNTH 9
DB 6 HPTKNH 11

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DR EMBL; AY319888; AA084644.1; -; Genomic DNA.
DR GO; GO:0016853; F:isomerase activity; IEA.
KW Isomerase.
FT NON_TER 1 1
FT NON_TER 18 18
SQ SEQUENCE 18 AA; 2088 MW; 2DEA7147E11DD6A6 CRC64;

Query Match
Best Local Similarity 21.7%; Score 25; DB 2; Length 18;
Pred. No. 1e+04;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 HPTNTH 9
DB 2 HPTKNH 7

RESULT 65
Q6VYB7_9NEOP
ID Q6VYB7_9NEOP PRELIMINARY; PRT; 18 AA.
AC Q6VYB7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Mannose phosphate isomerase (Fragment).
GN Name=Mpi;
OS Heliconius erato hydara.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Dictyota;
OC Papilionoidea; Nymphalidae; Heliconiinae; Heliconiini; Heliconius.
OX NCBI_TaxID=64529;
[1]
RN NUCLEOTIDE SEQUENCE.
RX PubMed=15210977; DOI=10.1073/pnas.0306243101;
RA Planagan N.S., Tobler A., Davison A., Pybus O.G., Kapan D.D.,
RA Planas S., Linares M., Heckel D., McMillan W.O.;
RT "Historical demography of Mullerian mimicry in the neotropical
RT Heliconius butterflies."
RL Proc. Natl. Acad. Sci. U.S.A. 101:9704-9709(2004).
DR EMBL; AY319880; AA084636.1; -; Genomic DNA.
DK GO; GO:0016853; F:isomerase activity; IEA.
KW Isomerase.
FT NON_TER 1 1
FT NON_TER 18 18
SQ SEQUENCE 18 AA; 2088 MW; 2DEA7147E11DD6A6 CRC64;

Query Match
Best Local Similarity 21.7%; Score 25; DB 2; Length 18;
Pred. No. 1e+04;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 HPTNTH 9
DB 2 HPTKNH 7

RESULT 66
Q4YEL0_PLABE
ID Q4YEL0_PLABE PRELIMINARY; PRT; 18 AA.
AC Q4YEL0;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=PB405193.00.0;
OS Plasmodium berghei.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5821;
[1]
RN NUCLEOTIDE SEQUENCE.
RX PubMed=15210977; DOI=10.1073/pnas.0306243101;
RA Hall N., Karras M., Raine J.D., Carlson J.M., Koof T.W.A.,
RA Berriman M., Florens L., Janseen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
RA Quail M.A., Omond D., Doggett J., Trueman H.E., Mendoza J.,
RA Bidwell S.L., Rajandream M.A., Carnuci D.J., Yates J.R., Kafatos F.C.,

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RA Janse C.J., Barrrell B., Turner C.M.R., Waters A.P., Sindén R.S.;  
 RT "A comprehensive survey of the Plasmodium life cycle by genomic,  
 RL transcriptomic, and proteomic analyses."  
 Science 307:82-86(2005).  
 CC -1- CAUTION: The sequence shown here is derived from an  
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
 CC preliminary data.  
 DR EMBL, CA01005914; CA103559.1; -; Genomic\_DNA.  
 KM Hypothetical protein.  
 SQ SEQUENCE 18 AA; 2133 MW; 29C0F93F153D0E3D CRC64;

Query Match 21.7%; Score 25; DB 2; Length 18;  
 Best Local Similarity 60.0%; Pred. No. 1e+04;  
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 9 HKTLV 13  
 DB 9 HKYII 13

RESULT 67  
 ID Q28069\_BOVIN PRELIMINARY; PRT; 18 AA.  
 AC Q28069;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-JUN-1999 (TrEMBLrel. 09, Last sequence update)  
 DT 01-JUN-1999 (TrEMBLrel. 09, Last annotation update)  
 DE Alpha-s1-casein (Fragment).  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;  
 OC Pecora; Bovidae; Bovinae; Bos.  
 OK NCBI\_TaxID=9913;  
 RN (1)  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Mammary gland;  
 RA Maki M., Nagao M., Hirose M., Chiba H.;  
 RT "Cloning of cDNA sequence coding for bovine alpha-s1-casein."  
 RL Agric. Biol. Chem. 47:441-444(1983).  
 DR EMBL, D00412; BAA00313.1; -; mRNA.  
 FT NON\_TER 1 18  
 FT NON\_TER 1 18  
 SQ SEQUENCE 18 AA; 1880 MW; 8DEDCL740674108C CRC64;

Query Match 21.7%; Score 25; DB 2; Length 18;  
 Best Local Similarity 80.0%; Pred. No. 1e+04;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIPHP 5  
 DB 12 DIPNP 16

RESULT 68  
 ID Q6VYD8\_9NEOP PRELIMINARY; PRT; 19 AA.  
 AC Q6VYD8;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Mannose phosphate isomerase (Fragment).  
 GN Name=Mpi;  
 OS Heliconius erato emma.  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Dictyssa;  
 OC Papilionoidea; Nymphalidae; Heliconiinae; Heliconiini; Heliconius.  
 OK NCBI\_TaxID=246809;  
 RN (1)  
 RP NUCLEOTIDE SEQUENCE.  
 RC PubMed=15210977; DOI=10.1073/pnas.0306243101;  
 RA Flanagan N.S., Tobler A., Davison A., Pybus O.G., Kapan D.D.,  
 RA Planas S., Liner M., Heckel D., McMillan W.O.;  
 RT "Historical demography of Mullerian mimicry in the neotropical

RT Heliconius butterflies."  
 RL Proc. Natl. Acad. Sci. U.S.A. 101:9704-9709(2004).  
 DR EMBL, AY19889; AA084645.1; -; Genomic\_DNA.  
 DR GO, GO:0016853; F:isomerase activity; IEA.  
 KM Isomerase.  
 FT NON\_TER 1 19  
 FT NON\_TER 19 19  
 SQ SEQUENCE 19 AA; 2186 MW; CE24942CE67DE35C CRC64;

Query Match 21.7%; Score 25; DB 2; Length 19;  
 Best Local Similarity 66.7%; Pred. No. 1.1e+04;  
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 HPTNIH 9  
 DB 6 HPTKNH 11

RESULT 69  
 ID Q6VYB1\_9NEOP PRELIMINARY; PRT; 19 AA.  
 AC Q6VYB1;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Mannose phosphate isomerase (Fragment).  
 GN Name=Mpi;  
 OS Heliconius erato hydra.  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Dictyssa;  
 OC Papilionoidea; Nymphalidae; Heliconiinae; Heliconiini; Heliconius.  
 OK NCBI\_TaxID=64529;  
 RN (1)  
 RP NUCLEOTIDE SEQUENCE.  
 RC PubMed=15210977; DOI=10.1073/pnas.0306243101;  
 RA Flanagan N.S., Tobler A., Davison A., Pybus O.G., Kapan D.D.,  
 RA Planas S., Liner M., Heckel D., McMillan W.O.;  
 RT "Historical demography of Mullerian mimicry in the neotropical  
 RT Heliconius butterflies."  
 RL Proc. Natl. Acad. Sci. U.S.A. 101:9704-9709(2004).  
 DR EMBL, AY19886; AA084642.1; -; Genomic\_DNA.  
 DR GO, GO:0016853; F:isomerase activity; IEA.  
 KM Isomerase.  
 FT NON\_TER 1 19  
 FT NON\_TER 19 19  
 SQ SEQUENCE 19 AA; 2216 MW; 2DEA1BF7911DD6A6 CRC64;

Query Match 21.7%; Score 25; DB 2; Length 19;  
 Best Local Similarity 66.7%; Pred. No. 1.1e+04;  
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 HPTNIH 9  
 DB 3 HPTKNH 8

RESULT 70  
 ID Q7RG13\_PLAYO PRELIMINARY; PRT; 19 AA.  
 AC Q7RG13;  
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Hypothetical protein (Fragment).  
 GN Name=PY04538;  
 OS Plasmodium yoelii yoelii.  
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
 OK NCBI\_TaxID=73239;  
 RN (1)  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=17XNL;  
 RC MEDLINE=2255706; PubMed=12368865; DOI=10.1038/nature01099;  
 RA Carlton J.M., Anguolli S.V., Suh B.B., Koof T.W., Petrea M.,

RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,  
 RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,  
 RA Shallow S.J., Van Aken S.E., Riedmiller S.B., Feldblyum T.V.,  
 RA Cho J.K., Quackenbush J., Sedegah M., Shostak A., Cummings L.M.,  
 RA Florens L., Yates J.R., III, Raine J.D., Sinden R.E., Harris M.A.,  
 RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,  
 RA van Lin L.H., Jance C.J., Waters A.P., Smith H.O., White O.R.,  
 RA Salzberg S.L., Venter J.C., Frazer C.M., Hoffman S.L., Gardner M.J.,  
 RA Carucci D.J.;  
 RT "Genome sequence and comparative analysis of the model rodent malaria  
 parasite Plasmodium yoelii yoelii.";  
 RL Nature 419:512-519(2002).  
 CC -1- CAUTION: The sequence shown here is derived from an  
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
 CC preliminary data.  
 DR EMBL: AABL01001387; EAA15415.1; -; Genomic\_DNA.  
 KM Hypothetical protein.  
 FT NON\_TER 1  
 SQ SEQUENCE 19 AA; 2346 MW; 5FAD63FC40D6B696 CRC64;  
 PT

Query Match 21.7%; Score 25; DB 2; Length 19;  
 Best Local Similarity 33.3%; Pred. No. 1.1e+04;  
 Matches 4; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 7 NIKHYLVCSVN 18  
 Db 6 NFINILICNYIN 17

RESULT 71  
 ID Q7YK42\_9FABA PRELIMINARY; PRT; 19 AA.  
 AC Q7YK42;  
 DT 01-OCT-2003 (T-EMBLrel. 25, Created)  
 DT 01-OCT-2003 (T-EMBLrel. 25, Last sequence update)  
 DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)  
 DE Paba (Fragment).  
 DE GN Name=paba;  
 OS Desmanthus bicornutus.  
 OS Chloropiast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eurosids I; Fabales; Fabaceae; Mimosoideae; Mimoseae; Desmanthus.  
 OC NCBI\_TaxID=196645;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Miller J.T., Grimes J.W., Murphy D.J., Bayer R.J., Ladiges P.Y.;  
 RT "A Phylogenetic Analysis of the Acaciace and Ingeae (Mimosoideae;  
 RT Fabaceae) based on trnK, matK, psbA-trnH, and trnL/trnF Sequence  
 RT Data.";  
 RL Syst. Bot. 28:558-566(2003).  
 DR EMBL: AF524960; AAP80478.1; -; Genomic\_DNA.  
 DR GO: 0009507; Chloropiast; IEA.  
 KW Chloropiast.  
 FT NON\_TER 1  
 SQ SEQUENCE 19 AA; 1364 MW; 4441E0C10D549D84 CRC64;  
 PT

Query Match 21.7%; Score 25; DB 2; Length 19;  
 Best Local Similarity 31.6%; Pred. No. 1.1e+04;  
 Matches 6; Conservative 3; Mismatches 4; Indels 6; Gaps 1;

QY 7 NIKHY-----LVCSVNG 19  
 Db 1 NAKKPLDLAAVAPSPING 19

RESULT 72  
 ID Q8CJ05\_MESAU PRELIMINARY; PRT; 19 AA.  
 AC Q8CJ05;  
 DT 01-MAR-2003 (T-EMBLrel. 23, Created)  
 DT 01-MAR-2003 (T-EMBLrel. 23, Last sequence update)  
 DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)

DR Cyclicin D1 (Fragment).  
 OS Mesocricetus auratus (Golden hamster).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Cricetinae; Mesocricetus.  
 OC NCBI\_TaxID=10036;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=22565058; PubMed=12569092; DOI=10.1074/jbc.M300412200;  
 RA Hilton T.L., Wang E.H.;  
 RT "Transcription factor IID recruitment and Sp1 activation. Dual  
 RT function of TAF1 in cyclin D1 transcription.";  
 RL J. Biol. Chem. 278:12992-13002(2003).  
 DR EMBL: AF539477; AAN59789.1; -; Genomic\_DNA.  
 FT NON\_TER 19  
 SQ SEQUENCE 19 AA; 2307 MW; 83E3341F29C52279 CRC64;  
 PT

Query Match 21.7%; Score 25; DB 2; Length 19;  
 Best Local Similarity 57.1%; Pred. No. 1.1e+04;  
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 HKYLVCE 15  
 Db 3 HQLLCCE 9

RESULT 73  
 ID Q7LZW5\_HHV1 PRELIMINARY; PRT; 19 AA.  
 AC Q7LZW5;  
 DT 01-MAR-2004 (T-EMBLrel. 26, Created)  
 DT 01-MAR-2004 (T-EMBLrel. 26, Last sequence update)  
 DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)  
 DE Capsid protein VP26 (Fragment).  
 OS Human herpesvirus 1 (HHV-1) (Human herpes simplex virus 1).  
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;  
 OC Alphaherpesvirinae; Simplexvirus.  
 OC NCBI\_TaxID=10298;  
 RN [1]  
 RP PROTEIN SEQUENCE.  
 RA Davison M.D., Rixon F.J., Davison A.J.;  
 RT "Identification of genes encoding two capsid proteins (VP24 and VP26)  
 RT of herpes simplex virus type 1.";  
 RL J. Gen. Virol. 73:2709-2713(1992).  
 RN [2]  
 RP PROTEIN SEQUENCE.  
 RX PubMed=1328483;  
 RA Davison M.D., Rixon F.J., Davison A.J.;  
 RT "Identification of genes encoding two capsid proteins (VP24 and VP26)  
 RT of herpes simplex virus type 1.";  
 RL J. Gen. Virol. 73 ( Pt 10):2709-2713(1992).  
 DR PIR: P00548; P00548.  
 FT NON\_TER 1  
 FT NON\_TER 19  
 SQ SEQUENCE 19 AA; 2060 MW; BBE855419135AC5A CRC64;  
 PT

Query Match 21.7%; Score 25; DB 2; Length 19;  
 Best Local Similarity 80.0%; Pred. No. 1.1e+04;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DIPHP 5  
 Db 11 DNPHP 15

RESULT 74  
 ID APY3\_PLECI STANDARD; PRT; 20 AA.  
 AC P83477;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 13-SEP-2005 (Rel. 48, Last annotation update)  
 DR Antiviral protein y3 (Fragment).

OS Pleurotus citrinopileatus (Golden oyster mushroom).  
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;  
OC Agaricales; Pleurotaceae; Pleurotus.  
OX NCBI\_TaxID=98342;  
RN [1]  
RP PROTEIN SEQUENCE.  
RA Wu L.-P., Wu Z.-J., Lin Q.-Y., Xie L.-H.;  
RL Submitted (OCT-2002) to Swiss-Prot.  
CC -1- FUNCTION: Unknown.  
CC -1- MISCELLANEOUS: Has antiviral activity against Tobacco mosaic virus  
and antitumor activity against stomach cancer cells in vitro.  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use as long as its content is in no way modified and this statement is not  
CC removed.  
CC Antiviral protein; Direct protein sequencing.  
KM Antiviral protein; Direct protein sequencing.  
FT NON\_TER 1 1  
FT NON\_TER 20 20  
SQ SEQUENCE 20 AA; 2237 MW; 3D2B0A20A8BB1172 CRC64;  
Query Match 21.7%; Score 25; DB 1; Length 20;  
Best Local Similarity 57.1%; Pred. No. 1.2e+04;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 11 YLVGESV 17  
DB 14 YVACEAV 20  
RESULT 75  
APR3\_PLECI STANDARD; PRT; 20 AA.  
ID APR3\_PLECI  
AC P83481;  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 13-SEP-2003 (Rel. 48, Last annotation update)  
DE Antiviral protein Yp3 (Fragment).  
OS Pleurotus citrinopileatus (Golden oyster mushroom).  
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;  
OC Agaricales; Pleurotaceae; Pleurotus.  
OX NCBI\_TaxID=98342;  
RN [1]  
RP PROTEIN SEQUENCE.  
RA Wu L.-P., Wu Z.-J., Lin Q.-Y., Xie L.-H.;  
RL Submitted (OCT-2002) to Swiss-Prot.  
CC -1- FUNCTION: Unknown.  
CC -1- MISCELLANEOUS: Has antiviral activity against Tobacco mosaic virus  
and antitumor activity against stomach cancer cells in vitro.  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use as long as its content is in no way modified and this statement is not  
CC removed.  
CC Antiviral protein; Direct protein sequencing.  
KM Antiviral protein; Direct protein sequencing.  
FT NON\_TER 1 1  
FT NON\_TER 20 20  
SQ SEQUENCE 20 AA; 2237 MW; 3D2B0A20A8BB1172 CRC64;  
Query Match 21.7%; Score 25; DB 1; Length 20;  
Best Local Similarity 57.1%; Pred. No. 1.2e+04;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 11 YLVGESV 17  
DB 14 YVACEAV 20  
RESULT 76

064619 RAT  
ID O64619\_RAT PRELIMINARY; PRT; 20 AA.  
AC O64619;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Polymerase-beta (BC 2.7.7.7) (Fragment).  
GN Namepold;  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Brain;  
RA MEDLINE=87257910; PubMed=3600656;  
RX Ymaguchi M., Hirose F., Hayashi Y., Nishimoto Y., Matsukage A.;  
RT "Murine DNA polymerase beta gene: mapping of transcription initiation  
RT sites and the nucleotide sequence of the putative promoter region.";  
RL Mol. Cell. Biol. 7:2012-2018(1987).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Brain;  
RA MEDLINE=88294046; PubMed=3042024;  
RX Date T., Yamaguchi M., Hirose F., Nishimoto Y., Tanihara K.,  
RA Matsukage A.;  
RT "Expression of active rat DNA polymerase beta in Escherichia coli.";  
RL Biochemistry 27:2983-2990(1988).  
DR EMBL: M19679; AAA41902.1; -; Genomic\_DNA.  
DR HSSP: P06766; IBNO.  
DR GO: GO:0003887; F:DNA-directed DNA polymerase activity; IEA.  
DR GO: GO:0016740; F:transferase activity; IEA.  
KW Nucleotidyltransferase; Transferase.  
FT NON\_TER 1 1  
SQ SEQUENCE 20 AA; 2190 MW; B7D8F9A3C5801825 CRC64;  
Query Match 21.7%; Score 25; DB 2; Length 20;  
Best Local Similarity 66.7%; Pred. No. 1.2e+04;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 15 ESYNGG 20  
DB 9 ETLNGG 14  
RESULT 77  
O9PRY1 TORCA  
ID O9PRY1 TORCA PRELIMINARY; PRT; 20 AA.  
AC O9PRY1;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE AGRIN receptor 190 kDa SUBUNIT-ALPHA-dystroglycan homolog  
(Fragment).  
OS Torpedo californica (Pacific electric ray).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;  
OC Elasmobranchii; Squalia; Hypnosqualea; Pristigaster; Batoidae;  
OC Torpediniformes; Torpedinidae; Torpedinidae; Torpedo.  
OX NCBI\_TaxID=7787;  
RN [1]  
RP PROTEIN SEQUENCE.  
RA MEDLINE=94242436; PubMed=8185951; DOI=10.1016/0896-6273(94)90324-7;  
RX Bove M.A., Deyat K.A., Leszyk J.D., Fallon J.R.;  
RT "Identification and purification of an agrin receptor from Torpedo  
RT postmyotonic membranes: a heteromeric complex related to the  
RT dystroglycans.";  
RL Neuron 12:1173-1180(1994).  
FT NON\_TER 1 1  
FT NON\_TER 20 20  
SQ SEQUENCE 20 AA; 2239 MW; 038622F02D189F90 CRC64;  
Query Match 21.7%; Score 25; DB 2; Length 20;

Best Local Similarity 33.3%; Pred. No. 1.2e+04;  
Matches 4; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 9 HKYLVCSYNGG 20  
DB 1 HEYFMHAXKGG 12

## RESULT 78

Q9R4Z4\_PROMI PRELIMINARY; PRT; 20 AA.  
AC Q9R4Z4;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE AMBIENT-temperature FIMBRIA; ATP (Fragment).  
OS Proteus mirabilis.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Proteus.  
OX NCBI\_TaxID=584;  
RN [1]  
RP PROTEIN SEQUENCE.  
RX MEDLINE=9422573; PubMed=7909538;  
RA Massad G., Bahran F.K., Mobley H.L.;  
RT "Proteus mirabilis fimbriae: identification, isolation, and  
characterization of a new ambient-temperature fimbria.",  
RL Infect. Immun. 62:1989-1994(1994).  
FT NON\_TER 1 1  
SQ SEQUENCE 20 AA; 2017 MW; B2FC481003883AE2 CRC64;

Query Match 21.3%; Score 24.5; DB 2; Length 20;  
Best Local Similarity 33.3%; Pred. No. 1.4e+04;  
Matches 6; Conservative 3; Mismatches 2; Indels 7; Gaps 1;

QY 3 PPHPTNHKYLVCESVNGG 20  
DB 6 PAPTEV-----TVDDGG 16

## RESULT 79

Q7M471\_VESOR PRELIMINARY; PRT; 9 AA.  
AC Q7M471;  
DT 01-MAR-2004 (TrEMBLrel. 26, Created)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Venom protein HR-3 (Fragment).  
OS Vespa orientalis (Oriental hornet).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Pterygota;  
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;  
OC Vespidae; Vespinae; Vespa.  
OX NCBI\_TaxID=7447;  
RN [1]  
RP PROTEIN SEQUENCE.  
RA Tulichbaev M.U., Akhmedova N.U., Kazakov I., Korneev A.S.,  
RA Gagul'gans A.I.;  
RT "low-molecular-weight peptides of venom of the giant hornet Vespa  
orientalis. Structure and function.",  
RL Biochemistry 53:183-190(1988).  
DR PIR; S10920; S10920.  
FT NON\_TER 1 1  
FT NON\_TER 9 9  
SQ SEQUENCE 9 AA; 1029 MW; 9C27C729CB11P2D5 CRC64;

Query Match 20.9%; Score 24; DB 2; Length 9;  
Best Local Similarity 42.9%; Pred. No. 2.2e+06;  
Matches 3; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 7 NHHKYIV 13  
DB 2 SVHEFLV 8

## RESULT 80

Q9UCI7\_HUMAN PRELIMINARY; PRT; 15 AA.  
AC Q9UCI7;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE 38 kDa MYELOPEROXIDASE (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP PROTEIN SEQUENCE.  
RX MEDLINE=93094240; PubMed=1334087;  
RA Taylor K.L., Pohl J., Kinkade J.M.Jr.;  
RT "Unique autolytic cleavage of human myeloperoxidase. Implications for  
the involvement of active site MET409."  
RL J. Biol. Chem. 267:25282-25286(1992).  
DR GO; GO:0004601; F:peroxidase activity; IEA.  
DR InterPro; IPR02007; Anim\_peroxidase.  
DR PROSITE; PS50292; PEROXIDASE\_3; 1.  
SQ SEQUENCE 15 AA; 1791 MW; 8B76949B5D087321 CRC64;

Query Match 20.9%; Score 24; DB 2; Length 15;  
Best Local Similarity 38.5%; Pred. No. 1.2e+04;  
Matches 5; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 3 PPHPTNHKYLVCESV 15  
DB 1 PELTSMHTLLARE 13

## RESULT 81

Q6R9U9\_HUMAN PRELIMINARY; PRT; 17 AA.  
AC Q6R9U9;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)  
DE Microcephalin (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX PubMed=15056608; DOI=10.1093/hmg/ddh127;  
RA Wang Y.Q., Su B.;  
RT "Molecular evolution of microcephalin, a gene determining human brain  
size.",  
RL Hum. Mol. Genet. 13:1131-1137(2004).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RA Wang Y., Su B.;  
RT Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY506297; AAS88650.1; -; Genomic DNA.  
DR EMBL; AY506293; AAS88656.1; -; Genomic DNA.  
FT NON\_TER 1 1  
SQ SEQUENCE 17 AA; 1921 MW; DC64EAF1C7785B5B CRC64;

Query Match 20.9%; Score 24; DB 2; Length 17;  
Best Local Similarity 41.7%; Pred. No. 1.4e+04;  
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 7 NHHKYIVCSVA 18  
DB 1 SITQHKVCASNV 12



```

RESULT 82
Q6R9P0_TRAFR PRELIMINARY; PRT; 17 AA.
ID Q6R9P0_TRAFR PRELIMINARY; PRT; 17 AA.
AC Q6R9P0;
DT 05-JUL-2004 (TEMBLrel. 27, Created)
DT 05-JUL-2004 (TEMBLrel. 27, Last sequence update)
DE Microcephalin (Fragment).
GN Name=McpH1;
OS Trachypithecus francoisi (Francois' langur) (Indochinese langur).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Cercopithecidae; Colobinae; Trachypithecus.
NCBI_TaxID=54180;
RN [1];
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15056608; DOI=10.1093/hmg/ddh127;
RA Wang Y.Q., Su B.;
RT "Molecular evolution of microcephalin, a gene determining human brain
RT size.";
RL Hum. Mol. Genet. 13:1131-1137(2004).
RN [2];
RP NUCLEOTIDE SEQUENCE.
RA Wang Y., Su B.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY506356; AAS88719.1; -; Genomic_DNA.
FT NON_TER 1 1
SQ SEQUENCE 17 AA; 1931 MW; DC663AF1C7785E5B CRC64;

Query Match 20.9%; Score 24; DB 2; Length 17;
Best Local Similarity 41.7%; Pred. No. 1.4e+04;
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 7 NIHKLVCESVN 18
DB 1 SITQHKVCASEN 12

RESULT 83
Q6R9P1_TRAFR PRELIMINARY; PRT; 17 AA.
ID Q6R9P1_TRAFR PRELIMINARY; PRT; 17 AA.
AC Q6R9P1;
DT 05-JUL-2004 (TEMBLrel. 27, Created)
DT 05-JUL-2004 (TEMBLrel. 27, Last sequence update)
DE Microcephalin (Fragment).
GN Name=McpH1;
OS Trachypithecus phayrei (Phayre's leaf monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Cercopithecidae; Colobinae; Trachypithecus.
NCBI_TaxID=61618;
RN [1];
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15056608; DOI=10.1093/hmg/ddh127;
RA Wang Y.Q., Su B.;
RT "Molecular evolution of microcephalin, a gene determining human brain
RT size.";
RL Hum. Mol. Genet. 13:1131-1137(2004).
RN [2];
RP NUCLEOTIDE SEQUENCE.
RA Wang Y., Su B.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY506355; AAS88718.1; -; Genomic_DNA.
FT NON_TER 1 1
SQ SEQUENCE 17 AA; 1931 MW; DC663AF1C7785E5B CRC64;

Query Match 20.9%; Score 24; DB 2; Length 17;
Best Local Similarity 41.7%; Pred. No. 1.4e+04;
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 7 NIHKLVCESVN 18
DB 1 SITQHKVCASEN 12

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DB 1 SITQHKVCASEN 12

RESULT 84
Q6R9P2_PYGBI PRELIMINARY; PRT; 17 AA.
ID Q6R9P2_PYGBI PRELIMINARY; PRT; 17 AA.
AC Q6R9P2;
DT 05-JUL-2004 (TEMBLrel. 27, Created)
DT 05-JUL-2004 (TEMBLrel. 27, Last sequence update)
DE Microcephalin (Fragment).
GN Name=McpH1;
OS Pygathrix hemaus (Dove langur) (Dove langur).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Cercopithecidae; Colobinae; Pygathrix.
NCBI_TaxID=54133;
RN [1];
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15056608; DOI=10.1093/hmg/ddh127;
RA Wang Y.Q., Su B.;
RT "Molecular evolution of microcephalin, a gene determining human brain
RT size.";
RL Hum. Mol. Genet. 13:1131-1137(2004).
RN [2];
RP NUCLEOTIDE SEQUENCE.
RA Wang Y., Su B.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY506354; AAS88717.1; -; Genomic_DNA.
FT NON_TER 1 1
SQ SEQUENCE 17 AA; 1931 MW; DC663AF1C7785E5B CRC64;

Query Match 20.9%; Score 24; DB 2; Length 17;
Best Local Similarity 41.7%; Pred. No. 1.4e+04;
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 7 NIHKLVCESVN 18
DB 1 SITQHKVCASEN 12

RESULT 85
Q6R9P3_PYGBI PRELIMINARY; PRT; 17 AA.
ID Q6R9P3_PYGBI PRELIMINARY; PRT; 17 AA.
AC Q6R9P3;
DT 05-JUL-2004 (TEMBLrel. 27, Created)
DT 05-JUL-2004 (TEMBLrel. 27, Last sequence update)
DE Microcephalin (Fragment).
GN Name=McpH1;
OS Pygathrix bieti (Black snub-nosed monkey) (Rhinopithecus bieti).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Cercopithecidae; Colobinae; Pygathrix.
NCBI_TaxID=61621;
RN [1];
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15056608; DOI=10.1093/hmg/ddh127;
RA Wang Y.Q., Su B.;
RT "Molecular evolution of microcephalin, a gene determining human brain
RT size.";
RL Hum. Mol. Genet. 13:1131-1137(2004).
RN [2];
RP NUCLEOTIDE SEQUENCE.
RA Wang Y., Su B.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY506353; AAS88716.1; -; Genomic_DNA.
FT NON_TER 1 1
SQ SEQUENCE 17 AA; 1931 MW; DC663AF1C7785E5B CRC64;

Query Match 20.9%; Score 24; DB 2; Length 17;
Best Local Similarity 41.7%; Pred. No. 1.4e+04;
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 7 NIHKLVCESVN 18
DB 1 SITQHKVCASEN 12

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Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 7 NIHXYLVCSVN 18  
: | : | | |  
Db 1 SITOHKVCASEN 12

RESULT 86  
Q6R9P4\_MACMU PRELIMINARY; PRT; 17 AA.

AC Q6R9P4;  
DT 05-JUL-2004 (TREMBLrel. 27, Created)  
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)  
DE Microcephalin (Fragment).  
GN Name=McpH1;  
OS Macaca mulatta (Rhesus macaque).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
OC Cercopithecidae; Cercopithecinae; Macaca.  
OX NCB1\_TaxID=9544;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX PubMed=15056608; DOI=10.1093/hmg/ddh127;  
RA Wang Y.Q., Su B.;  
RT "Molecular evolution of microcephalin, a gene determining human brain size."  
RL Hum. Mol. Genet. 13:1131-1137(2004).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RA Wang Y., Su B.;  
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY506342; AAS88715.1; -; Genomic\_DNA.  
FT NON\_TER 1 1  
SQ SEQUENCE 17 AA; 1931 MW; DC663AF1C7785B5B CRC64;

Query Match 20.9%; Score 24; DB 2; Length 17;  
Best Local Similarity 41.7%; Pred. No. 1.4e+04;  
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 7 NIHXYLVCSVN 18  
: | : | | |  
Db 1 SITOHKVCASEN 12

RESULT 87  
Q6R9Q1\_PONPY PRELIMINARY; PRT; 17 AA.

AC Q6R9Q1;  
DT 05-JUL-2004 (TREMBLrel. 27, Created)  
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)  
DT 01-FEB-2005 (TREMBLrel. 29, Last annotation update)  
DE Microcephalin (Fragment).  
GN Name=McpH1;  
OS Pongo pygmaeus (Orangutan).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;  
OC Pongo.  
OX NCB1\_TaxID=9600;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX PubMed=15056608; DOI=10.1093/hmg/ddh127;  
RA Wang Y.Q., Su B.;  
RT "Molecular evolution of microcephalin, a gene determining human brain size."  
RL Hum. Mol. Genet. 13:1131-1137(2004).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RA Wang Y., Su B.;  
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY506345; AAS88708.1; -; Genomic\_DNA.  
DR EMBL; AY506346; AAS88709.1; -; Genomic\_DNA.  
DR EMBL; AY506347; AAS88710.1; -; Genomic\_DNA.

FT NON\_TER 1 1  
SQ SEQUENCE 17 AA; 1921 MW; DC64EAF1C7785B5B CRC64;

Query Match 20.9%; Score 24; DB 2; Length 17;  
Best Local Similarity 41.7%; Pred. No. 1.4e+04;  
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 7 NIHXYLVCSVN 18  
: | : | | |  
Db 1 SITOHKVCASEN 12

RESULT 88  
Q6R9Q5\_PPRIM PRELIMINARY; PRT; 17 AA.

AC Q6R9Q5;  
DT 05-JUL-2004 (TREMBLrel. 27, Created)  
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)  
DT 01-FEB-2005 (TREMBLrel. 29, Last annotation update)  
DE Microcephalin (Fragment).  
GN Name=McpH1;  
OS Gorilla gorilla (gorilla).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;  
OC Gorilla.  
OX NCB1\_TaxID=9593;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX PubMed=15056608; DOI=10.1093/hmg/ddh127;  
RA Wang Y.Q., Su B.;  
RT "Molecular evolution of microcephalin, a gene determining human brain size."  
RL Hum. Mol. Genet. 13:1131-1137(2004).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RA Wang Y., Su B.;  
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY506341; AAS88704.1; -; Genomic\_DNA.  
DR EMBL; AY506342; AAS88705.1; -; Genomic\_DNA.  
DR EMBL; AY506343; AAS88706.1; -; Genomic\_DNA.  
DR EMBL; AY506344; AAS88707.1; -; Genomic\_DNA.  
FT NON\_TER 1 1  
SQ SEQUENCE 17 AA; 1921 MW; DC64EAF1C7785B5B CRC64;

Query Match 20.9%; Score 24; DB 2; Length 17;  
Best Local Similarity 41.7%; Pred. No. 1.4e+04;  
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 7 NIHXYLVCSVN 18  
: | : | | |  
Db 1 SITOHKVCASEN 12

RESULT 89  
Q6R9R4\_PANTR PRELIMINARY; PRT; 17 AA.

AC Q6R9R4;  
DT 05-JUL-2004 (TREMBLrel. 27, Created)  
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)  
DT 01-FEB-2005 (TREMBLrel. 29, Last annotation update)  
DE Microcephalin (Fragment).  
GN Name=McpH1;  
OS Pan troglodytes (Chimpanzee).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;  
OC Pan.  
OX NCB1\_TaxID=9598;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX PubMed=15056608; DOI=10.1093/hmg/ddh127;  
RA Wang Y.Q., Su B.;  
RT "Molecular evolution of microcephalin, a gene determining human brain size."  
RL Hum. Mol. Genet. 13:1131-1137(2004).

RL Hum. Mol. Genet. 13:1131-1137 (2004).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Wang Y., Su B.,  
 DR Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY506332; AAS88695.1; -; Genomic DNA.  
 DR EMBL; AY506333; AAS88696.1; -; Genomic DNA.  
 DR EMBL; AY506334; AAS88697.1; -; Genomic DNA.  
 DR EMBL; AY506335; AAS88698.1; -; Genomic DNA.  
 DR EMBL; AY506336; AAS88699.1; -; Genomic DNA.  
 DR EMBL; AY506337; AAS88700.1; -; Genomic DNA.  
 DR EMBL; AY506338; AAS88701.1; -; Genomic DNA.  
 DR EMBL; AY506339; AAS88702.1; -; Genomic DNA.  
 DR EMBL; AY506340; AAS88703.1; -; Genomic DNA.  
 FT NON TER 1  
 SQ SEQUENCE 17 AA; 1921 MW; DC64EAF1C7785B5B CRC64;  
 Query Match 20.9%; Score 24; DB 2; Length 17;  
 Best Local Similarity 41.7%; Pred. No. 1.4e+04;  
 Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
 QY 7 NHKYLVCESVN 18  
 DB 1 SITQHKVCASEN 12  
 RESULT 90  
 HEMTO\_THETS STANDARD; PRT; 18 AA.  
 ID P80155;  
 AC 01-DEC-1992 (Rel. 24, Created)  
 DT 01-DEC-1992 (Rel. 24, Last sequence update)  
 DT 10-MAY-2005 (Rel. 47, Last annotation update)  
 DE Ovoclemyrin (Yp14) (Fragment).  
 OS Theromyzon tessulatum (Leech).  
 OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinea; Hirudinea;  
 OC Rhynchobdellida; Glossiphoniidae; Theromyzon.  
 ON NCBI\_Taxid=13286;  
 RN [1]  
 RP PROTEIN SEQUENCE.  
 RC TISSUE=Oocyte;  
 RX MEDLINE=93049299; PubMed=1425663;  
 RA Baert J.-L., Britel M., Sautiere P., Malecha J.;  
 RT "Ovoclemyrin, a major 14-kDa yolk protein distinct from  
 vitellogenin in leech.";  
 RL Eur. J. Biochem. 209:563-569 (1992).  
 CC -1- FUNCTION: Major yolk protein. This iron protein may play a role in  
 the detoxification of free iron after a blood meal.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- SIMILARITY: Belongs to the hemerythrin family.  
 CC -----  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC -----  
 CC PIR; S29264; S29264.  
 DR HSSP; P02247; 2MR.  
 DR INTERPRO; IPR002063; Hemerythrin.  
 DR PROSITE; PS00550; HEMERYTHRINS, PARTIAL.  
 KW Direct protein sequencing; Iron; Metal-binding; Oxygen transport;  
 KW TRANSPORT.  
 FT NON TER 18  
 SQ SEQUENCE 18 AA; 2368 MW; 33397EEB57C81F1 CRC64;  
 Query Match 20.9%; Score 24; DB 1; Length 18;  
 Best Local Similarity 80.0%; Pred. No. 1.5e+04;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 DIPHP 5  
 DB 2 DIPHP 6

RESULT 91  
 Q92YV9\_9HYME PRELIMINARY; PRT; 18 AA.  
 ID Q92YV9;  
 AC Q92YV9;  
 DT 01-MAY-1999 (T-EMBLrel. 10, Created)  
 DT 01-MAY-1999 (T-EMBLrel. 10, Last sequence update)  
 DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)  
 DE Cytochrome oxidase II (Fragment).  
 OS Opilus kraussei.  
 OC Mitochondrion.  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Ichneumonidae;  
 OC Braconidae; Opiinae; Opius.  
 ON NCBI\_Taxid=64839;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=99152621; PubMed=10028295;  
 RA Dowton M., Austin A.D.;  
 RT "Evolutionary dynamics of a mitochondrial rearrangement 'hot spot' in  
 the Hymenoptera.";  
 RL Mol. Biol. Evol. 16:298-309 (1999).  
 DR EMBL; AF034602; AAC79750.1; -; Genomic DNA.  
 DR GO; GO:0005739; C.mitochondrion; IEA.  
 KW Mitochondrion.  
 FT NON TER 1  
 SQ SEQUENCE 18 AA; 2245 MW; F834BD4587B14D66 CRC64;  
 Query Match 20.9%; Score 24; DB 2; Length 18;  
 Best Local Similarity 71.4%; Pred. No. 1.5e+04;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 12 LVCESVN 18  
 DB 1 IYLVESVN 7  
 RESULT 92  
 Q4XS69\_PLACH PRELIMINARY; PRT; 18 AA.  
 ID Q4XS69;  
 AC Q4XS69;  
 DT 13-SEP-2005 (T-EMBLrel. 31, Created)  
 DT 13-SEP-2005 (T-EMBLrel. 31, Last sequence update)  
 DE Hypothetical protein (Fragment).  
 GN ORFNames=PC107016.00.0;  
 OS Plasmodium chabaudi.  
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
 ON NCBI\_Taxid=5825;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Hall N., Karras M., Raine J.D., Carlton J.M., Koof T.W.A.,  
 RA Bertman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,  
 RA James K., Rutherford K., Harris B., Harris D., Churcher C.,  
 RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,  
 RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,  
 RA Jansz C.J., Barrett B., Turner C.M.R., Waters A.P., Sinden R.S.;  
 RT "A comprehensive survey of the Plasmodium life cycle by genomic,  
 transcriptomic, and proteomic analyses.";  
 RL Science 307:82-86 (2005).  
 CC -1- CAUTION: The sequence shown here is derived from an  
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
 CC preliminary data.  
 DR EMBL; CAJ01003579; CAH80243.1; -; Genomic DNA.  
 KW Hypothetical protein.  
 FT NON TER 1  
 SQ SEQUENCE 18 AA; 2271 MW; 6113B4C4387EB7D8 CRC64;  
 Query Match 20.9%; Score 24; DB 2; Length 18;  
 Best Local Similarity 66.7%; Pred. No. 1.5e+04;  
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 NIKRYL 12  
| | | |  
DB 6 NIKRYI 11

RESULT 93  
Q5C5Z8 SCHJA PRELIMINARY; PRT; 19 AA.  
ID Q5C5Z8  
AC Q5C5Z8  
DT 10-MAY-2005 (TReMBLrel. 30, Created)  
DT 10-MAY-2005 (TReMBLrel. 30, Last sequence update)  
DE 10-MAY-2005 (TReMBLrel. 30, Last annotation update)  
OS Hypothetical protein.  
OC Schistosoma japonicum (Blood fluke).  
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidae;  
OC Schistosomatidae; Schistosomatidae; Schistosoma.  
OK NCBI\_TaxID=6182;  
RN (1)  
RP NUCLEOTIDE SEQUENCE.  
RA Han Z.;  
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF03037; AXK24926.1; -; mRNA.  
KW Hypothetical protein.  
SQ SEQUENCE 19 AA; 1908 MW; 442CDA5D856B3F21 CRC64;

Query Match 20.9%; Score 24; DB 2; Length 19;  
Best Local Similarity 66.7%; Pred. No. 1.6e+04;  
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 14 CESVNG 19  
| | | |  
DB 3 CELANG 8

RESULT 94  
Q9ZYW3\_9HYME PRELIMINARY; PRT; 19 AA.  
ID Q9ZYW3\_9HYME  
AC Q9ZYW3;  
DT 01-MAY-1999 (TReMBLrel. 10, Created)  
DT 01-MAY-1999 (TReMBLrel. 10, Last sequence update)  
DE 01-JUN-2003 (TReMBLrel. 24, Last annotation update)  
DE Cytochrome oxidase II (Fragment).  
OS Gnampodon pumilio.  
OS Mitochondrion.  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Ichneumonidae;  
OC Braconidae; Gnampodontinae; Gnampodon.  
OK NCBI\_TaxID=64833;  
RN (1)  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=99152621; PubMed=10028295;  
RA Dowton M., Austin A.D.;  
RT "Evolutionary dynamics of a mitochondrial rearrangement 'hot spot' in the Hymenoptera."  
RT Mol. Biol. Evol. 16:298-309(1999).  
RL EMBL; AF034598; AAC79746.1; -; Genomic\_DNA.  
DR GO; GO:0005739; C:mitochondrion; IEA.  
KW Mitochondrion.  
FT NON\_TER 1  
SQ SEQUENCE 19 AA; 2290 MW; 77F1B7E7B7BCA CRC64;

Query Match 20.9%; Score 24; DB 2; Length 19;  
Best Local Similarity 71.4%; Pred. No. 1.6e+04;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 12 LVCESVN 18  
| | | |  
DB 1 IYVESVN 7

RESULT 95  
Q9ZYX2\_9HYME PRELIMINARY; PRT; 19 AA.  
ID Q9ZYX2\_9HYME

AC Q9ZYX2;  
DT 01-MAY-1999 (TReMBLrel. 10, Created)  
DT 01-MAY-1999 (TReMBLrel. 10, Last sequence update)  
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)  
DE Cytochrome oxidase II (Fragment).  
OS Centistes sp.  
OS Mitochondrion.  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Ichneumonidae;  
OC Braconidae; Euphorinae; Centistes.  
OK NCBI\_TaxID=64856;  
RN (1)  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=99152621; PubMed=10028295;  
RA Dowton M., Austin A.D.;  
RT "Evolutionary dynamics of a mitochondrial rearrangement 'hot spot' in the Hymenoptera."  
RT Mol. Biol. Evol. 16:298-309(1999).  
RL EMBL; AF034589; AAC79737.1; -; Genomic\_DNA.  
DR GO; GO:0005739; C:mitochondrion; IEA.  
KW Mitochondrion.  
FT NON\_TER 1  
SQ SEQUENCE 19 AA; 2213 MW; 319C74242367B0FD CRC64;

Query Match 20.9%; Score 24; DB 2; Length 19;  
Best Local Similarity 71.4%; Pred. No. 1.6e+04;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 12 LVCESVN 18  
| | | |  
DB 1 IYVESVN 7

RESULT 96  
Q4Y3P1\_PLACH PRELIMINARY; PRT; 19 AA.  
ID Q4Y3P1\_PLACH  
AC Q4Y3P1;  
DT 13-SEP-2005 (TReMBLrel. 31, Created)  
DT 13-SEP-2005 (TReMBLrel. 31, Last sequence update)  
DT 13-SEP-2005 (TReMBLrel. 31, Last annotation update)  
DE Hypothetical protein (Fragment).  
GN ORFNames=PC102236.00.0;  
OS Plasmodium chabaudi.  
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
OK NCBI\_TaxID=5825;  
RN (1)  
RP NUCLEOTIDE SEQUENCE.  
RA Hall N., Kairas M., Raine J.D., Carlton J.M., Kooij T.W.A.,  
RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,  
RA James K., Rutherford K., Harris B., Harris D., Churcher C.,  
RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,  
RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,  
RA Jaffe C.J., Barrill B., Turner C.M.R., Waters A.P., Sinden R.S.;  
RT "A comprehensive survey of the Plasmodium life cycle by genomic, transcriptomic, and proteomic analyses."  
RL Science 307:82-86(2005).  
CC -!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is preliminary data.  
DR EMBL; CAU01001297; CAH76219.1; -; Genomic\_DNA.  
KW Hypothetical protein.  
FT NON\_TER 1  
SQ SEQUENCE 19 AA; 2341 MW; 215542A7D275C444 CRC64;

Query Match 20.9%; Score 24; DB 2; Length 19;  
Best Local Similarity 33.3%; Pred. No. 1.6e+04;  
Matches 5; Conservative 2; Mismatches 2; Indels 6; Gaps 1;

QY 10 KYLVC-----ESVN 18  
| | | | | | | | | |  
DB 2 KYIACILKKKEIN 16

```

RESULT 97
Q6R9P5_HYLL6
ID Q6R9P5_HYLL6 PRELIMINARY; PRT; 19 AA.
AC Q6R9P5;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Microcephalin (Fragment).
GN Name=McpH1;
OS Hylobates leucogenys (White-cheeked gibbon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Hylobatidae; Nomascus.
OX NCBI_TaxId=61853;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15056608; DOI=10.1093/hmg/ddh127;
RA Wang Y.Q., Su B.;
RT "Molecular evolution of microcephalin, a gene determining human brain
size."
RL Hum. Mol. Genet. 13:1131-1137(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Wang Y., Su B.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY506351; AAS88714.1; -; Genomic_DNA.
FT NON TER 1 1
SQ SEQUENCE 19 AA; 2216 MW; 099CEC663AFC1778 CRC64;

Query Match 20.9%; Score 24; DB 2; Length 19;
Best Local Similarity 41.7%; Pred. No. 1.6e+04;
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 7 NIKHYLVCSVN 18
:|:|:|:|:|
DB 1 SITQHKVCASEN 12

RESULT 98
Q6R9P6_9PRIM
ID Q6R9P6_9PRIM PRELIMINARY; PRT; 19 AA.
AC Q6R9P6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Microcephalin (Fragment).
GN Name=McpH1;
OS Bunopithecus hollock (Hollock gibbon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Hylobatidae; Bunopithecus.
OX NCBI_TaxId=61851;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15056608; DOI=10.1093/hmg/ddh127;
RA Wang Y.Q., Su B.;
RT "Molecular evolution of microcephalin, a gene determining human brain
size."
RL Hum. Mol. Genet. 13:1131-1137(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Wang Y., Su B.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY506350; AAS88713.1; -; Genomic_DNA.
FT NON TER 1 1
SQ SEQUENCE 19 AA; 2216 MW; 099CEC663AFC1778 CRC64;

Query Match 20.9%; Score 24; DB 2; Length 19;
Best Local Similarity 41.7%; Pred. No. 1.6e+04;
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 7 NIKHYLVCSVN 18
:|:|:|:|:|
DB 1 SITQHKVCASEN 12

```

```

DB 1 SITQHKVCASEN 12

RESULT 99
Q6R9P7_MACMU
ID Q6R9P7_MACMU PRELIMINARY; PRT; 19 AA.
AC Q6R9P7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Microcephalin (Fragment).
GN Name=McpH1;
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Cercopithecidae; Cercopithecinae; Macaca.
OX NCBI_TaxId=9544;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15056608; DOI=10.1093/hmg/ddh127;
RA Wang Y.Q., Su B.;
RT "Molecular evolution of microcephalin, a gene determining human brain
size."
RL Hum. Mol. Genet. 13:1131-1137(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Wang Y., Su B.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY506349; AAS88712.1; -; Genomic_DNA.
FT NON TER 1 1
SQ SEQUENCE 19 AA; 2169 MW; 09920C663AFC1778 CRC64;

Query Match 20.9%; Score 24; DB 2; Length 19;
Best Local Similarity 41.7%; Pred. No. 1.6e+04;
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 7 NIKHYLVCSVN 18
:|:|:|:|:|
DB 1 SITQHKVCASEN 12

RESULT 100
Q5EXA0_9LAMI
ID Q5EXA0_9LAMI PRELIMINARY; PRT; 19 AA.
AC Q5EXA0;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DE 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE STM2 protein (Fragment).
OS Streptocarpus pentherianus.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Lamiales; Gesneriaceae; Cyrtandroidae; Didymocarpaceae;
OC Streptocarpus.
OX NCBI_TaxId=167294;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15659624; DOI=10.1105/tpc.104.028936;
RA Harrison J., Moller M., Langdale J., Cronk Q., Hudson A.;
RT "The Role of KNOX Genes in the Evolution of Morphological Novelty in
Streptocarpus."
RL Plant Cell 17:430-443(2005).
DR EMBL; AY662104; AAW33758.1; -; Genomic_DNA.
FT NON TER 1 1
SQ SEQUENCE 19 AA; 1999 MW; 966867E782A63143 CRC64;

Query Match 20.9%; Score 24; DB 2; Length 19;
Best Local Similarity 35.7%; Pred. No. 1.6e+04;
Matches 5; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 3 PHTNHYLVCSVN 16
:|:|:|:|:|

```

Db 1 PXPESQKLAES 14

Search completed: January 20, 2006, 19:11:05  
Job time : 67.5385 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 20, 2006, 18:54:14 : Search time 75.5769 Seconds  
(without alignments)  
116.273 Million cell updates/sec

Title: US-09-662-293-4

Perfect score: 105

Sequence: 1 DPAKGMSPGFIVGSEGVLS 20

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 244163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 680474

Minimum DB seq length: 0  
Maximum DB seq length: 20

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing filter 100 summaries

Database :

A\_Geneseq\_21:\*

1: geneseq219808:\*

2: geneseq219808:\*

3: geneseq220008:\*

4: geneseq220018:\*

5: geneseq220028:\*

6: geneseq220038:\*

7: geneseq220038:\*

8: geneseq220048:\*

9: geneseq220058:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	105	100.0	20	3	AAV52513
2	105	100.0	20	3	AAV52513
3	105	100.0	20	3	AAV52513
4	105	100.0	20	3	AAV52513
5	105	100.0	20	3	AAV52513
6	105	100.0	20	3	AAV52513
7	105	100.0	20	3	AAV52513
8	105	100.0	20	3	AAV52513
9	105	100.0	20	3	AAV52513
10	105	100.0	20	3	AAV52513
11	105	100.0	20	3	AAV52513
12	105	100.0	20	3	AAV52513
13	105	100.0	20	3	AAV52513
14	105	100.0	20	3	AAV52513
15	105	100.0	20	3	AAV52513
16	105	100.0	20	3	AAV52513
17	105	100.0	20	3	AAV52513
18	105	100.0	20	3	AAV52513
19	105	100.0	20	3	AAV52513
20	105	100.0	20	3	AAV52513
21	105	100.0	20	3	AAV52513
22	105	100.0	20	3	AAV52513
23	105	100.0	20	3	AAV52513
24	105	100.0	20	3	AAV52513

25	33	31.4	15	8	AD036853	Ad036853 Majorly a
26	33	31.4	16	8	ADU54228	AdU54228 30 KD pro
27	33	31.4	16	8	ADU07809	ADU07809 Peptide e
28	33	31.4	20	5	ABP30905	ABP30905 OEB antib
29	33	31.4	20	7	ADAO8550	ADAO8550 Human OEB
30	33	31.4	20	7	ADP09099	ADP09099 Secreted
31	33	31.4	20	7	ADP08893	ADP08893 Secreted
32	33	31.4	20	7	ADG46180	ADG46180 OEB antib
33	33	31.4	20	7	ADK40495	ADK40495 KOR & VEG
34	33	31.4	20	8	ADRA40713	ADRA40713 KOR/ VEGF
35	33	31.4	20	9	ADX17776	ADX17776 Human ova
36	33	31.4	20	9	ADX17982	ADX17982 Human ova
37	33	31.4	20	5	AAO14949	AAO14949 Survivin-
38	33	31.4	15	7	ADN92606	ADN92606 Platelet
39	33	31.4	15	7	ADN92606	ADN92606 Platelet
40	33	31.4	16	5	AAU10333	AAU10333 Human PRO
41	33	31.4	16	6	ABP57840	ABP57840 A. margin
42	33	31.4	20	5	AAU71011	AAU71011 M. tuberc
43	33	31.4	20	7	ADK40519	ADK40519 KOR & VEG
44	33	31.4	20	8	ADRA40713	ADRA40713 KOR/ VEGF
45	33	31.4	20	9	ADX17776	ADX17776 Human ova
46	33	31.4	20	9	ADX17982	ADX17982 Human ova
47	33	31.4	20	5	AAO14949	AAO14949 Survivin-
48	33	31.4	15	7	ADN92606	ADN92606 Platelet
49	33	31.4	15	7	ADN92606	ADN92606 Platelet
50	33	31.4	16	5	AAU10333	AAU10333 Human PRO
51	33	31.4	16	6	ABP57840	ABP57840 A. margin
52	33	31.4	20	5	AAU71011	AAU71011 M. tuberc
53	33	31.4	20	7	ADK40519	ADK40519 KOR & VEG
54	33	31.4	20	8	ADRA40713	ADRA40713 KOR/ VEGF
55	33	31.4	20	9	ADX17776	ADX17776 Human ova
56	33	31.4	20	9	ADX17982	ADX17982 Human ova
57	33	31.4	20	5	AAO14949	AAO14949 Survivin-
58	33	31.4	15	7	ADN92606	ADN92606 Platelet
59	33	31.4	15	7	ADN92606	ADN92606 Platelet
60	33	31.4	16	5	AAU10333	AAU10333 Human PRO
61	33	31.4	16	6	ABP57840	ABP57840 A. margin
62	33	31.4	20	5	AAU71011	AAU71011 M. tuberc
63	33	31.4	20	7	ADK40519	ADK40519 KOR & VEG
64	33	31.4	20	8	ADRA40713	ADRA40713 KOR/ VEGF
65	33	31.4	20	9	ADX17776	ADX17776 Human ova
66	33	31.4	20	9	ADX17982	ADX17982 Human ova
67	33	31.4	20	5	AAO14949	AAO14949 Survivin-
68	33	31.4	15	7	ADN92606	ADN92606 Platelet
69	33	31.4	15	7	ADN92606	ADN92606 Platelet
70	33	31.4	16	5	AAU10333	AAU10333 Human PRO
71	33	31.4	16	6	ABP57840	ABP57840 A. margin
72	33	31.4	20	5	AAU71011	AAU71011 M. tuberc
73	33	31.4	20	7	ADK40519	ADK40519 KOR & VEG
74	33	31.4	20	8	ADRA40713	ADRA40713 KOR/ VEGF
75	33	31.4	20	9	ADX17776	ADX17776 Human ova
76	33	31.4	20	9	ADX17982	ADX17982 Human ova
77	33	31.4	20	5	AAO14949	AAO14949 Survivin-
78	33	31.4	15	7	ADN92606	ADN92606 Platelet
79	33	31.4	15	7	ADN92606	ADN92606 Platelet
80	33	31.4	16	5	AAU10333	AAU10333 Human PRO
81	33	31.4	16	6	ABP57840	ABP57840 A. margin
82	33	31.4	20	5	AAU71011	AAU71011 M. tuberc
83	33	31.4	20	7	ADK40519	ADK40519 KOR & VEG
84	33	31.4	20	8	ADRA40713	ADRA40713 KOR/ VEGF
85	33	31.4	20	9	ADX17776	ADX17776 Human ova
86	33	31.4	20	9	ADX17982	ADX17982 Human ova
87	33	31.4	20	5	AAO14949	AAO14949 Survivin-
88	33	31.4	15	7	ADN92606	ADN92606 Platelet
89	33	31.4	15	7	ADN92606	ADN92606 Platelet
90	33	31.4	16	5	AAU10333	AAU10333 Human PRO
91	33	31.4	16	6	ABP57840	ABP57840 A. margin
92	33	31.4	20	5	AAU71011	AAU71011 M. tuberc
93	33	31.4	20	7	ADK40519	ADK40519 KOR & VEG
94	33	31.4	20	8	ADRA40713	ADRA40713 KOR/ VEGF
95	33	31.4	20	9	ADX17776	ADX17776 Human ova
96	33	31.4	20	9	ADX17982	ADX17982 Human ova
97	33	31.4	20	5	AAO14949	AAO14949 Survivin-

98	31	29.5	15	8	Ado76801 Human 213
99	31	29.5	15	8	Ado77052 Human 213
100	31	29.5	15	8	Ado76676 Human 213

## ALIGNMENTS

## RESULT 1

AAV52513  
ID AAV52513 standard; peptide, 20 AA.

XX AAV52513;

DT 22-FEB-2000 (first entry)

DE House dust mite allergen protein (map) A/B fragment map(3).

XX Mite allergen protein; map; high molecular weight; HMW-map; allergy;

KW house dust mite; IGE; immunoglobulin E; allergen; mapA; mapB;

KW hypersensitivity reaction; therapy; treatment; diagnosis; human; feline;

KW canine; veterinary; antibody; vaccine; immunisation.

XX Dermatophagoides farinae.

XX WO954349-A2.

XX 28-OCT-1999.

XX 16-APR-1999; 99WO-US008524.

XX 17-APR-1998; 98US-00062013.

PR 13-MAY-1998; 98US-0085295P.

PR 02-SEP-1998; 98US-0098909P.

XX (HESK-) HESKA CORP.

XX Mccall CA, Hunter SW, Weber ER;

XX WPI; 2000-052700/04.

PT Novel high molecular weight Dermatophagoides nucleic acid polypeptides

XX used to modify an animals' hypersensitivity to mite allergens.

XX Claim 3; Page 69; 154pp; English.

Sequences AAV52510-Y52522 represent proteolytic fragments of Dermatophagoides farinae high molecular weight mite allergen protein (HMW-map) composition. The HMW-map composition was isolated from a D. farinae homogenate by gel filtration, with each fraction being analysed for the presence of proteins that bound to IGE present in mite-allergic dog antisera. The HMW-map composition comprises mapA (a 109 kD protein) and mapB (98 kD). Mite allergenic proteins and peptides, and nucleic acids encoding them, may be used in therapeutic compositions to modify an animal's hypersensitivity reaction to mite allergens. Animals that may be treated include mammals and birds, especially felines, canines, equines, humans, other pets, and work or domestic animals. The proteins or fragments may also be used to diagnose allergies via a skin test. The proteins and peptides can also be used to raise antibodies, which have a variety of potential uses. For example, they can be used as vaccines to passively immunise animals against dust mite hypersensitivity, as CC positive controls in test kits and as tools to recover desired dust mite CC allergens from a mixture of proteins

SQ Sequence 20 AA;

Query Match 100.0%; Score 105; DB 3; Length 20;  
Best Local Similarity 100.0%; Pred. No. 4,7e-09;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPAKMSPPGPIVGEVGLS 20  
DB 1 DPAKMSPPGPIVGEVGLS 20

RESULT 2  
AAV52522  
ID AAV52522 standard; peptide, 20 AA.

XX AAV52522;

DT 22-FEB-2000 (first entry)

DE House dust mite allergen protein (map) A/B fragment map(12).

XX Mite allergen protein; map; high molecular weight; HMW-map; allergy;

KW house dust mite; IGE; immunoglobulin E; allergen; mapA; mapB;

KW hypersensitivity reaction; therapy; treatment; diagnosis; human; feline;

KW canine; veterinary; antibody; vaccine; immunisation.

XX Dermatophagoides farinae.

XX WO954349-A2.

XX 28-OCT-1999.

XX 16-APR-1999; 99WO-US008524.

XX 17-APR-1998; 98US-00062013.

PR 13-MAY-1998; 98US-0085295P.

PR 02-SEP-1998; 98US-0098909P.

XX (HESK-) HESKA CORP.

XX Mccall CA, Hunter SW, Weber ER;

XX WPI; 2000-052700/04.

PT Novel high molecular weight Dermatophagoides nucleic acid polypeptides

XX used to modify an animals' hypersensitivity to mite allergens.

XX Claim 3; Page 70; 154pp; English.

Sequences AAV52510-Y52522 represent proteolytic fragments of Dermatophagoides farinae high molecular weight mite allergen protein (HMW-map) composition. The HMW-map composition was isolated from a D. farinae homogenate by gel filtration, with each fraction being analysed for the presence of proteins that bound to IGE present in mite-allergic dog antisera. The HMW-map composition comprises mapA (a 109 kD protein) and mapB (98 kD). Mite allergenic proteins and peptides, and nucleic acids encoding them, may be used in therapeutic compositions to modify an animal's hypersensitivity reaction to mite allergens. Animals that may be treated include mammals and birds, especially felines, canines, equines, humans, other pets, and work or domestic animals. The proteins or fragments may also be used to diagnose allergies via a skin test. The proteins and peptides can also be used to raise antibodies, which have a variety of potential uses. For example, they can be used as vaccines to passively immunise animals against dust mite hypersensitivity, as CC positive controls in test kits and as tools to recover desired dust mite CC allergens from a mixture of proteins

SQ Sequence 20 AA;

Query Match 100.0%; Score 105; DB 3; Length 20;  
Best Local Similarity 100.0%; Pred. No. 4,7e-09;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPAKMSPPGPIVGEVGLS 20  
DB 1 DPAKMSPPGPIVGEVGLS 20

RESULT 3  
AAU96317  
ID AAU96317 standard; peptide, 20 AA.



AC	AAU96317,
XX	
DT	15-JUL-2002 (first entry)
XX	
DE	Der HMW-map polypeptide #4.
XX	
KM	Der HMW-map; American house dust mite; anti-allergic; mite; IgE;
XX	mite allergenic protein; immunoglobulin E; hypersensitivity;
XX	immunocomplex formation.
OS	Dermatophagoides farinae.
PN	WO200222807-A2.
XX	
PD	21-MAR-2002.
XX	
PF	14-SEP-2001; 2001WO-US028730.
XX	
PR	14-SEP-2000; 2000US-00662293.
XX	
PA	(HESK-) HESKA CORP.
PI	Mccall CA, Hunter SW, Weber ER;
XX	WPI, 2002-351888/38.
PS	Claim 12; Page 70; 161pp; English.
XX	
CC	The invention relates to an isolated mite allergenic protein of
CC	Dermatophagoides, designated Der HMW-map protein, and its related nucleic
CC	acid. The Der HMW-map protein is useful for eliciting an immune response
CC	against Der HMW-map protein. The protein or a reagent comprising a non-
CC	proteinaceous epitope is useful for identifying an animal (e.g., dog,
CC	cat) susceptible to or having an allergic response to a mite. A
CC	therapeutic composition is useful for desensitizing a host animal to an
CC	allergic response to a mite. The DNA and protein can be used in the
CC	detection of anti-Der HMW-map antibodies in animal fluids, and inhibition
CC	of immunoglobulin (Ig) E or Der HMW-map protein activity associated with a
CC	disease. Antibodies that bind to Der HMW-map are useful for inhibiting
CC	binding of proteins to IgE, to prevent immunocomplex formation, thus
CC	reducing hypersensitivity responses to mite allergens, and as vaccines
CC	against mite allergen hypersensitivity. Sequences AAU96314-AAU96342
XX	represent Der HMW-map polypeptides of the invention
SO	
SQ	Sequence 20 AA:
	Query Match 100.0%; Score 105; DB 5; Length 20;
	Best Local Similarity 100.0%; Pred. No. 4.7e-09;
	Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
Oy	
Db	1 DPAKGMSPPGFIVGEGVLS 20   1 DPAKGMSPPGFIVGEGVLS 20
RESULT 4	
ID	AAU96326
AC	AAU96326 standard; peptide; 20 AA.
XX	
XX	AAU96326;
XX	
DT	15-JUL-2002 (first entry)
XX	
DE	Der HMW-map polypeptide #13.
XX	
KM	Der HMW-map; American house dust mite; anti-allergic; mite; IgE;
XX	mite allergenic protein; immunoglobulin E; hypersensitivity;
KM	immunocomplex formation.
XX	
OS	Dermatophagoides farinae.

[illegible]

DR	WP1; 2004-653416/63.
XX	
PT	New modified nitrilase polypeptides, useful for preparing carboxylic acids, preferably substituted chiral carboxylic acids.
XX	
PS	Disclosure; Page 13; 96pp; English.
XX	
CC	The present invention relates to modified nitrilase proteins, which are useful for preparing carboxylic acids, preferably substituted chiral carboxylic acids. Nitrilases are enzymes which catalyse the hydrolysis of nitriles into the corresponding carboxylic acids and ammonium ions. The modified nitrilases of the invention have a modification at position 286 and exhibit a modulated acceptance in comparison to wild-type nitrilase. The substitution of tyrosine at position 296 in wild-type Alcaligenes faecalis nitrilase comprising a sequence of 356 amino acids (ADR67405) was realised by site-directed mutagenesis utilising overlap-extension PCR. The present sequence is a fragment of a nitrilase used in a sequence alignment to illustrate the invention.
CC	
XX	Sequence 16 AA;
SQ	
Query Match	34.3%; Score 36; DB 8; Length 16;
Best Local Similarity	58.3%; Pred. No. 1.9e+02;
Matches	7; Conservative 1; Mismatches 4; Indels 0; Gaps 0
Oy	1 DPAKGMSPGPT 12       1 DPAGHYSTPGFL 12
Db	
RESULT 6	
AAB28728	
ID	AAB28728 standard; peptide; 9 AA.
AC	
XX	AAB28728;
DT	27-DEC-2002 (first entry)
XX	
DE	Human CASB88 antigenic epitope #19.
XX	
KW	CASB88 protein; Crohn's disease; Colitis ulcerosa; Preneoplastic lesion; colorectal cancer; Wilms' tumour; retinoblastoma; cancer; gene therapy; Rabinomyosarcoma; leiomyosarcoma; synovial sarcoma; vaccine; human; epitope.
XX	
OS	Homo sapiens.
XX	
PN	WO200250103-A2.
PD	27-JUN-2002.
XX	
PF	18-SEP-2001; 2001WO-EP010980.
XX	
PR	20-DEC-2000; 2000GB-00031095.
PR	27-MAR-2001; 2001GB-00007632.
PR	02-AUG-2001; 2001GB-00018926.
XX	
PA	(SMIK ) SMITHKLIN BECHAM BIOLOGICALS.
PI	Caseart J, Coche T, Gaulis SKJ, Orncoft T, Vinals Y De BassolsC;
DR	WPI; 2002-691493/74.
XX	
PT	Novel CASB88 polypeptide and polymucleotide useful for treating cancer, Crohn's disease, colitis ulcerosa, colorectal cancer, lung cancer and preneoplastic lesions, Wilms tumor, retinoblastoma and rhabdomyosarcoma.
XX	
PS	Claim 6; Page 77; 122pp; English.
XX	
CC	The invention relates to novel CASB88 polypeptides and polymucleotides. Sequences of the invention are used for the treatment of diseases e.g. Crohn's disease, Colitis ulcerosa, colorectal cancer, lung cancer and preneoplastic lesions, breast, brain, uterus, muscle, eye and germ cell
CC	

Query Match	33.3%	Score 35	DB 5	Length 9
Best Local Similarity	100.0%	Pred. No. 2e+06		
Matches 6	Conservative 0	Mismatches 0	Indels 0	Gaps 0
OY	5 GMSPPG 10			
DB	1 GMSPPG 6			
RESULT 7				
ID	AAE28775			
XX	AAE28775 standard; peptide; 10 AA.			
XX	AAE28775;			
XX	27-DEC-2002 (first entry)			
XX	Human CASB88 antigenic epitope #66.			
XX	CASB88 protein; Crohn's disease; Colitis ulcerosa; preneoplastic lesion;			
KW	colorectal cancer; Wilm's tumour; retinoblastoma; cancer; gene therapy;			
KW	rabdomyosarcoma; leiomyosarcoma; synovial sarcoma; vaccine; human;			
XX	epitope.			
OS	Homo sapiens.			
XX	WO200250103-A2.			
XX	27-JUN-2002.			
XX	18-SEP-2001; 2001WO-EP010980.			
XX	20-DEC-2000; 2000GB-00031095.			
PR	27-MAR-2001; 2001GB-00007632.			
PR	02-AUG-2001; 2001GB-00018926.			
XX	(SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.			
PI	Cassart J, Coche T, Gaulis SRJ, Ornloft T, Vinals Y De Basolac;			
XX	WPI; 2002-691493/74.			
XX	Novel CASB88 polypeptide and polynucleotide useful for treating cancer,			
PT	Crohn's disease, colitis ulcerosa, colorectal cancer, lung cancer and			
PT	preneoplastic lesions, Wilm's tumor, retinoblastoma and rabdomyosarcoma.			
XX	Claim 6; Page 81; 122pp; English.			
XX	The invention relates to novel CASB88 polypeptides and polynucleotides.			
CC	Sequences of the invention are used for the treatment of diseases e.g.			
CC	Crohn's disease, Colitis ulcerosa, colorectal cancer, lung cancer and			
CC	preneoplastic lesions, breast, brain, uterus, muscle, eye and germ cell			
CC	cancers, Wilm's tumour, retinoblastoma, rabdomyosarcoma, leiomyosarcoma			
CC	and synovial sarcoma. They are useful in gene therapy and as vaccines.			
CC	The present sequence is human CASB88 antigenic epitope			
XX	Sequence 10 AA;			
XX	Query Match	33.3%	Score 35	DB 5
XX	Best Local Similarity	100.0%	Pred. No. 1.6e+02	Length 10
XX	Matches 6	Conservative 0	Mismatches 0	Indels 0
OY	5 GMSPPG 10			
DB	3 GMSPPG 8			

## RESULT 8

ADC99464  
ID ADC99464 standard; peptide; 20 AA.

AC ADC99464;

DT 01-JAN-2004 (first entry)

DE Cancer-related DGI-5-binder peptide - SEQ ID 302.

XX cytosolic; cancer; gene therapy; DGI-2; DGI-5; DGI-7; DGI-9; Hras;  
XX leprtin; VEGF; vascular endothelial growth factor receptor; VEGF-R1;  
XX VEGF-R2; VEGF-R3; PLR1; PMS-related tyrosine kinase 1; Flk1; KDR;  
XX kinase insert domain protein receptor; EGFR; epidermal growth factor;  
XX FGFR1; fibroblast growth factor; Tie-1.

OS unidentified.

PN MO200305839-A2.

XX 01-MAY-2003.

PF 24-OCT-2002; 2002MO-US034021.

PR 24-OCT-2001; 2001US-0345471P.

PA (DGI-5) DGI BIOTECHNOLOGIES INC.

PI Piliutia RC, Brissette R, Spruyt M, Dedova O, Blume A;  
PI Prendergast J, Goldstein N;

XX MPI; 2003-457332/43.

PT Selecting target and target binder pairs for preparing a composition for  
PT treating cancer by mixing in a reaction vessel phase expressing  
PT biological targets and phase expressing target binders.

XX Claim 26; SEQ ID NO 302; 172pp; English.

CC The invention relates to a novel method of selecting target and target  
CC binder pairs comprising mixing in a reaction vessel phase expressing  
CC biological targets and phase expressing target binders, each having  
CC distinguishable selection markers and selecting target and target binder  
CC pairs based on the selection markers. The molecules of the invention  
CC demonstrate cytosolic activity whilst the method may be useful for  
CC selecting target and target binder pairs for preparing a composition for  
CC treating cancer. Furthermore, the method may be utilised during gene  
CC therapy procedures. The current sequence is that of the cancer-related  
CC DGI-5-binder peptide of the invention.

XX Sequence 20 AA;

Query Match 33.3%; Score 35; DB 7; Length 20;

Best Local Similarity 53.3%; Pred. No. 3.4e+02; Mismatches 6; Indels 0; Gaps 0;

QY 5 GMSPEFIVGEBSVL 19

DB 2 GRLPWGLVGRGL 16

## RESULT 9

AAW65590  
ID AAW65590 standard; peptide; 8 AA.

AC AAW65590;

DT 15-OCT-1998 (first entry)

XX Peptide #6.

DE Epstein-Barr virus; diagnostic test; autoimmune disease; vaccine;  
XX Infection; antibody; screening; genetic marker.

XX Synthetic.

OS WO9830586-A2.

XX 16-JUL-1998.

PF 13-JAN-1998; 98MO-US000342.

PR 13-JAN-1997; 97US-00781296.

PA (OKLA-) OKLAHOMA MEDICAL RES FOUND.

PI Harley JB, James JA;

XX MPI; 1998-399062/34.

PT Use of Epstein-Barr virus or component(s) - for developing product(s)  
PT which can be used for preventing, diagnosing, treating or determining  
PT risk of developing autoimmune disease.

PS Disclosure; Page 54; 81pp; English.

CC The invention relates to a vaccine for alleviating or preventing  
CC autoimmune disorders induced by infection with Epstein-Barr virus (EBV).  
CC It comprises EBV or a component in a carrier for administration of the  
CC virus or viral component to alleviate or prevent the autoimmune disorder.  
CC Also claimed are: (1) a diagnostic test kit comprising: (a) reagents  
CC which can be used to detect levels of antibodies to EBV, indicators of  
CC EBV infection of cells, or levels of EBV DNA or protein in a patient; (b)  
CC control samples from individuals not at risk of developing an autoimmune  
CC disease; and (c) a device for determining the differences in levels of a  
CC patient and control samples to distinguish individuals at higher risk of  
CC developing an autoimmune disease from those at lower risk of developing  
CC an autoimmune disease; and (2) a method for screening for genetic markers  
CC or risk factors for development of autoimmune disorders induced by  
CC infection with EBV comprising comparing the responses of different  
CC strains of the same species of an animal vaccinated with EBV or a  
CC component to induce an autoimmune response in at least one of the strains  
CC and comparing the differences in the genetics of the different strains to  
CC identify potential genetic markers or risk factors. The methods can be  
CC used for the prevention, diagnosis, and treatment of autoimmune diseases  
CC having EBV as an etiological agent. The autoimmune diseases may be e.g.  
CC systemic lupus erythematosus, Sjogren's syndrome, rheumatoid arthritis,  
CC juvenile onset diabetes mellitus, Wegener's granulomatosis, etc. The  
CC present sequence is shown in the specification

XX Sequence 8 AA;

Query Match 32.4%; Score 34; DB 2; Length 8;

Best Local Similarity 75.0%; Pred. No. 2e+06; Mismatches 2; Indels 0; Gaps 0;

QY 2 PAKGMSPP 9

DB 1 PAPGMRPP 8

## RESULT 10

AAE09067  
ID AAE09067 standard; peptide; 8 AA.

AC AAE09067;

DT 15-NOV-2001 (first entry)

XX Human autoantigen Sm B/B' octapeptide #3 used in the invention.

XX Vaccine; therapy; autoimmune disorder; Epstein-Barr virus; EBV; anaemia;  
XX polymyositis; systemic lupus erythematosus; SLE; rheumatoid arthritis;  
XX Sjogren's syndrome; diabetes mellitus; adrenalitis; multiple sclerosis;  
XX demyelinating disease; Hashimoto's thyroiditis; autoimmune infertility;  
XX hypoparathyroidism; primary biliary cirrhosis; ankylosing spondylitis;

KM inflammatory bowel disease; Addison's disease; thyroiditis; filariasis;  
 KM Graves' disease; ulcerative colitis; dermatomyositis; myasthenia gravis;  
 KM Crohn's disease; CREST syndrome; autoimmune cystitis; glomerulonephritis;  
 KM polyarthritis nodosa; hepatitis; atopic rhinitis; Goodpasture's syndrome;  
 KM sarcoidosis; rheumatic fever; anti-phospholipid syndrome; Farmer's lung;  
 KM Cushing's syndrome; bird-fancier's lung; alveolitis; erythema nodosum;  
 KM pyoderma gangrenosum; fibromyalgia; Kawasaki's disease; cardiomyopathy;  
 KM Sampter's syndrome; asthma; polymyalgia rheumatica; psoriasis; arteritis;  
 KM erythroblastosis foetalis; cystitis; IGA nephropathy; Hodgkin's lymphoma;  
 KM renal cell carcinoma; eosinophilia; immunosuppressive; ophthalmological;  
 KM thymomelic; neuroprotective; cytosolic; nephrotoxic; antiallergic;  
 KM dengue; antituber; vasotropic; antipyretic; hepatotropic; human.  
 OS Homo sapiens.  
 XX  
 XX MO200158481-A2.  
 XX  
 XX 16-AUG-2001.  
 XX  
 XX 09-FEB-2001; 2001WO-US004191.  
 XX  
 XX 09-FEB-2000; 2000US-00500904.  
 XX  
 XX (OKLA-) OKLAHOMA MEDICAL RES FOUND.  
 XX  
 XX Harley JB, James JA, Kaufman KM;  
 PI  
 XX WPI; 2001-522437/57.  
 DR  
 XX  
 PT Novel vaccine for alleviating or preventing autoimmune disorders induced  
 PT Epstein-Barr virus (EBV) infection e.g. systemic lupus erythematosus,  
 PT juvenile onset diabetes mellitus, comprises EBV virus or its component.  
 PT  
 XX  
 XX Example 1; Fig 3; 11app; English.

XX The present invention relates to a vaccine for alleviating or preventing  
 CC autoimmune disorders induced by infection with Epstein-Barr virus (EBV),  
 CC comprising EBV or its component in a carrier. The vaccine is useful for  
 CC preventing or alleviating autoimmune disorders induced by EBV, e.g.  
 CC systemic lupus erythematosus (SLE), Sjogren's syndrome, juvenile onset  
 CC diabetes mellitus, rheumatoid arthritis, Wegener's granulomatosis,  
 CC inflammatory bowel disease, polymyositis, dermatomyositis, multiple  
 CC endocrine failure, Schmidt's syndrome, autoimmune uveitis, Addison's  
 CC disease, adrenailitis, primary biliary cirrhosis, Graves' disease,  
 CC thyroiditis, Hashimoto's thyroiditis, autoimmune thyroid disease,  
 CC pernicious and haemolytic anaemia, lupoid hepatitis, demyelinating  
 CC disease, multiple sclerosis, subacute cutaneous lupus erythematosus,  
 CC hypoparathyroidism, Dressler's syndrome, myasthenia gravis, autoimmune  
 CC idiopathic thrombocytopenic purpura, autoimmune pemphigus vulgaris,  
 CC pemphigus, bullous pemphigoid, dermatitis herpetiformis, alopecia areata,  
 CC autoimmune cystitis, pemphigoid, scleroderma, progressive systemic  
 CC sclerosis, CREST syndrome (calcinosis, Reynaud's oesophageal dysmotility,  
 CC sclerodactyly and telangiectasia), adult onset diabetes mellitus (type II  
 CC diabetes), male or female autoimmune infertility, ankylosing spondylitis,  
 CC ulcerative colitis, Crohn's disease, mixed connective tissue disease,  
 CC polyarthritis nodosa, systemic necrotising vasculitis,  
 CC glomerulonephritis, atopic dermatitis, atopic rhinitis, Goodpasture's  
 CC syndrome, Chagas' disease, sarcoidosis, rheumatic fever, asthma,  
 CC recurrent abortion, anti-phospholipid syndrome, Farmer's lung, erythema  
 CC multiforme, postcardotomy syndrome, Cushing's syndrome, autoimmune  
 CC chronic active hepatitis, bird-fancier's lung, allergic  
 CC encephalomyelitis, toxic necrodermal lysis, alopecia, lungor's syndrome,  
 CC allergic alveolitis, fibrosing alveolitis, interstitial lung disease,  
 CC erythema nodosum, pyoderma gangrenosum, transfusion reaction, chronic  
 CC fatigue syndrome, fibromyalgia, Takayasu's arteritis, Kawasaki's disease,  
 CC polymyalgia rheumatica, temporal arteritis, giant cell arteritis, dengue,  
 CC Sampter's syndrome (triaditis), nasal polyps, eosinophilial and Behcet's  
 CC disease, Caplan's syndrome, encephalomyositis, erythema elevatum et  
 CC diuturnum, psoriasis, erythroblastosis foetalis, Shulman's syndrome, IGA  
 CC nephropathy, Felty's syndrome, fascitis with eosinophilia, Hilaria's,  
 CC chronic cystitis, heterochromic cystitis, Fuchs's cystitis, Hodgkins and  
 CC non-Hodgkin's lymphoma, cardiomyopathy, Henoch-Schönlein purpura, post  
 CC vaccination syndromes, renal cell carcinoma, Eaton-Lambert syndrome or

CC relapsing polychondritis. The present sequence is human autoantigen Sm  
 CC B/B' octapeptide used in the invention  
 XX  
 SQ Sequence 8 AA;  
 Query Match 32.4%; Score 34; DB 4; Length 8;  
 Best Local Similarity 75.0%; Pred. No. 2e+06;  
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 2 PAKGMSPP 9  
 DB 1 PAKGMRPP 8  
 RESULT 11  
 AAB97330  
 ID AAB97330 standard; peptide; 8 AA.  
 XX  
 XX AAB97330;  
 AC  
 XX  
 DT 13-AUG-2001 (first entry)  
 XX  
 DE UI RNP with A and C proteins epitope peptide.  
 XX  
 KM B cell; toxin; antigen specific; antibody mediated disease; virucide;  
 KM immunosuppressive; antiinflammatory; antiallergic; antidiabetic;  
 KM thymomelic; antithyroid; vasotropic; cardiac; antituber;  
 KM neuroprotective; antirheumatic; antiarthritic; dermatological;  
 KM ophthalmological; nephrotoxic; allergy; autoimmune disorder;  
 KM skin diseases; autoimmune endocrinopathy; vasculitic syndrome;  
 KM cardiovascular disease; immunohaematologic disorder; neurologic disease;  
 KM gastrointestinal disease; collagen vascular disease; renal diseases;  
 KM pulmonary disease; infertility disorder; UI-U6 RNP;  
 KM systemic lupus erythematosus.  
 XX  
 XX  
 XX Unidentified.  
 OS  
 XX  
 XX WO200132853-A1.  
 PN  
 XX  
 PD 10-MAY-2001.  
 XX  
 PF 12-OCT-2000; 2000WO-US028157.  
 XX  
 PR 29-OCT-1999; 99US-0162464P.  
 XX  
 PA (BIOM-) INST APPLIED BIOMEDICINE.  
 XX  
 PI Chaplin JW;  
 XX  
 DR WPI; 2001-316435/33.  
 XX  
 PT B cell clonal toxin useful for treating autoimmune disorders such as  
 PT Grave's disease, myocardial infarction, Crohn's disease, multiple  
 PT sclerosis, comprises a group that causes toxin to be internalized by B  
 PT cell.  
 XX  
 XX  
 PS Disclosure; Page 33; 46pp; English.  
 XX  
 XX This invention relates to a B cell clonal toxin. The toxin is made from  
 CC two moieties, the first causes the toxin to be internalized by a B cell,  
 CC and the second is a biologically acceptable toxin. The invention includes  
 CC a method for inactivating/filling an antigen specific B cell. A target B  
 CC cell is contacted with an effective amount of a B cell clonal toxin. The  
 CC method is useful for selective immunosuppression in conditions  
 CC characterised by the presence of an unwanted or deleterious immune  
 CC response, e.g. in the treatment of antigen specific antibody mediated  
 CC disease conditions. Use of the B cell clonal toxin can result in  
 CC immunosuppressive; antiinflammatory; antiallergic; virucide; antidiabetic  
 CC ; thymomelic; antithyroid; vasotropic; cardiac; antituber;  
 CC neuroprotective; antirheumatic; antiarthritic; dermatological;  
 CC ophthalmological; and nephrotoxic activity. The toxin is particularly  
 CC useful for treating a host suffering from an antigen specific antibody  
 CC mediated disease condition, where the antigen specific antibody is

CC produced by an antigen-reactive B cell population present in a host. The  
 CC toxin is useful for treating allergies, viral disease conditions, and  
 CC autoimmune disorders. Also treated are skin diseases; autoimmune  
 CC endocrinopathies; vasculitic syndromes; cardiovascular disease;  
 CC immunohematologic disorders; gastrointestinal diseases; neurologic  
 CC diseases; collagen vascular diseases; renal diseases; pulmonary diseases;  
 CC and infertility disorders. The present sequence represents a UI RNP with  
 CC A and C proteins epitope. An antibody response to this antigen is  
 CC implicated in systemic lupus erythematosus, a disorder which may be  
 CC treated using the toxin of the invention

CC Sequence 8 AA;

Query Match 32.4%; Score 34; DB 4; Length 8;  
 Best Local Similarity 75.0%; Pred. No. 2e+06;  
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PAKGMSPP 9  
 Db 1 PAKGMRPP 8

RESULT 12  
 ABU07632 standard; peptide; 8 AA.  
 XX ABU07632;

DT 23-OCT-2003 (revised)  
 DT 10-MAY-2003 (first entry)

DE Epstein-Barr virus nuclear antigen peptide #6.

KM EBV, viral, Epstein-Barr virus nuclear antigen; vaccine;  
 KM autoimmune disorder; Epstein-Barr virus infection; diabetes mellitus;  
 KM arthritis; multiple sclerosis; dermatitis; psoriasis; asthma; anaemia;  
 KM allergy.

OS Human herpesvirus 4.

PN US2002164355-A1.

PD 07-NOV-2002.

PF 24-OCT-2001; 2001US-00012756.

PR 30-NOV-1993; 93US-00160604.

PR 16-MAY-1996; 96US-0019053P.

PR 13-JAN-1997; 97US-00781296.

PA (HARL/) HARLEY J B.

PA (JAME/) JAMES J A.

PI Harley JB, James JA;

PI MPI; 2003-298686/29.

PT New vaccine preventing or alleviating autoimmune disorders induced by the  
 PT Epstein-Barr virus, such as diabetes mellitus, rheumatoid arthritis,  
 PT multiple sclerosis, systemic lupus erythematosus, atopic dermatitis and  
 PT psoriasis.

XX Example 1; Fig 3, 41pp; English.

CC The invention relates to a vaccine for alleviating or preventing  
 CC autoimmune disorders induced by infection with Epstein-Barr virus,  
 CC comprising an Epstein-Barr virus or a component in a carrier for  
 CC administration to alleviate or prevent the autoimmune disorders. The  
 CC methods and compositions of the present invention are useful for  
 CC diagnosing, preventing, treating and/or alleviating autoimmune disorders,  
 CC such as diabetes mellitus, rheumatoid arthritis, juvenile rheumatoid  
 CC arthritis, osteoarthritis, psoriatic arthritis, multiple sclerosis,  
 CC encephalomyelitis, myasthenia gravis, systemic lupus erythematosus,

CC autoimmune thyroiditis, atopic dermatitis, eczematous dermatitis,  
 CC psoriasis, Sjogren's Syndrome, Crohn's disease, aphthous ulcer, iritis,  
 CC conjunctivitis, keratoconjunctivitis, ulcerative colitis, asthma,  
 CC allergic asthma, cutaneous lupus erythematosus, scleroderma, vaginitis,  
 CC proctitis, drug eruptions, leprosy reversal reactions, erythema  
 CC nodosum/leprosum, autoimmune uveitis, allergic encephalomyelitis, acute  
 CC necrotising haemorrhagic encephalopathy, idiopathic bilateral progressive  
 CC sensorineural hearing loss, aplastic anaemia, pure red cell anaemia,  
 CC idiopathic thrombocytopenia, polychondritis, Wegener's granulomatosis,  
 CC chronic active hepatitis, Stevens-Johnson syndrome, idiopathic sprue,  
 CC lichen planus, Graves' disease, sarcoidosis, primary biliary cirrhosis,  
 CC uveitis posterior, interstitial lung fibrosis, graft-versus-host disease,  
 CC and allergy. The present sequence represents an Epstein-Barr virus  
 CC nuclear antigen peptide used in the method of the invention. (Updated on  
 CC 23-Oct-2003 to standardise OS field)

CC Sequence 8 AA;

Query Match 32.4%; Score 34; DB 6; Length 8;  
 Best Local Similarity 75.0%; Pred. No. 2e+06;  
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PAKGMSPP 9  
 Db 1 PAKGMRPP 8

RESULT 13  
 ADR43749 standard; peptide; 11 AA.  
 XX ADR43749;

DT 04-NOV-2004 (first entry)

DE Maximakinin 8-18 as a bradykinin agonist.

KM bradykinin; Cardiovascular; Vasoactive; Hypotensive; Cytostatic;  
 KM vascular stenosis; hypertension; tumour; cancer; Maximakinin.

OS Unidentified.

PN MO2004069857-A2.

PD 19-AUG-2004.

PF 06-FEB-2004; 2004WO-GB000470.

PR 06-FEB-2003; 2003GB-00002623.

PR 06-JUN-2003; 2003GB-00012992.

PA (UTTE-) UTTECH LTD.

PA Shaw C, Hirst D, Chen T, O'Rourke M, Rao P;

PI MPI; 2004-604409/58.

PT Bradykinin agonists comprising maximakinin and its fragments, useful for  
 PT selectively stimulating arterial smooth muscle bradykinin receptors and  
 PT for treating cardiovascular disease e.g. ischemic heart disease.

XX Claim 7; SEQ ID NO 3; 67pp; English.

CC The present invention relates to a bradykinin agonist, useful in the  
 CC selective stimulation of arterial smooth muscle bradykinin receptors or  
 CC treatment of cardiovascular disease comprises maximakinin, its analogue  
 CC or fragment or their encoding nucleic acids. Maximakinin derivatives are  
 CC used in the preparation of a medicament for selectively stimulating  
 CC arterial smooth muscle bradykinin receptors; for treating cardiovascular  
 CC disease (claimed) e.g. ischemic heart disease, ischemic disease of other  
 CC organs or organ systems, vascular stenosis, occlusion to peripheral  
 CC vessels (such as limb), hypertension, and on the treatment of a condition  
 CC or disorder that can be ameliorated with the selective bradykinin

CC receptor agonist. Also useful for treatment of a condition for which  
CC dilation of vessels is required e.g. treatment of tumours and cancers,  
CC and for gene therapy. Maximaklinin is a selective bradykinin receptor,  
CC agonist and exhibits both tissue and receptor specific targeting. This  
CC tissue selectivity enables the use of the peptides in the treatment of  
CC diseases of the cardiovascular system while minimizing the side effects  
CC associated with the use of less selective agents. The present sequence  
CC represents a maxmaklinin derivative as a bradykinin agonist  
XX  
SQ Sequence 11 AA;

Query Match 32.4%; Score 34; DB 8; Length 11;  
Best Local Similarity 75.0%; Pred. No. 2.6e+02;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 KGMSPPGF 11  
DB 1 KGPRPPGF 8

## RESULT 14

ID ADR43750 standard; peptide; 12 AA.

XX ADR43750;

DT 04-NOV-2004 (first entry)

DE Maximaklinin 8-19 as a bradykinin agonist.

XX bradykinin; Cardiovascular; Vasotropic; Hypotensive; Cytostatic;  
KW vascular stenosis; hypertension; tumour; cancer; Maximaklinin.

XX Unidentified.

PN WO2004069857-A2.

PD 19-AUG-2004.

PF 06-FEB-2004; 2004WO-GB000470.

PR 06-FEB-2003; 2003GB-00002623.

PR 06-JUN-2003; 2003GB-00012992.

PA (UTRE-) UTRECH LTD.

PI Shaw C, Hirst D, Chen T, O'Rourke M, Rao P;

PS WPI; 2004-604409/58.

PT Bradykinin agonists comprising maxmaklinin and its fragments, useful for  
PT selectively stimulating arterial smooth muscle bradykinin receptors and  
PT for treating cardiovascular disease e.g. Ischemic heart disease.

XX Claim 7, SEQ ID NO 4; 67pp; English.

CC The present invention relates to a bradykinin agonist, useful in the  
CC selective stimulation of arterial smooth muscle bradykinin receptors or  
CC treatment of cardiovascular disease comprises maxmaklinin, its analogue  
CC or fragment or their encoding nucleic acids. Maximaklinin derivatives are  
CC used in the preparation of a medicament for selectively stimulating  
CC arterial smooth muscle bradykinin receptors; for treating cardiovascular  
CC disease (claimed) e.g. ischemic heart disease, ischemic disease of other  
CC organs or organ systems, vascular stenosis, occlusion to peripheral  
CC vessels (such as limb), hypertension; and on the treatment of a condition  
CC or disorder that can be ameliorated with the selective bradykinin  
CC receptor agonist. Also useful for treatment of a condition for which  
CC dilation of vessels is required e.g. treatment of tumours and cancers,  
CC and for gene therapy. Maximaklinin is a selective bradykinin receptor  
CC agonist and exhibits both tissue and receptor specific targeting. This  
CC tissue selectivity enables the use of the peptides in the treatment of  
CC diseases of the cardiovascular system while minimizing the side effects  
CC associated with the use of less selective agents. The present sequence

CC represents a maxmaklinin derivative as a bradykinin agonist  
XX  
SQ Sequence 12 AA;

Query Match 32.4%; Score 34; DB 8; Length 12;  
Best Local Similarity 75.0%; Pred. No. 2.8e+02;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 KGMSPPGF 11  
DB 1 KGPRPPGF 8

## RESULT 15

ID ADR43752 standard; peptide; 13 AA.

XX ADR43752;

DT 04-NOV-2004 (first entry)

DE Maximaklinin 7-19 as a bradykinin agonist.

XX bradykinin; Cardiovascular; Vasotropic; Hypotensive; Cytostatic;  
KW vascular stenosis; hypertension; tumour; cancer; Maximaklinin.

XX Unidentified.

PN WO2004069857-A2.

PD 19-AUG-2004.

PF 06-FEB-2004; 2004WO-GB000470.

PR 06-FEB-2003; 2003GB-00002623.

PR 06-JUN-2003; 2003GB-00012992.

PA (UTRE-) UTRECH LTD.

PI Shaw C, Hirst D, Chen T, O'Rourke M, Rao P;

PS WPI; 2004-604409/58.

PT Bradykinin agonists comprising maxmaklinin and its fragments, useful for  
PT selectively stimulating arterial smooth muscle bradykinin receptors and  
PT for treating cardiovascular disease e.g. ischemic heart disease.

XX Claim 7, SEQ ID NO 6; 67pp; English.

CC The present invention relates to a bradykinin agonist, useful in the  
CC selective stimulation of arterial smooth muscle bradykinin receptors or  
CC treatment of cardiovascular disease comprises maxmaklinin, its analogue  
CC or fragment or their encoding nucleic acids. Maximaklinin derivatives are  
CC used in the preparation of a medicament for selectively stimulating  
CC arterial smooth muscle bradykinin receptors; for treating cardiovascular  
CC disease (claimed) e.g. ischemic heart disease, ischemic disease of other  
CC organs or organ systems, vascular stenosis, occlusion to peripheral  
CC vessels (such as limb), hypertension; and on the treatment of a condition  
CC or disorder that can be ameliorated with the selective bradykinin  
CC receptor agonist. Also useful for treatment of a condition for which  
CC dilation of vessels is required e.g. treatment of tumours and cancers,  
CC and for gene therapy. Maximaklinin is a selective bradykinin receptor  
CC agonist and exhibits both tissue and receptor specific targeting. This  
CC tissue selectivity enables the use of the peptides in the treatment of  
CC diseases of the cardiovascular system while minimizing the side effects  
CC associated with the use of less selective agents. The present sequence  
CC represents a maxmaklinin derivative as a bradykinin agonist  
XX

SQ Sequence 13 AA;

Query Match 32.4%; Score 34; DB 8; Length 13;  
Best Local Similarity 75.0%; Pred. No. 3.1e+02;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 KGMSPPGF 11  
 DB 2 KGPRPGF 9

## RESULT 16

ABP48137  
 ID ABP48137 standard; peptide; 18 AA.

AC ABP48137;

DT 23-AUG-2002 (first entry)

DE GHR binding H5 peptide secondary library sequence #13.

KM Growth hormone; receptor; osteopapthic; endocrine; hormonal; dwarfism;  
 KW acromegaly; animal husbandry; milk production; GHR.

OS Synthetic.

PN US6387879-B1.

PD 14-MAY-2002.

PF 15-DEC-1997; 97US-00990888.

PR 15-DEC-1997; 97US-00990888.

PA (DGIB-) DGI BIOTECHNOLOGIES INC.

PI Blume AJ, Bissette R, Carcamo J, Mandeckl WS, Tang PM;

DR WPI, 2002-478462/51.

PT New amino acid sequences fully defined in the specification mimic growth  
 hormones and are useful to treat conditions such as dwarfism and  
 acromegaly, and to promote growth and milk production in cows.

PS Claim 1; Fig 15A; 46pp; English.

XX The invention relates to novel amino acid sequences which bind  
 CC specifically to growth hormone receptor (GHR). The peptides of the  
 CC invention have osteopapthic, endocrine; and hormonal activity. The amino  
 CC acid sequences are useful to treat dwarfism and acromegaly, and in animal  
 CC husbandry to promote growth and milk production in cows. The sequence  
 CC represents a growth hormone receptor binding peptide of the invention  
 XX

SO Sequence 18 AA;

Query Match 32.4%; Score 34; DB 5; Length 18;  
 Best Local Similarity 60.0%; Pred. No. 4.4e+02;  
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 5 GMSPPGFVIG 14  
 DB 6 GVSYPGWLVG 15

## RESULT 17

ADR43748  
 ID ADR43748 standard; peptide; 18 AA.

AC ADR43748;

DT 04-NOV-2004 (first entry)

DE Maximakinin 1-18 as a bradykinin agonist.

KM bradykinin; Cardiovascular; Vasotrophic; Hypotensive; Cytostatic;  
 KW vascular stenosis; hypertension; tumour; cancer; Maximakinin.

OS Unidentified.

XX NO2004069857-A2.  
 PN  
 XX  
 PD 19-AUG-2004.  
 XX

PF 06-FEB-2004; 2004WO-GB000470.

PR 06-FEB-2003; 2003GB-00002623.

PR 06-JUN-2003; 2003GB-00012992.

XX (UUTR-) UUTRCH LTD.

PI Shaw C, Hirst D, Chen T, O'Rourke M, Rao P;

DR WPI, 2004-604409/58.

PT Bradykinin agonists comprising maximakinin and its fragments, useful for  
 selectively stimulating arterial smooth muscle bradykinin receptors and  
 PT for treating cardiovascular disease e.g. ischemic heart disease.

PS Claim 7; SEQ ID NO 2; 67pp; English.

XX The present invention relates to a bradykinin agonist, useful in the  
 CC selective stimulation of arterial smooth muscle bradykinin receptors or  
 CC treatment of cardiovascular disease comprises maximakinin, its analogue  
 CC or fragment or their encoding nucleic acids. Maximakinin derivatives are  
 CC used in the preparation of a medicament for selectively stimulating  
 CC arterial smooth muscle bradykinin receptors; for treating cardiovascular  
 CC disease (claimed) e.g. ischemic heart disease, ischemic disease of other  
 CC organs or organ systems, vascular stenosis, occlusion to peripheral  
 CC vessels (such as limb), hypertension; and on the treatment of a condition  
 CC or disorder that can be ameliorated with the selective bradykinin  
 CC receptor agonist. Also useful for treatment of a condition for which  
 CC dilation of vessels is required e.g. treatment of tumours and cancers,  
 CC and for gene therapy. Maximakinin is a selective bradykinin receptor  
 CC agonist and exhibits both tissue and receptor specific targeting. This  
 CC tissue selectivity enables the use of the peptides in the treatment of  
 CC diseases of the cardiovascular system while minimizing the side effects  
 CC associated with the use of less selective agents. The present sequence  
 CC represents a maximakinin derivative as a bradykinin agonist  
 XX

SO Sequence 18 AA;

Query Match 32.4%; Score 34; DB 8; Length 18;  
 Best Local Similarity 75.0%; Pred. No. 4.4e+02;  
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 KGMSPPGF 11  
 DB 8 KGPRPGF 15

RESULT 18  
 ADN17072  
 ID ADN17072 standard; peptide; 19 AA.

AC ADN17072;

DT 15-JUL-2004 (first entry)

DE Second generation G protein library g-alpha peptide, SEQ ID No 81.

KW G alpha subunit; G protein; G protein coupled receptor; GPCR;  
 KW allosteric modulator; g-alpha.

OS Unidentified.

PN WO2004035614-A1.

PD 29-APR-2004.

PF 15-JAN-2003; 2003WO-EP000352.

PR 18-OCT-2002; 2002US-0419143P.  
 XX (KARO-) KARO BIO AB.  
 XX  
 XX Fowlkes DM, Christensen DJ, Hamilton PT, Blasius R, Ramer JK;  
 PI Hyde-Denyscher R, Duffin D, Fredericks Z,  
 XX  
 XX WPI; 2004-365151/34.  
 DR  
 PT New synthetic or partially purified peptides that can bind to specific  
 PT subunits of G proteins, useful for detecting the activation or  
 PT deactivation of a G protein-coupled receptor (GPCR) or for identifying  
 PT allosteric modulators of GPCR.  
 XX  
 XX Example 300d; SEQ ID NO 81; 242pp; English.  
 PS  
 XX The invention relates to a novel non-naturally occurring and/or at least  
 CC partially purified peptide, which does not comprise a V-H or V-L homology  
 CC unit of an antibody and specifically binds to an activated G alpha  
 CC subunit of a G protein. The invention further comprises: an assay kit for  
 CC the identification of the activation state of a G protein coupled  
 CC receptor (GPCR), the kit comprising a first peptide cited above labeled  
 CC with a first label; methods of identifying the activation state of a GPCR  
 CC ; a method of identifying a modulator of a GPCR; a method of determining  
 CC the presence or amount of a modulator of a GPCR in a sample; methods of  
 CC identifying a substance as an agonist or antagonist of GPCR; and a method  
 CC of identifying a G-alpha subunit which interacts with a GPCR. The  
 CC composition and methods are useful in detecting the activation or  
 CC deactivation of a G protein-coupled receptor or in monitoring the  
 CC activation state of a GPCR within a cell. These may also be used for  
 CC identifying allosteric modulators of GPCRs. This sequence represents a G  
 CC protein library 9-alpha peptide oligo of the invention.  
 XX  
 SO Sequence 19 AA;

Query Match 32.4%; Score 34; DB 8; Length 19;  
 Best Local Similarity 72.7%; Pred. No. 4.6e+02;  
 Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 10 GIVGEGVLS 20  
 DB 8 GIWVGBEGRSL 18

RESULT 19  
 ADR43747  
 ID ADR43747 standard; peptide; 19 AA.  
 XX  
 XX ADR43747;  
 AC  
 XX  
 XX 04-NOV-2004 (first entry)  
 DT  
 XX  
 XX Maximakinin 1-19 as a bradykinin agonist.  
 DE  
 XX  
 XX bradykinin; Cardiovascular; Vasotrophic; Hypotensive; Cytostatic;  
 KW  
 KW vascular stenosis; hypertension; tumour; cancer; Maximakinin.  
 XX  
 XX Unidentified.  
 OS  
 XX  
 XX WO2004069857-A2.  
 PN  
 XX  
 XX 19-AUG-2004.  
 PD  
 XX  
 XX 06-FEB-2004; 2004WO-GB000470.  
 PR  
 XX  
 XX 06-FEB-2003; 2003GB-00002623.  
 PR  
 XX  
 XX 06-JUN-2003; 2003GB-00012992.  
 XX  
 XX (UTRE-) UTRECH LTD.  
 PA  
 XX  
 XX Shaw C, Hirst D, Chen T, O'Rourke M, Rao P;  
 PI  
 XX  
 XX WPI; 2004-604409/58.  
 DR

XX  
 XX Bradykinin agonists comprising maximakinin and its fragments, useful for  
 PT selectively stimulating arterial smooth muscle bradykinin receptors and  
 PT for treating cardiovascular disease e.g. ischemic heart disease.  
 PT  
 PS Disclosure; SEQ ID NO 1; 67pp; English.  
 XX

CC The present invention relates to a bradykinin agonist, useful in the  
 CC selective stimulation of arterial smooth muscle bradykinin receptors or  
 CC treatment of cardiovascular disease comprises maximakinin, its analogue  
 CC or fragment or their encoding nucleic acids. Maximakinin derivatives are  
 CC used in the preparation of a medicament for selectively stimulating  
 CC arterial smooth muscle bradykinin receptors; for treating cardiovascular  
 CC disease (claimed) e.g. ischemic heart disease, ischemic disease of other  
 CC organs or organ systems, vascular stenosis, occlusion to peripheral  
 CC vessels (such as limb), hypertension; and on the treatment of a condition  
 CC or disorder that can be ameliorated with the selective bradykinin  
 CC receptor agonist. Also useful for treatment of a condition for which  
 CC dilation of vessels is required e.g. treatment of tumours and cancers,  
 CC and for gene therapy. Maximakinin is a selective bradykinin receptor  
 CC agonist and exhibits both tissue and receptor specific targeting. This  
 CC tissue selectivity enables the use of the peptides in the treatment of  
 CC diseases of the cardiovascular system while minimizing the side effects  
 CC associated with the use of less selective agents. The present sequence  
 CC represents maximakinin 1-19 as a bradykinin agonist  
 XX

SO Sequence 19 AA;

Query Match 32.4%; Score 34; DB 8; Length 19;  
 Best Local Similarity 75.0%; Pred. No. 4.6e+02;  
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 4 KGMSPPGF 11  
 DB 8 KGMPPPGF 15

RESULT 20  
 AAM18175  
 ID AAM18175 standard; peptide; 15 AA.  
 XX  
 XX AAM18175;  
 AC  
 XX  
 XX 13-AUG-1997 (first entry)  
 DT  
 XX  
 XX Immunodominant epitope from Mycobacterium tuberculosis 30KD protein.  
 DE  
 XX  
 XX Vaccine; vaccinating agent; M. tuberculosis; pathogen; bacteria; virus;  
 KW  
 KW fungus; protozoan; HIV.  
 KW  
 XX  
 XX Mycobacterium tuberculosis.  
 OS  
 XX  
 XX WO9637219-A1.  
 PN  
 XX  
 XX 28-NOV-1996.  
 PD  
 XX  
 XX 23-MAY-1996; 96WO-US007781.  
 PR  
 XX  
 XX 23-MAY-1995; 95US-00447398.  
 PR  
 XX  
 XX 20-OCT-1995; 95US-00545926.  
 PR  
 XX  
 XX 31-OCT-1995; 95US-00551149.  
 PR  
 XX  
 XX 06-DEC-1995; 95US-00568357.  
 XX  
 XX (REGC ) UNIV CALIFORNIA.  
 PA  
 XX  
 XX Horwitz MA, Harth G;  
 PI  
 XX  
 XX WPI; 1997-020936/02.  
 DR  
 XX  
 XX Vaccines derived from M. tuberculosis major abundant extracellular  
 PT proteins - are easy to prepare and less toxic than conventional killed or  
 PT attenuated vaccines, useful for protecting against or treating  
 PT Mycobacterial infections.  
 PT



XX Claim 49; Page 162; 193pp; English.  
 PS  
 XX A vaccinating agent for promoting an immune response in a mammal against  
 CC Mycobacterium pathogens comprises at least one immunodominant epitope of  
 CC at least one majorly abundant extracellular protein, i.e. the  
 CC M.tuberculosis 110, 80, 71, 58, 45, 32A, 32B, 30, 24, 23.5, 23, 16, 14 or  
 CC 12 kD proteins, or their analogues, homologues and subunits. The present  
 CC sequence represents an immunodominant epitope from the major abundant  
 CC extracellular product 30 kD protein. The vaccinating agents are used to  
 CC protect against (or to treat existing) infections by Mycobacterium  
 CC (especially M. tuberculosis) while the epitopes can also be used to  
 CC detect presence of an immune response to a Mycobacterium pathogen. The  
 CC vectors, containing the DNA for the extracellular proteins, are used to  
 CC transform cells for production of recombinant DNA molecules. More  
 CC generally the DNA from other pathogens can be used in vaccines, e.g.  
 CC against other bacteria, viruses, fungi and protozoa. Since different  
 CC combinations of DNA can be used, a wide range of effective compositions  
 CC can be produced. They generate a response against the antigens most often  
 CC found on infected cells during the infection, regardless of the strength  
 CC or specificity of the immune response. The vaccines are easy to produce  
 CC and less toxic than known killed or attenuated vaccines, so can be given  
 CC to immunocompromised subjects, e.g. those with HIV infection  
 XX  
 SQ Sequence 15 AA;  
 Query Match 31.4%; Score 33; DB 2; Length 15;  
 Best Local Similarity 62.5%; Pred. No. 5.1e+02;  
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 DPAKGMP 8  
 Db 4 DPGQGMGP 11  
 RESULT 21  
 AAW75617  
 ID AAW75617 standard; peptide; 15 AA.  
 AC AAW75617;  
 XX  
 DT 23-OCT-1998 (first entry)  
 XX  
 DE M. tuberculosis 30 kD protein derived peptide 31 (residues 151-165).  
 XX  
 KW Mycobacterium tuberculosis; vaccination; extracellular product;  
 KM immunodominant epitope; interleukin-12; Mf59; immune response;  
 XX opsonising humoral response; intracellular pathogen.  
 OS Synthetic.  
 OS Mycobacterium tuberculosis.  
 XX  
 PN WO9831388-A1.  
 XX  
 PD 23-JUL-1998.  
 XX  
 PF 15-JAN-1998; 98WO-US000942.  
 XX  
 PR 21-JAN-1997; 97US-00786533.  
 XX  
 PA (REGC ) UNITV CALIFORNIA.  
 XX  
 PI Horwitz MA, Harth G, Lee B;  
 XX  
 DR WPI; 1998-413815/35.  
 XX  
 PT Vaccines against Mycobacterium containing major extracellular proteins -  
 PT used to, e.g. induce protective and therapeutic immune responses, and for  
 PT detecting an immune response.  
 XX  
 PS Example 28; Page 96; 236pp; English.  
 XX  
 CC Sequences shown in AAW75587 to AAW75641 represent synthetic peptides

CC derived from the native 30kD major secretory protein of M. tuberculosis.  
 CC These peptides are used for splenic lymphocyte proliferation assays to  
 CC identify the immunodominant T-cell epitope of the 30kD protein. The  
 CC invention provides an agent for vaccinating mammals against  
 CC Mycobacterium. The agent comprises at least one of the major abundant  
 CC extracellular 110, 80, 71, 58, 45, 32A, 32B, 30, 24, 23.5, 23, 16, 14 or  
 CC 12 kD proteins of M. tuberculosis, or at least 1 of their immunodominant  
 CC epitopes and interleukin-12 (IL-12) or Mf59 as adjuvants. The agent  
 CC containing the nucleic acid encoding the extracellular products are used  
 CC to raise a protective or therapeutic immune response against  
 CC Mycobacterium, specifically M. tuberculosis. The immunodominant epitopes  
 CC can also be used (typically in a cutaneous hypersensitivity test) to  
 CC detect an immune response to vaccination. Preparation of the agent does  
 CC not require selection of the most immunogenic products, so large scale  
 CC production and purification are easy, resulting in a consistent,  
 CC standardised formulation, having lower toxicity than killed or attenuated  
 CC vaccines. The agents provide a rapid and effective response (including a  
 CC strong cell-mediated component) and are safe even in immunocompromised  
 CC subjects. They prevent development of an opsonising humoral response that  
 CC might spread intracellular pathogens  
 XX  
 SQ Sequence 15 AA;  
 Query Match 31.4%; Score 33; DB 2; Length 15;  
 Best Local Similarity 62.5%; Pred. No. 5.1e+02;  
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 DPAKGMP 8  
 Db 4 DPGQGMGP 11  
 RESULT 22  
 ABUS6381  
 ID ABUS6381 standard; peptide; 15 AA.  
 XX  
 AC ABUS6381;  
 XX  
 DT 31-MAR-2003 (first entry)  
 XX  
 DE Mycobacterium tuberculosis 30kDa protein fragment #21.  
 XX  
 KW Antibacterial; tuberculosis; vaccine; gene therapy; 30kDa protein.  
 XX  
 OS Synthetic.  
 OS  
 PN US2002131975-A1.  
 XX  
 PD 19-SEP-2002.  
 XX  
 XX 14-SEP-2001; 2001US-00953510.  
 XX  
 PR 23-NOV-1993; 94US-00156358.  
 PR 12-AUG-1994; 94US-00289867.  
 PR 23-MAY-1995; 95US-00447398.  
 PR 31-OCT-1995; 95US-00551149.  
 PR 06-DEC-1995; 95US-00568357.  
 PR 23-MAY-1996; 96US-00652842.  
 PR 21-SEP-1998; 98US-00157689.  
 XX  
 PA (REGC ) UNITV CALIFORNIA.  
 XX  
 PI Horwitz MA, Harth G;  
 XX  
 DR WPI; 2003-174073/17.  
 XX  
 PT New vaccine, useful for promoting an immune response against infectious  
 PT pathogens of the genus Mycobacterium in a mammalian host.  
 XX  
 PS Claim 3; Page 66; 82pp; English.  
 XX  
 CC The invention describes a vaccine for promoting an immune response, in a  
 CC mammalian host, against infectious pathogens of the genus Mycobacterium,

```

CC comprising at least 1 immunodominant epitope of at least one majority
CC abundant extracellular product comprising Mycobacterium tuberculosis 110,
CC 80, 71, 58, 45, 32A, 32B, 30, 24, 23, 5, 23, 16, 14, 12 KD protein or
CC their analogues, homologues or subunits. The proteins and polypeptides of
CC the invention are useful in gene therapy and treatment of diseases caused
CC by Mycobacterium such as tuberculosis. This sequence represents a
CC fragment of the Mycobacterium tuberculosis 30kDa protein
CC
SQ Sequence 15 AA;

Query Match          31.4%; Score 33; DB 6; Length 15;
Best Local Similarity 62.5%; Pred. No. 5.1e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 DPAKGMSP 8
   ||:|||||
Db 4 DPGQGMGP 11

RESULT 23
AAE39326
ID AAE39326 standard; peptide; 15 AA.
XX
AC AAE39326;
XX
DT 18-DEC-2003 (first entry)
XX
DE M. tuberculosis 30 KD protein immunodominant T-cell epitope peptide #31.
XX
KM Vaccine; antibacterial; fungicide; protozoacide; immunostimulant;
XX
OS Mycobacterium tuberculosis.
XX
PN US6599510-B1.
XX
PD 29-JUL-2003.
XX
PF 21-SEP-1998; 98US-00157689.
XX
PR 23-NOV-1993; 93US-00156358.
PR 12-AUG-1994; 94US-00289667.
PR 23-MAY-1995; 95US-00447398.
PR 31-OCT-1995; 95US-00551149.
PR 06-DEC-1995; 95US-00568357.
PR 23-MAY-1996; 96US-00652842.
XX
PA (RBGC ) UNITV CALIFORNIA.
XX
PI Horwitz MA, Harth G;
XX
DR WPI, 2003-669607/63.
XX
PT A nucleic acid encoding an abundant extracellular protein of
PT Mycobacterium tuberculosis useful as vaccines for generating protective
PT or therapeutic immune response against viral, bacterial, fungal or
PT protozoal infections.
XX
PS Example 25; Col 64; 82pp; English.
XX
CC The invention relates to a novel nucleic acid encoding an abundant
CC extracellular protein of Mycobacterium tuberculosis useful as vaccines
CC for generating protective or therapeutic immune response against viral,
CC bacterial, fungal and protozoal infections. They are also used as
CC immunotherapeutic agents. The present sequence is M. tuberculosis strain
CC Erdman 30 KD major secretory protein immunodominant T-cell epitope
CC peptide
CC
SQ Sequence 15 AA;

Query Match          31.4%; Score 33; DB 7; Length 15;
Best Local Similarity 62.5%; Pred. No. 5.1e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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```

QY 1 DPAKGMSP 8
   ||:|||||
Db 4 DPGQGMGP 11

RESULT 24
ADP45168
ID ADP45168 standard; peptide; 15 AA.
XX
AC ADP45168;
XX
DT 12-FEB-2004 (first entry)
XX
DE M. tuberculosis 30kDa extracellular protein fragment seq id 67.
XX
KM antibacterial; vaccine; immune response; extracellular product;
KM Mycobacterium; 30KD; extracellular protein.
XX
OS Mycobacterium tuberculosis.
XX
PN US2003152584-A1.
XX
PD 14-AUG-2003.
XX
PF 15-MAY-2002; 2002US-00147255.
XX
PR 23-NOV-1993; 93US-00156358.
PR 12-AUG-1994; 94US-00289667.
PR 23-MAY-1995; 95US-00447398.
PR 31-OCT-1995; 95US-00551149.
PR 23-MAY-1996; 96US-00652842.
PR 06-DEC-1995; 96US-00568357.
PR 21-SEP-1998; 98US-00157689.
PR 06-JAN-1999; 99US-00226539.
XX
PA (HORW/) HORWITZ M A.
XX
PI Horwitz MA;
XX
DR WPI, 2003-897688/82.
XX
PT Vaccinating agent useful for promoting an immune response in a mammalian
PT host against Mycobacterium, comprising an immunodominant epitope of a
PT majorly abundant extracellular product comprising an M. tuberculosis 30
PT KD protein.
XX
PS Claim 3; SEQ ID NO 67; 83pp; English.
XX
CC The invention describes a new vaccinating agent for promoting an immune
CC response in a mammalian host against Mycobacterium comprising at least
CC one immunodominant epitope of at least one majority abundant extracellular
CC product comprising M. tuberculosis 110, 80, 71, 58, 45, 32A, 32B, 30, 24,
CC 23.5, 23, 16, 14 or 12 KD protein, or its analogue, homologue or subunit.
CC The bacterium is M. tuberculosis. The vaccinating agent is useful for
CC promoting an immune response in a mammalian host against Mycobacterium.
CC This is the amino acid sequence of a Mycobacterium tuberculosis 30KD
CC extracellular protein fragment that can be used to illicit and immune
CC response.
XX
SQ Sequence 15 AA;

Query Match          31.4%; Score 33; DB 7; Length 15;
Best Local Similarity 62.5%; Pred. No. 5.1e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 DPAKGMSP 8
   ||:|||||
Db 4 DPGQGMGP 11

RESULT 25
AD036853

```

ID ADO36853 standard; peptide; 15 AA.  
 XX  
 AC ADO36853;  
 XX  
 DT 15-JUL-2004 (first entry)  
 XX  
 DE Majorly abundant extracellular 30kd protein fragment #31.  
 XX  
 KM antibacterial; virucide; fungicide; protozoacide; vaccine;  
 KM vaccinating agent; immune response; infectious pathogen; Mycobacterium;  
 KM 110 kDa protein; 80 kDa protein; 71 kDa protein; 58 kDa protein;  
 KM 45 kDa protein; 32A kDa protein; 32B kDa protein; 30 kDa protein;  
 KM 24 kDa protein; 23.5 kDa protein; 23 kDa protein; 16 kDa protein;  
 KM 14 kDa protein; 12 kDa protein; vaccine; immunotherapeutic agent;  
 KM 30kd protein.  
 XX  
 OS Synthetic.  
 XX  
 PN US2004018209-A1.  
 XX  
 PD 29-JAN-2004.  
 XX  
 PF 14-SEP-2001; 2001US-00953413.  
 XX  
 PR 23-NOV-1993; 93US-00156358.  
 PR 12-AUG-1994; 94US-00289667.  
 PR 23-MAY-1995; 95US-00447398.  
 PR 31-OCT-1995; 95US-00551149.  
 PR 23-MAY-1996; 96US-00652842.  
 PR 06-DEC-1996; 96US-00568357.  
 PR 21-SEP-1998; 98US-00157689.  
 XX  
 PA (REGC ) UNIV CALIFORNIA.  
 XX  
 PI Horwitz MA, Harth G;  
 XX  
 DR WPI; 2004-121994/12.  
 XX  
 PT New vaccinating agent comprising at least a portion of at least one  
 PT majorly abundant extracellular product, useful for promoting an immune  
 PT response in a mammalian host against an infectious pathogen from the  
 PT genus Mycobacterium.  
 XX  
 PS Example 25; SEQ ID NO 67; 83pp; English.  
 XX  
 CC The invention describes a vaccinating agent useful in promoting an immune  
 CC response in a mammalian host against an infectious pathogen from the  
 CC genus Mycobacterium. The vaccinating agent comprising at least a portion  
 CC of at least one majorly abundant extracellular product or a DNA construct  
 CC encoding at least a portion of at least one majorly abundant  
 CC extracellular product selected from M. tuberculosis 110 kDa protein, 80  
 CC kDa protein, 71 kDa protein, 58 kDa protein, 45 kDa protein, 32A kDa  
 CC protein, 32B kDa protein, 30 kDa protein, 24 kDa protein, 23.5 kDa  
 CC protein, 23 kDa protein, 16 kDa protein, 14 kDa protein or 12 kDa protein  
 CC and its analogs, homologs or subunits, and capable of inducing the  
 CC expression of the extracellular product upon in vivo introduction into  
 CC and resultant uptake by cells of the mammalian host. Also described are:  
 CC a DNA molecule containing a coding sequence for at least a portion of the  
 CC amino acid sequence of M. tuberculosis 16 kDa protein and fragments and  
 CC derivatives; an amino acid sequence encoded by the DNA molecule of (1);  
 CC and immunizing a mammalian host against an infectious pathogen of the  
 CC genus Mycobacterium. The agent is useful as a vaccine for promoting an  
 CC immune response in a mammalian host, against pathogen from genus  
 CC Mycobacterium and for producing compounds for use as vaccines and/or  
 CC immunotherapeutic agents. It can also be used to protect a mammalian host  
 CC against infection by viral, bacterial, fungal or protozoan pathogens.  
 CC This is the amino acid sequence of a synthetic Mycobacterium tuberculosis  
 CC majorly abundant extracellular 30kd protein fragment used to identify  
 CC immunodominant-cell epitopes of the 30kd protein.  
 CC  
 XX  
 SO Sequence 15 AA;  
 XX  
 Query Match 31.4%; Score 33; DB 8; Length 15;

Best Local Similarity 62.5%; Pred. No. 5, 1e+02;  
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 DPAKGMSP 8  
 DB 4 DPEQGMGP 11  
 RESULT 26  
 ID ADU64228 standard; peptide; 15 AA.  
 XX  
 AC ADU64228;  
 XX  
 DT 10-FEB-2005 (first entry)  
 XX  
 DE 30 KD protein peptide fragment residues 151-165, SEQ ID 67.  
 XX  
 KM Antibacterial; Tuberculostatic; Protozoacide; Fungicide; Virucide;  
 KM Anti-HIV, Vaccine.  
 XX  
 OS Mycobacterium tuberculosis.  
 XX  
 PN US2004228873-A1.  
 XX  
 PD 18-NOV-2004.  
 XX  
 PF 27-OCT-2003; 2003US-00695155.  
 XX  
 PR 23-NOV-1993; 93US-00156358.  
 PR 12-AUG-1994; 94US-00289667.  
 PR 23-MAY-1995; 95US-00447398.  
 PR 20-OCT-1995; 95US-00545926.  
 PR 31-OCT-1995; 95US-00551149.  
 PR 23-MAY-1996; 96US-00652842.  
 PR 06-DEC-1996; 96US-00568357.  
 PR 21-JAN-1997; 97US-00786533.  
 XX  
 PA (HORN/) HORWITZ M A.  
 PA (HART/) HARTH G.  
 PA (LEEB/) LEE B.  
 XX  
 PI Horwitz MA, Harth G, Lee B;  
 XX  
 DR WPI; 2004-813210/80.  
 XX  
 PT New vaccinating agent for promoting an immune response against infectious  
 PT Mycobacterium pathogen and HIV infection using majorly abundant  
 PT extracellular products from Mycobacterium tuberculosis.  
 XX  
 PS Example 28; SEQ ID NO 67; 109pp; English.  
 XX  
 CC The present invention relates to a vaccinating agent for promoting an  
 CC immune response in a mammalian host against an infectious Mycobacterium  
 CC pathogen. The vaccinating agent comprises at least a portion or at least  
 CC one immunodominant epitope of at least one majorly abundant extracellular  
 CC product selected from M. tuberculosis 110, 80, 71, 58, 45, 32A, 32B, 30,  
 CC 24, 23.5, 23, 16, 14 or 12 kDa protein and their analogs, homologs, and  
 CC subunits, and an IL-12 or KP 59 adjuvant. The compositions of the present  
 CC invention are useful for stimulating a protective immune response in  
 CC mammalian hosts against intracellular pathogens, such as bacteria,  
 CC protozoa, viruses and fungus, particularly Mycobacterium tuberculosis and  
 CC the HIV virus. The present sequence is a peptide fragment of M.  
 CC tuberculosis 30 KD protein which was used for immunodominant epitope  
 CC mapping of the 30 KD protein.  
 CC  
 XX  
 SO Sequence 15 AA;  
 XX  
 Query Match 31.4%; Score 33; DB 8; Length 15;  
 Best Local Similarity 62.5%; Pred. No. 5, 1e+02;  
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 DPAKGMSP 8

Db 4 DPGGKGP 11

RESULT 27  
AAU07809 standard; peptide; 16 AA.  
AAU07809;  
07-NOV-2001 (first entry)  
Peptide encoded by oligonucleotide ONV510.  
Vascular endothelial growth factor receptor-1; VEGF, psoriasis;  
angiogenesis mediated disease; birth control; neovascularisation;  
inflammatory disorder; neoplastic disorder; anti tumour; anti rheumatic;  
anti arthritic; anti psoriatic; anti diabetic; anti atherosclerotic;  
anti ulcer; osteopathic; cycostatic; anti inflammatory; ophthalmological;  
dermatological.  
Synthetic.  
WO200157067-A1.  
09-AUG-2001.  
02-FEB-2001; 2001WO-1B000135.  
04-FEB-2000; 2000US-0180568P.  
(SUPR-) SUPRATEK PHARMA INC.  
Tcheltakova L, Li S, Pietrynski G, Alakhov V;  
WPI; 2001-529780/58.  
N-PSDB; AAS09208.  
Composition for treating angiogenesis mediated diseases such as tumor and  
psoriasis, comprises a peptide or its derivative capable of specific  
binding with high affinity vascular endothelial growth factor receptor-1.  
Example 16; Page 70; 86bp; English.  
The present invention relates to a pharmaceutical composition comprising  
of a peptide ligand, or its derivative, which is capable of specific  
binding with high affinity to vascular endothelial growth factor (VEGF)  
receptor-1 or its derivative and structurally similar receptors. The  
invention also provides peptide ligands that are capable of inhibiting  
angiogenesis induced by VEGF. The peptide ligands of the invention are  
useful for treating a disease associated with angiogenesis in a patient.  
They are also useful for treating angiogenesis mediated diseases e.g.  
solid tumours, rheumatoid arthritis and psoriasis, for treating diseases  
of excessive or abnormal stimulation of endothelial cells e.g. Crohn's  
disease, atherosclerosis and scleroderma, for treating diseases that have  
angiogenesis as a pathological consequence e.g. cat scratch disease and  
ulcers, as a birth control agent, and for treating diseases associated  
with neovascularisation of the eye e.g. atopic keratitis and Paget's  
disease, inflammatory disorders e.g. ulcerative colitis and inflammatory  
bowel disease, and neoplastic and non-neoplastic diseases and disorders.  
The peptide ligands are also useful as a targeting group to improve the  
delivery of a biological agent used for therapeutic or diagnostic  
purpose. The present sequence represents peptide encoded by  
oligonucleotide ONV5.10  
Sequence 16 AA;

Query Match 31.4%; Score 33; DB 4; Length 16;  
Best Local Similarity 50.0%; Pred. No. 5.5e+02;  
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
1 DPAKMSPPGFI 12

Db 2 EPEVRLSPGH 13

RESULT 28  
ABP30905 standard; protein; 20 AA.  
ABP30905;  
02-JUL-2002 (first entry)  
OE8 antibody epitope peptide #4.  
Human; immunostimulant; cycostatic; cancer; ovarian carcinoma.  
Homo sapiens.  
WO200206317-A2.  
24-JAN-2002.  
17-JUL-2001; 2001WO-US022635.  
17-JUL-2000; 2000US-00617747.  
10-AUG-2000; 2000US-00636801.  
20-SEP-2000; 2000US-00667857.  
04-APR-2001; 2001US-00827271.  
18-JUN-2001; 2001US-00884441.  
(CORI-) CORIXA CORP.  
Mitcham JL, King GE, Algate PA, Fling SP, Retter MW, Fanger GR,  
Reed SG, Vedrick TS, Carter D, Hill P, Albone B;  
WPI; 2002-164781/21.  
Polypeptides comprising an immunogenic portion of an ovarian carcinoma  
protein or its variants, useful for stimulating an immune response in a  
patient and treating ovarian cancer.  
Claim 34; Page 323; 408bp; English.  
This invention relates to polypeptides comprising an immunogenic portion  
of an ovarian carcinoma protein which acts as an immunostimulant and is  
cytostatic. The polypeptides, polynucleotides, antibodies, fusion  
proteins, T cell populations and antigen presenting cells that express  
the polypeptides are useful for eliciting an immune response in a  
patient and treating ovarian cancer. This sequence represents protein  
related to the invention  
Sequence 20 AA;

Query Match 31.4%; Score 33; DB 5; Length 20;  
Best Local Similarity 62.5%; Pred. No. 7e+02;  
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;  
13 VGEBSVLS 20

Db 3 IGBDGLIS 10  
RESULT 29  
ADA08550 standard; peptide; 20 AA.  
ADA08550;  
06-NOV-2003 (first entry)

Query Match 31.4%; Score 33; DB 5; Length 20;  
Best Local Similarity 62.5%; Pred. No. 7e+02;  
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;  
13 VGEBSVLS 20  
ADA08550 standard; peptide; 20 AA.  
ADA08550;  
06-NOV-2003 (first entry)  
Human OE8 antibody epitope #4.  
epitope; human; gene therapy; ovarian cancer; cancer.

OS Homo sapiens.  
 XX  
 PN US2003091580-A1.  
 XX  
 PD 15-MAY-2003.  
 XX  
 PP 17-JUL-2001; 2001US-00907969.  
 XX  
 PR 18-JUN-2001; 2001US-00884441.  
 XX  
 PA (MITC/) MITCHAM J L.  
 PA (KING/) KING G B.  
 PA (ALGA/) ALGATE P A.  
 PA (PLIN/) FLING S P.  
 PA (RETT/) RETTER M W.  
 PA (FANG/) FANGER G R.  
 PA (VEDV/) VEDVICK T S.  
 PA (CART/) CARTER D.  
 PA (HILL/) HILL P.  
 PA (ALBO/) ALBONE B.  
 XX  
 PI Mitcham JL, King GB, Algate PA, Fling SP, Retter MW, Fanger GR;  
 PI Reed SG, Vedvick TS, Carter D, Hill P, Albone B;  
 XX  
 DR WPI, 2003-532352/50.  
 XX  
 PI New isolated 0772P polypeptides and polynucleotides, useful in gene  
 PT therapy, particularly for treating or diagnosing cancer, e.g. ovarian  
 PT cancer.  
 XX  
 PS Claim 34; SEQ ID NO 397; 371bp; English.  
 XX  
 CC The invention relates to an isolated 0772P polypeptide, which has the  
 CC structure fully defined in the specification. The composition containing  
 CC the polypeptides, polynucleotides, fusion proteins, antibodies, T-cells  
 CC or antigen presenting cells are useful for stimulating an immune response  
 CC and treating ovarian cancer. Detecting the presence of the  
 CC polynucleotides and polypeptides is useful for diagnosing cancer. Ovarian  
 CC carcinoma cDNAs and protein cDNAs were identified using microarray  
 CC technology. The present sequence represents a human OES antibody epitope.  
 CC  
 SQ Sequence 20 AA;  
 XX  
 XX  
 Query Match 31.4%; Score 33; DB 7; Length 20;  
 Best Local Similarity 62.5%; Pred. No. 7e+02;  
 Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;  
 QY 13 VGBEGVLS 20  
 Db :||:|:  
 3 IGBDGILS 10  
 XX  
 RESULT 30  
 ADF09099  
 ID ADF09099 standard; peptide; 20 AA.  
 XX  
 AC ADF09099;  
 XX  
 DT 12-FEB-2004 (first entry)  
 XX  
 DE Secreted ovarian carcinoma antigen seqid 603.  
 XX  
 KW gene therapy; protein therapy; vaccine; antibody inhibition;  
 KW breast cancer; restorative therapy; diagnostic agent; immunoassay;  
 KW secreted ovarian carcinoma antigen.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2003124140-A1.  
 XX  
 PD 03-JUL-2003.  
 XX

PF 17-JUL-2002; 2002US-00198053.  
 XX  
 PR 17-DEC-1998; 98US-00215681.  
 PR 17-DEC-1998; 98US-00216003.  
 PR 23-JUN-1999; 99US-00338933.  
 PR 24-SEP-1999; 99US-00404879.  
 PR 17-JUL-2000; 2000US-00617747.  
 PR 10-AUG-2000; 2000US-00635801.  
 PR 20-SEP-2000; 2000US-00667857.  
 PR 04-APR-2001; 2001US-00827271.  
 PR 18-JUN-2001; 2001US-00884441.  
 PR 17-JUL-2001; 2001US-00907969.  
 XX  
 PA (CORI-) CORIXA CORP.  
 XX  
 PI Bangur CS, Retter MW, Fanger GR, Hill P;  
 PI WPI, 2003-897152/82.  
 XX  
 DR WPI, 2003-897152/82.  
 XX  
 PT Oncogenic nucleic acids useful for the prevention, diagnosis and  
 PT treatment of breast cancer.  
 XX  
 PS Claim 2; SEQ ID NO 603; 399bp; English.  
 XX  
 CC The invention describes nucleic acids (I) and the polypeptides (II) they  
 CC encode. The nucleic acids (I) may be used for preventing, diagnosing and  
 CC treating diseases related to their aberrant expression i.e. breast  
 CC cancers. For example, (I) and (II) may be used to treat disorders  
 CC associated with decreased expression by rectifying mutations or deletions  
 CC in a patient's genome that affect the activity of (II) by expressing  
 CC inactive proteins or to supplement the patient's own production of (II).  
 CC Additionally, (I) may be used to produce (II), by inserting (I) into a  
 CC host cell and culturing the cell to express the protein (II). (I) and its  
 CC complementary sequences may also be used as DNA probes in diagnostic  
 CC assays to detect and quantitate the presence of similar nucleic acids in  
 CC samples. The host cell may also be used as antigens in the production of  
 CC antibodies against (II) and in assays to identify modulators of (II)'s  
 CC expression and activity. The anti-(II) antibodies, agonists and  
 CC antagonists may be used to regulate expression and activity and as  
 CC diagnostic agents for detecting the presence of (II) in samples (e.g. by  
 CC immunoassay). This sequence represents a secreted ovarian carcinoma  
 CC antigen.  
 CC  
 SQ Sequence 20 AA;  
 XX  
 XX  
 Query Match 31.4%; Score 33; DB 7; Length 20;  
 Best Local Similarity 62.5%; Pred. No. 7e+02;  
 Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;  
 QY 13 VGBEGVLS 20  
 Db :||:|:  
 3 IGBDGILS 10  
 XX  
 RESULT 31  
 ADF08893  
 ID ADF08893 standard; peptide; 20 AA.  
 XX  
 AC ADF08893;  
 XX  
 DT 12-FEB-2004 (first entry)  
 XX  
 DE Secreted ovarian carcinoma antigen seqid 397.  
 XX  
 KW gene therapy; protein therapy; vaccine; antibody inhibition;  
 KW breast cancer; restorative therapy; diagnostic agent; immunoassay;  
 KW secreted ovarian carcinoma antigen.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2003124140-A1.  
 XX

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PD 03-JUL-2003.
XX
XX 17-JUL-2002; 2002US-00198053.
XX
XX 17-DEC-1998; 98US-00215681.
XX 17-DEC-1998; 98US-00216003.
XX 23-JUN-1999; 99US-00338933.
XX 24-SEP-1999; 99US-00404879.
XX 17-JUL-2000; 2000US-00617747.
XX 10-AUG-2000; 2000US-00636801.
XX 20-SEP-2000; 2000US-00667857.
XX 04-APR-2001; 2001US-00827271.
XX 18-JUN-2001; 2001US-00884441.
XX 17-JUL-2001; 2001US-00907969.
XX
XX (CORI-) CORIXA CORP.
XX
XX Bangur CS, Reltter MW, Fanger GR, Hall P;
XX WPI; 2003-897152/82.
XX
XX Oncogenic nucleic acids useful for the prevention, diagnosis and
XX treatment of breast cancer.
XX
XX Example 3; SEQ ID NO 397; 399pp; English.
XX
XX The invention describes nucleic acids (I) and the polypeptides (II) they
XX encode. The nucleic acids (I) may be used for preventing, diagnosing and
XX treating diseases related to their aberrant expression i.e. breast
XX cancers. For example, (I) and (II) may be used to treat disorders
XX associated with decreased expression by rectifying mutations or deletions
XX in a patient's genome that affect the activity of (II) by expressing
XX inactive proteins or to supplement the patient's own production of (II).
XX Additionally, (I) may be used to produce (II), by inserting (I) into a
XX host cell and culturing the cell to express the protein (II). (I) And its
XX complementary sequences may also be used as DNA probes in diagnostic
XX assays to detect and quantitate the presence of similar nucleic acids in
XX samples, and therefore which patients may be in need of restorative
XX therapy. The host cell may also be used as antigens in the production of
XX antibodies against (II) and in assays to identify modulators of (II)'s
XX expression and activity. The anti-(II) antibodies, agonists and as
XX antagonists may be used to regulate expression and activity and as
XX diagnostic agents for detecting the presence of (II) in samples (e.g. by
XX immunoassay). This sequence represents a secreted ovarian carcinoma
XX antigen.
XX
XX Sequence 20 AA;
XX
XX Query Match 31.4%; Score 33; DB 7; Length 20;
XX Best Local Similarity 62.5%; Pred. No. 7e+02;
XX Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 13 VGEBCVLS 20
XX :||:|:|
XX DB 3 IGSDGILS 10
XX
XX RESULT 32
XX ADG46180
XX ID ADG46180 standard; peptide; 20 AA.
XX
XX AC ADG46180;
XX
XX DT 26-FEB-2004 (first entry)
XX
XX DE O8E antibody epitope #4.
XX
XX KW Human; ovarian carcinoma; O8E; ovarian cancer; secreted tumour antigen;
XX cytostatic; O772P; epitope.
XX
XX OS Homo sapiens.
XX
XX PN US2003165504-A1.

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XX
XX 04-SEP-2003.
XX
XX 04-APR-2001; 2001US-00827271.
XX
XX 17-DEC-1998; 98US-00215681.
XX 17-DEC-1998; 98US-00216003.
XX 23-JUN-1999; 99US-00338933.
XX 24-SEP-1999; 99US-00404879.
XX 17-JUL-2000; 2000US-00617747.
XX 10-AUG-2000; 2000US-00636801.
XX 20-SEP-2000; 2000US-00667857.
XX
XX (RETT/) RETTER M W.
XX (FANG/) FANGER G R.
XX
XX Reltter MW, Fanger GR;
XX WPI; 2003-898035/82.
XX
XX New isolated O8E or O772P polypeptides, useful for diagnosing,
XX preventing, treating and monitoring cancer, e.g. ovarian cancer,
XX stimulating the immune response in patient.
XX
XX Example 3; SEQ ID NO 397; 290pp; English.
XX
XX The invention relates to human ovarian carcinoma polypeptides, designated
XX O8E or O772P, and the polynucleotides encoding them. The invention also
XX relates to methods for inhibiting the development of cancer, e.g. ovarian
XX cancer in a patient, methods for stimulating and/or expanding T cells and
XX methods for identifying secreted tumour antigens. The polypeptides,
XX compositions, antibodies to the polypeptides and methods are useful for
XX diagnosing, preventing, treating and monitoring cancer, e.g. ovarian
XX cancer. The composition is particularly useful for stimulating an immune
XX response in patient. This sequence represents an O8E antibody epitope of
XX the invention.
XX
XX Sequence 20 AA;
XX
XX Query Match 31.4%; Score 33; DB 7; Length 20;
XX Best Local Similarity 62.5%; Pred. No. 7e+02;
XX Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 13 VGEBCVLS 20
XX :||:|:|
XX DB 3 IGSDGILS 10
XX
XX RESULT 33
XX ADK40495
XX ID ADK40495 standard; peptide; 20 AA.
XX
XX AC ADK40495;
XX
XX DT 06-MAY-2004 (first entry)
XX
XX DE KDR & VEGF/KDR complex binding peptide of a Lin20 peptide library ID146.
XX
XX KW endothelial cell; vacular endothelial growth factor; VEGF;
XX receptor tyrosine kinase; VEGF-2; kinase domain region; KDR;
XX foetal liver kinase-1; Flk-1; VEGF/KDR complex; angiogenesis;
XX neoplastic tumour; radiotherapeutic; malaria; HIV; SIV infection;
XX simian haemorrhagic fever virus;
XX enterohaemorrhagic Escherichia coli infection; protozoacidal; anti-HIV;
XX virucidal; antibacterial; cytostatic.
XX
XX OS Synthetic.
XX
XX PN WO2003074005-A2.
XX
XX PD 12-SEP-2003.
XX
XX PF 03-MAR-2003; 2003WO-US006731.

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PF 02-JUN-2004; 2004US-00860790.
XX
PR 17-DEC-1998; 98US-00216003.
PR 23-JUN-1999; 99US-00338933.
PR 24-SEP-1999; 99US-00404879.
PR 17-JUL-2000; 2000US-00617747.
PR 10-AUG-2000; 2000US-00636801.
PR 20-SEP-2000; 2000US-00667857.
PR 04-APR-2001; 2001US-00827271.
PR 18-JUN-2001; 2001US-00884441.
PR 17-JUL-2001; 2001US-00907969.
PR 17-JUL-2002; 2002US-00198053.
XX
PA (CORI-) CORIXA CORP.
XX
PI Bangur CS, Retter MW, Fanger GR, Hill P;
XX
DR WPI; 2005-151645/16.
XX
PT New ovarian carcinoma polynucleotides, preferably cDNAs, useful for
PT diagnosing, preventing and treating diseases, such as ovarian cancer, and
PT for eliciting humoral and/or cellular immune response.
XX
PS Disclosure; SEQ ID NO 397; 398bp; English.
XX
CC The invention relates to an isolated polynucleotide comprising a sequence
CC of, a sequence hybridizing under highly stringent conditions to, or
CC having at least 75, or 90% identity to a 849 or 1399 bp, fully defined in
CC the specification, its complement or degenerate variants, or a sequence
CC of at least 20 contiguous residues of the 849 or 1399 bp sequence. The
CC polynucleotides and polypeptides are useful for diagnosing, preventing
CC and treating diseases, such as ovarian cancer, and for eliciting humoral
CC and/or cellular immune response. This sequence corresponds to an ovarian
CC carcinoma antigen peptide of the invention.
XX
SQ Sequence 20 AA;

Query Match          31.4%; Score 33; DB 9; Length 20;
Best Local Similarity 62.5%; Pred. No. 7e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 13 VGEQGVLS 20
   :||:|:|
Db 3 IGEDGILS 10

RESULT 36
ADX17982
ID ADX17982 standard; peptide; 20 AA.
XX
AC ADX17982;
XX
DT 21-APR-2005 (first entry)
XX
DE Human ovarian carcinoma antigen O8B peptide #4.
XX
KW diagnosis; cytostatic; immunostimulant; gene therapy; tumor;
KW ovarian tumor; cancer; carcinoma; antigen.
XX
OS Homo sapiens.
XX
PN US2005031634-A1.
XX
PD 10-FEB-2005.
XX
PF 02-JUN-2004; 2004US-00860790.
XX
PR 17-DEC-1998; 98US-00216003.
PR 23-JUN-1999; 99US-00338933.
PR 24-SEP-1999; 99US-00404879.
PR 17-JUL-2000; 2000US-00617747.
PR 10-AUG-2000; 2000US-00636801.
PR 20-SEP-2000; 2000US-00667857.
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PR 04-APR-2001; 2001US-00827271.
PR 18-JUN-2001; 2001US-00884441.
PR 17-JUL-2001; 2001US-00907969.
PR 17-JUL-2002; 2002US-00198053.
XX
PA (CORI-) CORIXA CORP.
XX
PI Bangur CS, Retter MW, Fanger GR, Hill P;
XX
DR WPI; 2005-151645/16.
XX
PT New ovarian carcinoma polynucleotides, preferably cDNAs, useful for
PT diagnosing, preventing and treating diseases, such as ovarian cancer, and
PT for eliciting humoral and/or cellular immune response.
XX
PS Claim 2; SEQ ID NO 603; 398bp; English.
XX
CC The invention relates to an isolated polynucleotide comprising a sequence
CC of, a sequence hybridizing under highly stringent conditions to, or
CC having at least 75, or 90% identity to a 849 or 1399 bp, fully defined in
CC the specification, its complement or degenerate variants, or a sequence
CC of at least 20 contiguous residues of the 849 or 1399 bp sequence. The
CC polynucleotides and polypeptides are useful for diagnosing, preventing
CC and treating diseases, such as ovarian cancer, and for eliciting humoral
CC and/or cellular immune response. This sequence corresponds to an ovarian
CC carcinoma antigen peptide of the invention.
XX
SQ Sequence 20 AA;

Query Match          31.4%; Score 33; DB 9; Length 20;
Best Local Similarity 62.5%; Pred. No. 7e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 13 VGEQGVLS 20
   :||:|:|
Db 3 IGEDGILS 10

RESULT 37
AAO14949
ID AAO14949 standard; peptide; 10 AA.
XX
AC AAO14949;
XX
DT 06-AUG-2002 (first entry)
XX
DE Survivin-like protein-related peptide.
XX
KW Survivin-like protein; diagnosis; screening; cancer;
KW apoptosis abnormality; gene therapy.
XX
OS Unidentified.
XX
PN WO200233071-A1.
XX
PD 25-APR-2002.
XX
PF 16-OCT-2001; 2001WO-0P009071.
XX
PR 17-OCT-2000; 2000JP-00316721.
PR 20-DEC-2000; 2000JP-00386809.
XX
PA (TAKE ) TAKEDA CHEM IND LTD.
XX
PI Tanaka H, Kaleda I;
XX
DR WPI; 2002-435536/46.
XX
PT Baculovirus TAP repeat domain or RING-finger domain-containing survivin-
PT like polypeptides and encoded DNAs, applicable in diagnosis and screening
PT compounds for treating various cancers and apoptosis abnormality.
XX
PS Example 4; Page 91; 136pp; Japanese.
```



XX The invention comprises the amino acid and coding sequences of survivin-  
 CC like proteins. The survivin-like DNA and protein sequences are useful in  
 CC diagnostics and screening compounds for treating various cancers and  
 CC apoptosis abnormally, including gene therapy. The present amino acid  
 CC sequence was used in an example of the invention  
 XX

Sequence 10 AA;  
 SQ

Query Match 30.5%; Score 32; DB 5; Length 10;  
 Best Local Similarity 50.0%; Pred. No. 4.7e+02;  
 Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 DPAKGMSPG 10  
 DB 1 BRGAGPPPG 10

RESULT 38  
 ADS92606  
 ID ADS92606 standard; peptide; 10 AA.  
 AC ADS92606;  
 XX  
 DT 02-DEC-2004 (first entry)  
 XX  
 DE Platelet aggregation inhibition method-related mutated gp38p peptide #3.  
 XX  
 KW platelet aggregation inhibition; gp44-expressing; screening;  
 KW colon cancer; rectal cancer; testicular cancer; seminoma;  
 KW flat-epithelial carcinoma; cancer metastasis; pulmonary thrombosis;  
 KW cerebral infarction; myocardial infarction; arteriosclerosis;  
 KW bleeding tendency; blood clotting disorder; haemophilia; uremia;  
 KW chronic myeloproliferative disorder; gp38p; mutant; mutein.  
 XX  
 OS Synthetic.  
 OS Unidentified.  
 XX  
 PN WO2004033681-A1.  
 XX  
 PD 22-APR-2004.  
 XX  
 PF 09-OCT-2003; 2003WO-JP012996.  
 XX  
 PR 11-OCT-2002; 2002JP-00298400.  
 PR 08-MAY-2003; 2003JP-00129954.  
 XX  
 PA (SANY ) SANKYO CO LTD.  
 XX  
 PI Teunuo T, Fujita N, Osawa M, Kato Y,  
 XX  
 DR WPI; 2004-330453/30.  
 XX  
 PT Substances with activity of promoting or inhibiting platelet aggregation  
 PT screened by using factor gp4, applicable in treatment of its  
 PT accompanying diseases like colon cancer, myocardial infarction and  
 PT arteriosclerosis.  
 XX  
 PS Example 12; SEQ ID NO 46; 219pp; Japanese.  
 XX  
 CC The invention comprises a method for screening substances for promoting  
 CC or inhibiting platelet aggregation. The method involves: culturing gp44-  
 CC expressing cells in the presence/absence of a test substance, detecting  
 CC expression of mRNAs, and measuring the expression doses of the detected  
 CC mRNAs for comparison and selection. The method of the invention is useful  
 CC in the development of drugs for the treatment of: colon cancer, rectal  
 CC cancer, testicular cancer, seminoma, flat-epithelial carcinoma, cancer  
 CC metastasis, pulmonary thrombosis, cerebral infarction, myocardial  
 CC infarction, arteriosclerosis, bleeding tendency, blood clotting disorder,  
 CC haemophilia, uremia and chronic myeloproliferative disorder. The present  
 CC amino acid sequence represents a mutated gp38p peptide that was used in  
 CC an example of the invention.  
 XX

SQ Sequence 10 AA;  
 CC

Query Match 30.5%; Score 32; DB 8; Length 10;  
 Best Local Similarity 83.3%; Pred. No. 4.7e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 5 GMSPPG 10  
 DB 2 GMAAPG 7

RESULT 39  
 ADB49200  
 ID ADB49200 standard; peptide; 15 AA.  
 AC ADB49200;  
 XX  
 DT 04-DEC-2003 (first entry)  
 XX  
 DE Biotinylated peptide recognition unit #1.  
 XX  
 KW WW domain; drug candidate screening; drug discovery; drug modification;  
 KW drug refinement; immunogen; WW binding protein; WW domain;  
 KW peptide recognition unit.  
 XX  
 OS Synthetic.  
 XX  
 PN US2003077577-A1.  
 XX  
 PD 24-APR-2003.  
 XX  
 PF 28-JUN-2002; 2002US-00185050.  
 XX  
 PR 03-APR-1996; 96US-00630916.  
 PR 03-APR-1997; 97US-00826516.  
 XX  
 PA (PIRO/) PIROZZI G.  
 PA (KAYB/) KAY B K.  
 PA (FOWL/) FOWLKES D M.  
 XX  
 PI Pirozzi G, Kay BK, Fowlkes DM,  
 XX  
 DR WPI; 2003-635075/60.  
 XX  
 PT Novel purified polypeptide comprising WW domain, useful for drug  
 PT discovery, modification and refinement, for discovering polypeptides  
 PT involved in pharmacological activities, or as an immunogen to generate  
 PT antibodies.  
 XX  
 PS Example; Page 22; 133pp; English.  
 XX  
 CC The invention describes a purified polypeptide (I) comprising a WW domain  
 CC which has a sequence (S1) selected from 11 sequences fully defined in the  
 CC specification, a sequence (S2) selected from 48 sequences fully defined  
 CC in the specification or a sequence (S3) comprising 683, 906, 224 or 725  
 CC amino acids fully defined in the specification. (I) is useful for  
 CC screening a potential drug candidate, by allowing (I) to come into  
 CC contact with at least one recognition unit having a selective affinity  
 CC for the WW domain in (I), in the presence of an amount of a potential  
 CC drug candidate, such that (I) and the recognition unit are capable of  
 CC interacting when brought into contact with one another in the absence of  
 CC the drug candidate, and determining the effect, if any, of the presence  
 CC of the amount of the drug candidate on the interaction of (I) with the  
 CC recognition unit. (I) is useful for drug discovery, modification and  
 CC refinement, for discovering polypeptides involved in pharmacological  
 CC activities, or as an immunogen to generate antibodies. This is the amino  
 CC acid sequence of a peptide recognition unit used to screen cDNA  
 CC expression libraries for WW domain binding proteins.  
 CC  
 SQ Sequence 15 AA;  
 CC

Query Match 30.5%; Score 32; DB 7; Length 15;  
 Best Local Similarity 46.2%; Pred. No. 7.3e+02;  
 XX

Matches 6; Conservative 1; Mismatches 6; Indels 0; Gaps 0;  
QY 2 PAKGMSPPGFIVG 14  
DB 2 PPHGTTPPPYIVG 14

RESULT 40  
AAU10333  
ID AAU10333 standard; peptide; 16 AA.

AC AAU10333;

DT 14-FEB-2002 (first entry)

DE Human PROST 03 immunogenic fragment, Pep8.

KW Human; PROST 03; metastasis; prostate cancer; tumour; immune response;  
KW cytostatic; vaccine; immunogenic.

OS Homo sapiens.

PN WO200181577-A2.

PD 01-NOV-2001.

PF 26-APR-2001; 2001WO-US013323.

PR 27-APR-2000; 2000US-0200065P.

PR 20-APR-2001; 2001US-00838785.

PA (SCHD) SCHERING AG.

PI Lau T, Lin RJ, Parkes D, Parry G, Schneider DW, Streibbrecher R;  
PI Van Heut PT, Wu J;

DR WPI; 2002-041404/05.

PT Novel PROST 03 polypeptides and polynucleotides useful in research,  
PT diagnosis and therapeutic applications, particularly for use in cancer  
PT therapeutics.

PS Claim 18; Page 50; 77pp; English.

XX The invention relates to an isolated PROST 03 polypeptide (I) and to the  
CC polynucleotide (II) encoding PROST 03. Fragments of (I) were used to  
CC generate antibodies (III) to PROST 03. (III) is useful for selectively  
CC destroying a cell expressing (I), and for treating a disease-state  
CC associated with expression of PROST 03 in a human patient. (III) is  
CC useful for diagnosing metastasis associated with (I), in a subject. (I)  
CC is also useful for diagnosing and treating diseases of cell proliferation  
CC such as prostate cancer. (I) is also useful for generating antibodies to  
CC PROST 03. (III) is useful in detecting the levels of PROST 03  
CC polypeptides in cells and tissues, and in targeting drugs to primary and  
CC metastatic tumours. (I) is also useful for stimulating immune response to  
CC PROST 03 containing cells. (II) is useful in diagnostic assays for  
CC detecting the levels of polynucleotides encoding PROST 03 in cells and  
CC tissues. (II) is useful as DNA probes, as targets for antisense and  
CC ribozyme therapy, and as templates for the production of antisense  
CC polynucleotides. (I) and (II) are useful in research, biological,  
CC clinical and therapeutic purposes. The present sequence represents the  
CC amino acid sequence of human PROST 03 immunogenic fragment Pep8, used to  
CC generate anti-PROST 03 antibodies  
XX

SO Sequence 16 AA;

Query Match 30.5%; Score 32; DB 5; Length 16;  
Best Local Similarity 55.6%; Pred. No. 7.9e+02;  
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 DPAKGMSP 9  
DB 3 BPBAGLSAP 11

RESULT 41  
AEC13757  
ID AEC13757 standard; peptide; 16 AA.  
XX  
AC AEC13757;

DT 20-OCT-2005 (first entry)

DE Staphylococcus aureus lysyl-tRNA synthetase peptide.

KW protein purification; antibacterial; antimicrobial; infection;  
KW drug screening; lysyl-tRNA synthetase.

OS Staphylococcus aureus.

PN US2005181464-A1.

PD 18-AUG-2005.

PF 29-SEP-2004; 2004US-00953901.

PR 04-APR-2002; 2002US-0369819P.

PR 04-APR-2002; 2002US-0369826P.

PR 04-APR-2002; 2002US-0369831P.

PR 04-APR-2002; 2002US-0370060P.

PR 08-APR-2002; 2002US-0370681P.

PR 08-APR-2002; 2002US-0370805P.

PR 08-APR-2002; 2002US-0370852P.

PR 09-APR-2002; 2002US-0370959P.

PR 09-APR-2002; 2002US-0370979P.

PR 09-APR-2002; 2002US-0371008P.

PR 09-APR-2002; 2002US-0371014P.

PR 09-APR-2002; 2002US-0371025P.

PR 09-APR-2002; 2002US-0371064P.

PR 09-APR-2002; 2002US-0371065P.

PR 09-APR-2002; 2002US-0371094P.

PR 09-APR-2002; 2002US-0371114P.

PR 09-APR-2002; 2002US-0371180P.

PR 09-APR-2002; 2002US-0371189P.

PR 31-MAY-2002; 2002US-0384634P.

PR 31-MAY-2002; 2002US-0385157P.

PR 04-JUN-2002; 2002US-0385542P.

PR 04-JUN-2002; 2002US-0385611P.

PR 04-JUN-2002; 2002US-0385747P.

PR 04-JUN-2002; 2002US-0385750P.

PR 04-JUN-2002; 2002US-0385752P.

PR 04-JUN-2002; 2002US-0385773P.

PR 04-JUN-2002; 2002US-0385780P.

PR 04-JUN-2002; 2002US-0385785P.

PR 04-JUN-2002; 2002US-0385797P.

PR 05-JUN-2002; 2002US-0385962P.

PR 05-JUN-2002; 2002US-0385962P.

PR 05-JUN-2002; 2002US-0386022P.

PR 05-JUN-2002; 2002US-0386024P.

PR 05-JUN-2002; 2002US-0386027P.

PR 05-JUN-2002; 2002US-0386141P.

PR 05-JUN-2002; 2002US-0386350P.

PR 05-JUN-2002; 2002US-0386586P.

PR 06-JUN-2002; 2002US-0386368P.

PR 06-JUN-2002; 2002US-0386369P.

PR 06-JUN-2002; 2002US-0386436P.

PR 06-JUN-2002; 2002US-0386441P.

PR 06-JUN-2002; 2002US-0386528P.

PR 06-JUN-2002; 2002US-0386573P.

PR 06-JUN-2002; 2002US-0386834P.

PR 31-JUL-2002; 2002US-0399839P.

PR 31-JUL-2002; 2002US-0399861P.

PR 31-JUL-2002; 2002US-0399869P.

PR 31-JUL-2002; 2002US-0399970P.

PR 31-JUL-2002; 2002US-0399983P.

PR 31-JUL-2002; 2002US-0399984P.  
 PR 31-JUL-2002; 2002US-0399985P.  
 PR 01-AUG-2002; 2002US-0400154P.  
 PR 01-AUG-2002; 2002US-0400230P.  
 PR 01-AUG-2002; 2002US-0400268P.  
 PR 01-AUG-2002; 2002US-0400363P.  
 PR 01-AUG-2002; 2002US-0400365P.  
 PR 01-AUG-2002; 2002US-0400374P.  
 PR 01-AUG-2002; 2002US-0400380P.  
 PR 01-AUG-2002; 2002US-0400433P.  
 PR 01-AUG-2002; 2002US-0400434P.  
 PR 01-AUG-2002; 2002US-0400436P.  
 PR 01-AUG-2002; 2002US-0400442P.  
 PR 01-AUG-2002; 2002US-0400463P.  
 PR 04-APR-2003; 2003MO-CA000465.  
 PR 08-APR-2003; 2003MO-CA000482.  
 PR 08-APR-2003; 2003MO-CA000483.  
 PR 02-JUN-2003; 2003MO-CA000786.  
 PA (AFPI-) AFINITUM PHARM INC.  
 XX  
 PI Edwards A, Dharami A, Vedadi M, Alam MZ, Arrowsmith C, Awrey DE,  
 PI Beattie B, Busadziya K, Clarke T, Domagala M, Houston S,  
 PI Kanagarajah D, Li Q, Mansoury K, McDonald M, Nethery-Brooks K, Ng I,  
 PI Ouyang H, Richards D, Vallee F, Virag C,  
 XX  
 DR WPI; 2005-628190/64.  
 XX  
 PT Novel crystallized, recombinant bacterial polypeptide, useful as targets  
 PT for pathogenic bacteria such as *Helicobacter pylori*, *Staphylococcus*  
 PT aureus, for detecting pathogenic species in biological sample, and in  
 PT drug designing.  
 XX  
 XX Example 1; Fig 8; 637pp; English.  
 XX  
 CC The invention relates to a composition (I) comprising purified  
 CC polypeptides from bacteria. Also described: (1) a crystallized,  
 CC recombinant polypeptide comprising an amino acid sequence of (I), where  
 CC the polypeptide is in crystal form; (2) a crystallized complex comprising  
 CC the crystallized, recombinant polypeptide and a co-factor or a small  
 CC organic molecule, where the complex is in crystal form; and (3) a host  
 CC cell comprising a nucleic acid encoding a polypeptide of (I), where a  
 CC culture of the host cell produces at least about 1 mg of the polypeptide  
 CC per liter of culture and the polypeptide is at least about one-third  
 CC soluble as measured by gel electrophoresis. (I) can be used as a target  
 CC for pathogenic bacteria, useful for detecting the presence of a  
 CC pathogenic species in a biological sample. (I) is useful for monitoring  
 CC the effectiveness of anti-pathogenic treatments in an individual  
 CC suffering from a disease or disorder caused by a pathogenic bacteria.  
 CC such as infections. (I) is also useful in drug design and screening, for  
 CC identifying inhibitors of (I), for designing a potential compound that is  
 CC useful for treating or preventing pathogenic diseases or disorders, for  
 CC assessing the activity of small molecules and other modulators in in  
 CC vitro assay, and for developing antimicrobial agents. The present  
 CC sequence represents a *Staphylococcus aureus* lysyl-tRNA synthetase  
 CC peptide, which is used in an example from the present invention.  
 XX  
 XX Sequence 16 AA;  
 SQ  
 Query Match 30.5%; Score 32; DB 9; Length 16;  
 Best Local Similarity 70.0%; Pred. No. 7.9e+02;  
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

XX  
 DT 03-FEB-2003 (first entry)  
 XX  
 DE A. marginale Ana32 fragment.  
 XX  
 KM Ehrlichiae; Rickettsiae; pathogen; antimicrobial; vaccine;  
 KM immune response; Ana32.  
 XX  
 OS Anaplasma marginale.  
 XX  
 PN WO200283724-A1.  
 XX  
 PD 24-OCT-2002.  
 XX  
 PF 11-APR-2002; 2002MO-AU000468.  
 XX  
 PF 12-APR-2001; 2001AU-00004400.  
 PR 10-SEP-2001; 2001AU-00007597.  
 PR 01-MAR-2002; 2002AU-00000861.  
 XX  
 PA (COUN-) COUNCIL QUEENSLAND INST MEDICAL RES.  
 PA  
 XX  
 XX Riding GA, Hope MA, Willadsen P;  
 PI  
 DR WPI; 2003-093001/08.  
 XX  
 PT New vaccine, useful for the manufacture of a medicament for raising an  
 PT immune response against Ehrlichiae and/or Rickettsiae pathogens.  
 PT  
 PS Example 6; Page 45; 102pp; English.  
 XX  
 CC The invention relates to a novel vaccine comprising at least one  
 CC polypeptide which raises an immune response against Ehrlichiae and/or  
 CC Rickettsiae pathogens when administered to a subject. The vaccine of the  
 CC invention has antimicrobial activity. The vaccine is useful for the  
 CC manufacture of a medicament for raising an immune response against  
 CC Ehrlichiae and/or Rickettsiae pathogens or for treating or preventing  
 CC Ehrlichiae or Rickettsiae infection in a subject. The present sequence  
 CC represents a fragment of the A. marginale Ana32 polypeptide  
 XX  
 SQ Sequence 18 AA;  
 Query Match 30.5%; Score 32; DB 6; Length 18;  
 Best Local Similarity 50.0%; Pred. No. 8.9e+02;  
 Matches 9; Conservative 1; Mismatches 6; Indels 2; Gaps 1;  
 QY 2 PAKGSPPGPIVGBEVL 19  
 DB 3 PNVGSAAPG-VGABSEL 18  
 XX  
 XX  
 XX  
 DT 25-FEB-2002 (first entry)  
 DT  
 XX  
 DE M. tuberculosis Rv0284 protein immunogenic peptide P24.  
 XX  
 KM Tuberculosis; Tuberculoaetatic; antibacterial; vaccine; Rv0284; Rv0285;  
 KM Rv0455c; Rv0569; Rv1195; Rv1386; Rv3477; Rv3878; Rv3879; MT3106.1;  
 KM ORF13A; Rv0284ct; Mycobacterium bovis; Mycobacterium africanum;  
 KM BCG vaccine; immunogenic peptide.  
 XX  
 OS Mycobacterium tuberculosis.  
 XX  
 PN WO200179274-A2.  
 XX  
 PD 25-OCT-2001.  
 XX  
 PF 19-APR-2001; 2001WO-DK000276.  
 XX

XX 19-APR-2000; 2000DK-00000666.  
PR 21-FEB-2001; 2001DK-00000283.  
XX (STAT-) STATENS SERUM INST.

XX Agger EM, Andersen P, Okkels LMW, Wellingh K;  
XX WPI; 2002-061970/08.

PT New Mycobacterium tuberculosis antigens, useful for diagnosing  
PT tuberculosis, and as a vaccine for treating or preventing infections  
caused by species of tuberculosis complex.

PS Example 3; Page 96; 11pp; English.

XX The invention relates to a substantially pure polypeptide comprising an  
CC amino acid sequence selected from RV0284, RV0285, RV0455C, RV0569,  
CC RV1195, RV1386, RV3477, RV3878, RV3879C or MT3106.1 (also disclosed are  
CC ORP13A and RV0284Ct), or their immunogenic portion, nucleic acids  
CC encoding them and an amino acid sequence analogue having at least 70%  
CC sequence identity to the polypeptide and is immunogenic. The protein is  
CC useful in preparing a pharmaceutical composition for diagnosing  
CC tuberculosis and in preparing a vaccine against tuberculosis caused by  
CC virulent mycobacteria. The vaccine or immunogenic/ pharmaceutical  
CC composition can be used prophylactically in a subject not infected with a  
CC virulent mycobacterium, or therapeutically in a subject already infected  
CC with a virulent mycobacterium. The protein is useful for preventing,  
CC treating and detecting infections caused by species of tuberculosis  
CC complex (M. tuberculosis, M. bovis, M. africanum). The nucleic acids may  
CC be used for effecting in vivo expression of the antigen, and in  
CC diagnostic assays for detecting the presence of pathogenic organisms in a  
CC sample. The vaccine is an improvement of the living BCG vaccine presently  
CC available, where one or more copies of the DNA sequence encoding one or  
CC more polypeptide has been incorporated into the genome of the  
CC microorganism to allow the microorganism to express and secrete the  
CC polypeptide. Incorporation of more than one copy of a nucleotide sequence  
CC enhances the immune response. The present sequence represents an  
CC immunogenic peptide derived from an M. tuberculosis protein of the  
CC invention

XX SQ Sequence 20 AA;

Query Match 30.5%; Score 32; DB 5; Length 20;  
Best Local Similarity 50.0%; Pred. No. 1e+03;  
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 5 GMSPPGPIVG 14  
DB 9 GMSPPGPIVG 18

RESULT 44  
ADR40519  
ID ADR40519 standard; peptide; 20 AA.

AC ADR40519;

DT 06-MAY-2004 (first entry)

DE KDR & VEGF/KDR complex binding peptide of a Lin20 peptide library ID170.

XX endothelial cell; vascular endothelial growth factor; VEGF;  
XX receptor tyrosine kinase; VEGF-2; kinase domain region; KDR;  
XX foetal liver kinase-1; Flk-1; VEGF/KDR complex; angiogenesis;  
XX neoplastic tumour; radiotherapeutic; malaria; HIV; SIV infection;  
XX simian haemorrhagic fever virus;  
XX enterohaemorrhagic Escherichia coli infection; protozoacidal; anti-HIV;  
XX virucidal; antibacterial; cytostatic.

OS Synthetic.

XX WO2003074005-A2.

XX 12-SEP-2003.  
PD 03-MAR-2003; 2003WO-US006731.  
XX 01-MAR-2002; 2002US-0360851P.  
PR 15-JAN-2003; 2003US-0440411P.

XX (DYAX-) DYAX CORP.  
PA (BRAC) BRACCO INT BV.

PI Sato AK, Sexton DJ, Ladner RC, Dransfield DT, Swenson RE;  
PI Marinelli ER, Ramalingam K, Nunn AD, Von Wronski MA, Shrivastava A;  
PI Pochon S, Buesat P, Arbogast C, Pillai R, Fan H, Linder KE, Song B;  
PI Nanjappa P;

XX WPI; 2003-779009/73.

PT New polypeptide that binds to vascular endothelial growth factor receptor  
PT -2, useful for diagnosis and treatment of e.g. tumors, and its conjugates  
PT with therapeutic or imaging agents.

PS Claim 80; SEQ ID NO 170; 350pp; English.

XX This invention relates to novel peptides useful for detecting and  
CC targeting primary receptors on endothelial cells that bind vascular  
CC endothelial growth factor (VEGF). Specifically, it refers to detecting  
CC the receptor tyrosine kinase identified as VEGF-2, which is also known as  
CC kinase domain region (KDR) and foetal liver kinase-1 (Flk-1). The present  
CC invention describes the involvement of the VEGF/KDR complex as important  
CC in angiogenesis, and that VEGF/KDR complex binding or KDR binding  
CC polypeptides can be used for imaging neoplastic tumours. Furthermore,  
CC these compositions are useful for targeting radiotherapeutics to specific  
CC sites for treating diseases associated with KDR activation, which include  
CC malaria, HIV, SIV infection, simian haemorrhagic fever virus and  
CC enterohaemorrhagic Escherichia coli infection. Accordingly, these  
CC compositions exhibit various activities including protozoacidal, anti-  
CC HIV, virucidal, antibacterial and cytostatic. This peptide sequence is a  
CC high affinity binding peptide of KDR and the VEGF/KDR complex, part of  
CC the Lin20 peptide library of the invention.

XX SQ Sequence 20 AA;

Query Match 30.5%; Score 32; DB 7; Length 20;  
Best Local Similarity 50.0%; Pred. No. 1e+03;  
Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 8 PPGFVSGEVL 19  
DB 2 PPGFVSGEVL 13

RESULT 45  
ADR40737  
ID ADR40737 standard; peptide; 20 AA.

AC ADR40737;

DT 21-OCT-2004 (first entry)

DE KDR/ VEGF binding peptide of the secondary linear Lin20 library Seq 170.

XX kinase domain region; KDR; vascular endothelial growth factor; VEGF;  
XX VEGF receptor 2; VEGFR2; foetal liver kinase 1; Flk-1; angiogenesis;  
XX neoplastic tumour; malaria; HIV infection; SIV infection;  
XX simian haemorrhagic fever virus infection;  
XX enterohaemorrhagic Escherichia coli infection; cytostatic;  
XX antiangiogenic; antimalarial; anti-HIV; virucidal; antibacterial;  
XX Lin20 library.

OS Synthetic.

XX WO2004065621-A1.

XX 05-AUG-2004.  
 PD  
 XX  
 PF 11-SEP-2003; 2003MO-US028787.  
 PR 15-JAN-2003; 2003US-0440411P.  
 PR 03-MAR-2003; 2003US-00382082.  
 PR 03-MAR-2003; 2003MO-US006731.  
 XX  
 PA (DYAX-) DYAX CORP.  
 PA (BRAC) BRACCO INT BV.  
 XX  
 PI Sato AK, Sexton DJ, Dransfield DT, Ladner RC, Arhogaast C;  
 PI Buseat P, Fan H, Khurana S, Linder KE, Martinelli ER, Nanjappa P;  
 PI Nunn A, Pillai R, Pochon S, Ramalingam K, Shrivastava A, Song B;  
 PI Swenson RE, Von Wronski MA;  
 XX  
 DR WPI, 2004-580734/56.  
 XX  
 PT Novel isolated polypeptide having ability to bind to kinase domain region  
 PT or vascular endothelial growth factor/kinase domain region complex,  
 PT useful in inhibiting vascular endothelial growth factor activation of  
 PT kinase domain region.  
 XX  
 PS Claim 12; SEQ ID NO 170; 470bp; English.  
 XX  
 CC This invention relates to novel isolated peptides that can bind to a  
 CC kinase domain region (KDR) or vascular endothelial growth factor  
 CC (VEGF)/KDR complex. Specifically, it refers to polypeptides, peptide  
 CC dimers and multimeric complexes that bind with high affinity to KDR (also  
 CC known as the VEGF receptor 2 (VEGFR2) and foetal liver kinase 1 (Flk-1))  
 CC or the VEGF/KDR complex, and as such due to the involvement of VEGF and  
 CC KDR in angiogenesis these binding peptides can be used for imaging  
 CC important sites of angiogenesis, as well as in targeting therapeutics to  
 CC such sites. The present invention describes these peptides as useful for  
 CC promoting or inhibiting angiogenesis and pathogenic conditions associated  
 CC thereof such as neoplastic tumours. Furthermore, these binding peptides  
 CC are useful for treating malaria, HIV infection, SIV infection, simian  
 CC haemorrhagic fever virus infection and enterohaemorrhagic Escherichia  
 CC coli infection. Accordingly, they exhibit cytostatic, antiangiogenic,  
 CC antimalarial, anti-HIV, virucidal and antibacterial activities. In  
 CC particular, they inhibit VEGF activation of its receptor (i.e. KDR), and  
 CC enable efficient detection, imaging and localisation of activated  
 CC endothelial cells exhibiting upregulated KDR expression. This peptide  
 CC sequence is a high affinity KDR and VEGF/KDR binding peptide belonging to  
 CC the secondary linear Lin20 library of the invention.  
 XX  
 SQ Sequence 20 AA;  
 XX  
 Query Match 30.5%; Score 32; DB 8; Length 20;  
 Best Local Similarity 50.0%; Pred. No. 1e+03;  
 Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;  
 QY 8 PPGFIVGEGVL 19  
 |||||  
 :  
 Db 2 PPGFSYMBQAL 13  
 |||||  
 :  
 RESULT 46  
 ID AAM49486  
 AAM49486 standard; peptide; 9 AA.  
 AC  
 XX AAM49486;  
 XX  
 DT 05-JUN-1998 (first entry)  
 XX  
 DE Human leucocyte antigen DQ4 binding peptide #377.  
 XX  
 KM Human leucocyte antigen; HLA-DQ4; combinatorial library;  
 KW autoimmune disease; chronic articular rheumatism.  
 XX  
 OS Synthetic.  
 XX

PN JF08151396-A.  
 XX  
 PD 11-JUN-1996.  
 XX  
 XX 28-NOV-1994; 94JP-00292657.  
 PP  
 XX 28-NOV-1994; 94JP-00292657.  
 PR 28-NOV-1994; 94JP-00292657.  
 XX  
 PA (TEIJU) TEIJIN LTD.  
 XX  
 DR WPI; 1996-329479/33.  
 XX  
 PT HLA-binding oligopeptide and an immunoregulator contg it - used in the  
 PT treatment of autoimmune disease.  
 XX  
 PS Claim 4; Page 43; 61pp; Japanese.  
 XX  
 CC This peptide is an example of a peptide which binds to a human leucocyte  
 CC antigen HLA-DQ4 molecule. The peptide was isolated from a phagemid  
 CC combinatorial library comprising the sequence AAV0553, by screening with  
 CC an HLA-DQ4 molecule. The peptide is used for the treatment of autoimmune  
 CC disease, or especially for treatment of viral diseases  
 CC  
 XX  
 SQ Sequence 9 AA;  
 XX  
 Query Match 29.5%; Score 31; DB 2; Length 9;  
 Best Local Similarity 57.1%; Pred. No. 2e+06;  
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;  
 QY 7 SPFGIV 13  
 :|||:  
 :|||:  
 Db 1 APFGIV 7  
 :|||:  
 :|||:  
 RESULT 47  
 ID ADO68173  
 ADO68173 standard; peptide; 9 AA.  
 AC  
 XX ADO68173;  
 XX  
 DT 15-JUL-2004 (first entry)  
 XX  
 DE Human 213P1F11 HLA motif bearing epitope #4263.  
 XX  
 KM cytostatic; gene therapy; 213P1F11, 213P1F11 modulation; cancer;  
 KW transgenic; cytotoxic agent delivery; diagnostic agent delivery;  
 KW immune response; pancreatic cancer; rectal cancer; bladder cancer; human;  
 KW human leucocyte antigen; HLA; class I; class II; epitope; HLA motif;  
 KM HLA vaccine.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2004019915-A1.  
 XX  
 PD 29-JAN-2004.  
 XX  
 PF 01-APR-2002; 2002US-00114432.  
 PR 01-APR-2002; 2002US-00114432.  
 PR 01-APR-2002; 2002US-00114432.  
 XX  
 PA (CHAL/) CHALLITA-ETD P M.  
 PA (RAT/) RAITANO A B.  
 PA (FARI/) FARIS M.  
 PA (HUBS/) HUBERT R S.  
 PA (MORR/) MORRISON R K.  
 PA (GEWW/) GR W.  
 PA (JAKO/) JAKOBYITS A.  
 XX  
 PI Chalita-ETD PM, Raitano AB, Faris M, Hubert RS, Morrison RK;  
 PI Ge W, Jakobovits A;  
 XX  
 DR WPI, 2004-132240/13.  
 XX

PT New composition comprising a substance that modulates the status of  
PT 213P1F11, or a molecule that is modulated by 213P1F11, useful for  
PT detecting or treating cancer, e.g. pancreatic or rectal cancer.

XX Example 13; Page 130; 334pp; English.

XX The invention describes a composition comprising a substance that  
CC modulates the status of 213P1F11, or a molecule that is modulated by  
CC 213P1F11, where the status of the cell that expresses 213P1F11 is  
CC modulated and 213P1F11 is a gene overexpressed in many cancers. Also  
CC described are: a pharmaceutical composition comprising the composition  
CC cited above in a unit dose form; an antibody or its fragment; a non-human  
CC transgenic animal that produced the antibody; a hybridoma that produces  
CC the antibody; delivering a cytotoxic agent or a diagnostic agent to the  
CC cell that expresses 213P1F11; a polynucleotide that encodes the protein;  
CC inhibiting growth of cancer cells that expresses 213P1F11; generating a  
CC mammalian immune response; detecting the presence of 213P1F11-related  
CC protein or polynucleotide in a sample; and detecting the presence of  
CC cancer in an individual. The compositions, molecules and methods are  
CC useful for detecting and treating cancer, e.g. pancreatic or rectal  
CC cancer. This is the amino acid sequence of a human 213P1F11 peptide  
CC epitope bearing a human leukocyte antigen (HLA) class I or class II motif  
CC useful in the creation of an HLA vaccine to modulate 213P1F11.

CC Sequence 9 AA;

Query Match 29.5%; Score 31; DB 8; Length 9;  
Best Local Similarity 62.5%; Pred. No. 2e+06; 1; Indels 0; Gaps 0;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 10 GRTVGEEG 17  
||: ||:|  
DB 1 GFLKGEEDG 8

RESULT 48

ADO69472  
ID ADO69472 standard; peptide; 9 AA.

XX ADO69472;

DT 15-JUL-2004 (first entry)

DE Human 213P1F11 HLA motif bearing epitope #5562.

XX cytostatic; gene therapy; 213P1F11; 213P1F11 modulation; cancer;  
KW transgenic; cytotoxic agent delivery; diagnostic agent delivery;  
KW immune response; pancreatic cancer; rectal cancer; bladder cancer; human;  
KW human leukocyte antigen; HLA; class I; class II; epitope; HLA motif;  
KW HLA vaccine.

XX Homo sapiens.

XX US2004019915-A1.

PD 29-JAN-2004.

PF 01-APR-2002; 2002US-00114432.

PR 01-APR-2002; 2002US-00114432.

PA (CHAL/) CHALLITA-EID P M.

PA (RAIT/) RAITANO A B.

PA (FARI/) PARIS M.

PA (HUBB/) HUBERT R S.

PA (MORR/) MORRISON R K.

PA (GEWW/) GE W.

PA (JAKO/) JAKOBOVITS A.

PI Challita-Eid PM, Raitano AB, Paris M, Hubert RS, Morrison RK;

PI Ge W, Jakobovits A;

XX WPI; 2004-132240/13.

XX New composition comprising a substance that modulates the status of  
PT 213P1F11, or a molecule that is modulated by 213P1F11, useful for  
PT detecting or treating cancer, e.g. pancreatic or rectal cancer.

XX Example 13; Page 151; 334pp; English.

XX The invention describes a composition comprising a substance that  
CC modulates the status of 213P1F11, or a molecule that is modulated by  
CC 213P1F11, where the status of the cell that expresses 213P1F11 is  
CC modulated and 213P1F11 is a gene overexpressed in many cancers. Also  
CC described are: a pharmaceutical composition comprising the composition  
CC cited above in a unit dose form; an antibody or its fragment; a non-human  
CC transgenic animal that produced the antibody; a hybridoma that produces  
CC the antibody; delivering a cytotoxic agent or a diagnostic agent to the  
CC cell that expresses 213P1F11; a polynucleotide that encodes the protein;  
CC inhibiting growth of cancer cells that expresses 213P1F11; generating a  
CC mammalian immune response; detecting the presence of 213P1F11-related  
CC protein or polynucleotide in a sample; and detecting the presence of  
CC cancer in an individual. The compositions, molecules and methods are  
CC useful for detecting and treating cancer, e.g. pancreatic or rectal  
CC cancer. This is the amino acid sequence of a human 213P1F11 peptide  
CC epitope bearing a human leukocyte antigen (HLA) class I or class II motif  
CC useful in the creation of an HLA vaccine to modulate 213P1F11.

CC Sequence 9 AA;

Query Match 29.5%; Score 31; DB 8; Length 9;  
Best Local Similarity 62.5%; Pred. No. 2e+06; 1; Indels 0; Gaps 0;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 10 GRTVGEEG 17  
||: ||:|  
DB 2 GFLKGEEDG 9

RESULT 49

ADO69312  
ID ADO69312 standard; peptide; 9 AA.

XX ADO69312;

DT 15-JUL-2004 (first entry)

DE Human 213P1F11 HLA motif bearing epitope #5402.

XX cytostatic; gene therapy; 213P1F11; 213P1F11 modulation; cancer;  
KW transgenic; cytotoxic agent delivery; diagnostic agent delivery;  
KW immune response; pancreatic cancer; rectal cancer; bladder cancer; human;  
KW human leukocyte antigen; HLA; class I; class II; epitope; HLA motif;  
KW HLA vaccine.

XX Homo sapiens.

XX US2004019915-A1.

PD 29-JAN-2004.

PF 01-APR-2002; 2002US-00114432.

PR 01-APR-2002; 2002US-00114432.

PA (CHAL/) CHALLITA-EID P M.

PA (RAIT/) RAITANO A B.

PA (FARI/) PARIS M.

PA (HUBB/) HUBERT R S.

PA (MORR/) MORRISON R K.

PA (GEWW/) GE W.

PA (JAKO/) JAKOBOVITS A.

PI Challita-Eid PM, Raitano AB, Paris M, Hubert RS, Morrison RK;

PI Ge W, Jakobovits A;

XX

DR WPI, 2004-132240/13.  
XX  
PT New composition comprising a substance that modulates the status of  
XX 213P1F11, or a molecule that is modulated by 213P1F11, useful for  
XX detecting or treating cancer, e.g. pancreatic or rectal cancer.  
PS Example 13; Page 149; 334pp; English.

The invention describes a composition comprising a substance that  
modulates the status of 213P1F11, or a molecule that is modulated by  
213P1F11, where the status of the cell that expresses 213P1F11 is  
modulated and 213P1F11 is a gene overexpressed in many cancers. Also  
described are: a pharmaceutical composition comprising the composition  
cited above in a unit dose form; an antibody or its fragment; a non-human  
transgenic animal that produced the antibody; a hybridoma that produces  
the antibody; delivering a cytotoxic agent or a diagnostic agent to the  
cell that expresses 213P1F11; a polynucleotide that encodes the protein;  
inhibiting growth of cancer cells that express 213P1F11; generating a  
mammalian immune response; detecting the presence of 213P1F11-related  
protein or polynucleotide in a sample; and detecting the presence of  
cancer in an individual. The compositions, molecules and methods are  
useful for detecting and treating cancer, e.g. pancreatic or rectal  
cancer. This is the amino acid sequence of a human 213P1F11 peptide  
epitope bearing a human leukocyte antigen (HLA) class I or class II motif  
useful in the creation of an HLA vaccine to modulate 213P1F11.

Sequence 9 AA;

Query Match	29.5%	Score 31	DB 8	Length 9
Best Local Similarity	62.5%	Pred. No. 26+06		
Matches	5	Conservative	2	Mismatches 1
				Indels 0
				Gaps 0
QY	10	GFIVGEEG	17	
		:    :		
Db	2	GPLKGEDG	9	

RESULT 50  
ADO69700  
ID ADO69700 standard; peptide; 9 AA.

AC	ADO69700;
XX	
DT	15-JUL-2004 (first entry)

DE Human 213P1F11 HLA motif bearing epitope #5790.

KM cysoarectic; gene therapy; 231p11; 231p11 modulation; cancer;  
KM transgenic; cytotoxic agent delivery; diagnostic agent delivery;  
KM immune response; pancreatic cancer; rectal cancer; bladder cancer;  
KM human leukocyte antigen; HLA; class I; class II; epitope; HLA motif;  
KM HLA vaccine.

03 Homo sapiens.

PN US2004019915-A1.

PD 29-JAN-2004

PF 01-APR-2002; 2002US-00114432.

PR 01-APR-2002; 2002US-00114432.

PA (CHAL/) CHALLITA-BID P M.

PA (PARI/) PARIS M.

PA (MORR/) MORRISON R K.

РА (JAKO/) JAKOBOVITS A.

PI Chalilta-Eld PM, Raltano AB, Faris M, Hubert RS, Morrison RK,

XX  
DR MPI, 2004-132240/13.  
XX  
XX  
PT New composition comprising a substance that modulates the status of  
213p11, or a molecule that is modulated by 213p11, useful for  
XX detecting or treating cancer, e.g. pancreatic or rectal cancer.  
XX  
PS Example 13: Page 155; 334pp; English.  
XX  
XX The invention describes a composition comprising a substance that  
modulates the status of 213p11, or a molecule that is modulated by  
213p11, where the status of the cell that expresses 213p11 is  
modulated, and 213p11 is a gene overexpressed in many cancers. Also  
described are: a pharmaceutical composition comprising the composition  
cited above in a unit dose form; an antibody or its fragment; a non-human  
transgenic animal that produced the antibody; a hybridoma that produces  
the antibody; delivering a cytotoxic agent or a diagnostic agent to the  
cell that expresses 213p11; a polynucleotide that encodes the protein;  
inhibiting growth of cancer cells that expresses 213p11; generating a  
mammalian immune response; detecting the presence of 213p11-related  
protein or polynucleotide in a sample; and detecting the presence of  
cancer in an individual. The compositions, molecules and methods are  
useful for detecting and treating cancer, e.g. pancreatic or rectal  
cancer. This is the amino acid sequence of a human 213p11 peptide  
epitope bearing a human leukocyte antigen (HLA) class I or class II motif  
useful in the creation of an HLA vaccine to modulate 213p11.  
XX  
XX  
Sequence 9 AA:

Query Match	29.5%	Score 31	DB 8	Length 9
Best Local Similarity	62.5%	Pred. NO. 2e+06		
Matches	5	Conservative	2	Mismatches 1
				Indels 0
				Gaps 0
QY	10	GTIVGEG	17	
		:   :		
Db	2	GFLKGEDG	9	

RESULT 51  
ADO71975  
ID ADO71975 standard; peptide; 9 AA.

AC ADO71975;

DT 15-JUL-2004 (first entry)

DE Human 213P1F11 HLA motif bearing epitope #6074.

KM cytostatic; gene therapy; 213P.F11; 213P.F11 modulation; cancer;  
KM transgenic; cytotoxic agent delivery; diagnostic agent delivery;  
KM immune response; pancreatic cancer; rectal cancer; bladder cancer; human,  
KM human leukocyte antigen; HLA; class I; class II; epitope; HLA motif;  
KM HLA vaccine.

**Homo sapiens.**

PN US2004019915-A1.

PD 29-JAN-2004

PF 01-APR-2002; 2002US-00114432.

PR 01-APR-2002; 2002US-00114432.

PA (CHAL/) CHALLITA-EID P M.

PA (FARI/) FARIS M.

PA (MORR/) MORRISON R K

PA (JAKO/) JAKOBOVITS A

PI Chailita-Eld PM, Rattano AB, Faris M, Hubert RS, Morrison RK;

PI Ge W, Jakobovits A;  
XX  
DR WPI: 2004-132240/13.  
XX  
PT New composition comprising a substance that modulates the status of  
XX 213p1f1, or a molecule that is modulated by 213p1f1, useful for  
PT detecting or treating cancer, e.g. pancreatic or rectal cancer.  
XX  
PS Example 13; Page 160; 334pp; English.  
XX  
CC The invention describes a composition comprising a substance that  
CC modulates the status of 213p1f1, or a molecule that is modulated by  
CC 213p1f1, where the status of the cell that expresses 213p1f1 is  
CC modulated and 213p1f1 is a gene overexpressed in many cancers. Also  
CC described are: a pharmaceutical composition comprising the composition  
CC cited above in a unit dose form, an antibody or its fragment; a non-human  
CC transgenic animal that produced the antibody; a hybridoma that produces  
CC the antibody; delivering a cytotoxic agent or a diagnostic agent to the  
CC cell that expresses 213p1f1; a polynucleotide that encodes the protein;  
CC inhibiting growth of cancer cells that expresses 213p1f1; generating a  
CC mammalian immune response; detecting the presence of 213p1f1-related  
CC protein or polynucleotide in a sample; and detecting the presence of  
CC cancer in an individual. The compositions, molecules and methods are  
CC useful for detecting and treating cancer, e.g. pancreatic or rectal  
CC cancer. This is the amino acid sequence of a human 213p1f1 peptide  
CC epitope bearing a human leukocyte antigen (HLA) class I or class II motif  
CC useful in the creation of an HLA vaccine to modulate 213p1f1.  
XX  
SQ Sequence 9 AA;  
XX  
Query Match 29.5%; Score 31; DB 8; Length 9;  
Best Local Similarity 62.5%; Pred. No. 2e+06;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
QY 10 GETVGEEG 17  
DB 1 GFLKGEDG 8  
XX  
RESULT 52  
AD068215  
ID AD068215 standard; peptide; 9 AA.  
XX  
AC AD068215;  
XX  
DT 15-JUL-2004 (first entry)  
XX  
DE Human 213p1f1 HLA motif bearing epitope #4305.  
XX  
KW cytostatic; gene therapy; 213p1f1; 213p1f1 modulation; cancer;  
KW transgenic; cytotoxic agent delivery; diagnostic agent delivery;  
KW immune response; pancreatic cancer; rectal cancer; bladder cancer; human;  
KW human leukocyte antigen; HLA; class I; class II; epitope; HLA motif;  
KW HLA vaccine.  
XX  
OS Homo sapiens.  
XX  
PN US2004019915-A1.  
XX  
PD 29-JAN-2004.  
XX  
PF 01-APR-2002; 2002US-00114432.  
XX  
PR 01-APR-2002; 2002US-00114432.  
XX  
PA (CHAL/) CHALLITA-BID P M.  
PA (RAIT/) RAITANO A B.  
PA (FARI/) FARIS M.  
PA (HUBE/) HUBERT R S.  
PA (MORR/) MORRISON R K.  
PA (GEWM/) GE W.  
PA (JAKO/) JAKOBOVITS A.  
XX

PI Challita-Bid PM, Raitano AB, Faris M, Hubert RS, Morrison RK,  
PI Ge W, Jakobovits A;  
XX  
DR WPI: 2004-132240/13.  
XX  
PT New composition comprising a substance that modulates the status of  
XX 213p1f1, or a molecule that is modulated by 213p1f1, useful for  
PT detecting or treating cancer, e.g. pancreatic or rectal cancer.  
XX  
PS Example 13; Page 131; 334pp; English.  
XX  
CC The invention describes a composition comprising a substance that  
CC modulates the status of 213p1f1, or a molecule that is modulated by  
CC 213p1f1, where the status of the cell that expresses 213p1f1 is  
CC modulated and 213p1f1 is a gene overexpressed in many cancers. Also  
CC described are: a pharmaceutical composition comprising the composition  
CC cited above in a unit dose form, an antibody or its fragment; a non-human  
CC transgenic animal that produced the antibody; a hybridoma that produces  
CC the antibody; delivering a cytotoxic agent or a diagnostic agent to the  
CC cell that expresses 213p1f1; a polynucleotide that encodes the protein;  
CC inhibiting growth of cancer cells that expresses 213p1f1; generating a  
CC mammalian immune response; detecting the presence of 213p1f1-related  
CC protein or polynucleotide in a sample; and detecting the presence of  
CC cancer in an individual. The compositions, molecules and methods are  
CC useful for detecting and treating cancer, e.g. pancreatic or rectal  
CC cancer. This is the amino acid sequence of a human 213p1f1 peptide  
CC epitope bearing a human leukocyte antigen (HLA) class I or class II motif  
CC useful in the creation of an HLA vaccine to modulate 213p1f1.  
XX  
SQ Sequence 9 AA;  
XX  
Query Match 29.5%; Score 31; DB 8; Length 9;  
Best Local Similarity 62.5%; Pred. No. 2e+06;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
QY 10 GETVGEEG 17  
DB 2 GFLKGEDG 9  
XX  
RESULT 53  
AD068624  
ID AD068624 standard; peptide; 9 AA.  
XX  
AC AD068624;  
XX  
DT 15-JUL-2004 (first entry)  
XX  
DE Human 213p1f1 HLA motif bearing epitope #4714.  
XX  
KW cytostatic; gene therapy; 213p1f1; 213p1f1 modulation; cancer;  
KW transgenic; cytotoxic agent delivery; diagnostic agent delivery;  
KW immune response; pancreatic cancer; rectal cancer; bladder cancer; human;  
KW human leukocyte antigen; HLA; class I; class II; epitope; HLA motif;  
KW HLA vaccine.  
XX  
OS Homo sapiens.  
XX  
PN US2004019915-A1.  
XX  
PD 29-JAN-2004.  
XX  
PF 01-APR-2002; 2002US-00114432.  
XX  
PR 01-APR-2002; 2002US-00114432.  
XX  
PA (CHAL/) CHALLITA-BID P M.  
PA (RAIT/) RAITANO A B.  
PA (FARI/) FARIS M.  
PA (HUBE/) HUBERT R S.  
PA (MORR/) MORRISON R K.  
PA (GEWM/) GE W.  
PA (JAKO/) JAKOBOVITS A.  
XX



XX Cha11ita-B1d PM, Raitano AB, Paris M, Hubert RS, Morrison RK;  
 PI Ge W, Jakobovits A;  
 XX WPI, 2004-132240/13.  
 XX  
 PT Now composition comprising a substance that modulates the status of  
 PT 213P1F11, or a molecule that is modulated by 213P1F11, useful for  
 PT detecting or treating cancer, e.g. pancreatic or rectal cancer.  
 XX  
 PS Example 13, Page 137, 334pp; English.  
 XX  
 CC The invention describes a composition comprising a substance that  
 CC modulates the status of 213P1F11, or a molecule that is modulated by  
 CC 213P1F11, where the status of the cell that expresses 213P1F11 is  
 CC modulated and 213P1F11 is a gene overexpressed in many cancers. Also  
 CC described are: a pharmaceutical composition comprising the composition  
 CC cited above in a unit dose form; an antibody or its fragment; a non-human  
 CC transgenic animal that produced the antibody; a hybridoma that produces  
 CC the antibody; delivering a cytotoxic agent or a diagnostic agent to the  
 CC cell that expresses 213P1F11; a polynucleotide that encodes the protein;  
 CC inhibiting growth of cancer cells that expresses 213P1F11; generating a  
 CC mammalian immune response; detecting the presence of 213P1F11-related  
 CC protein or polynucleotide in a sample; and detecting the presence of  
 CC cancer in an individual. The compositions, molecules and methods are  
 CC useful for detecting and treating cancer, e.g. pancreatic or rectal  
 CC cancer. This is the amino acid sequence of a human 213P1F11 peptide  
 CC epitope bearing a human leukocyte antigen (HLA) class I or class II motif  
 CC useful in the creation of an HLA vaccine to modulate 213P1F11.  
 XX  
 SQ Sequence 9 AA;

Query Match 29.5%; Score 31; DB 8; Length 9;  
 Best Local Similarity 62.5%; Pred. No. 2e+06;  
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 QY 10 GFIYGEBSG 17  
 ||: ||: ||:  
 Db 2 GFLKGRDQ 9

RESULT 54  
 ADO72059  
 ID ADO72059 standard; peptide; 9 AA.  
 XX  
 AC ADO72059;  
 XX  
 DT 15-JUL-2004 (first entry)  
 XX  
 DE Human 213P1F11 HLA motif bearing epitope #6158.  
 XX  
 KW cytostatic; gene therapy; 213P1F11; 213P1F11 modulation; cancer;  
 KW transgenic; cytotoxic agent delivery; diagnostic agent delivery;  
 KW immune response; pancreatic cancer; rectal cancer; bladder cancer; human;  
 KW human leukocyte antigen; HLA; class I; class II; epitope; HLA motif;  
 XX HLA vaccine.  
 OS Homo sapiens.  
 XX  
 PN US2004019915-A1.  
 XX  
 PD 29-JAN-2004.  
 XX  
 PF 01-APR-2002; 2002US-00114432.  
 XX  
 PR 01-APR-2002; 2002US-00114432.  
 XX  
 PA (CHAL/) CHALLITA-BID P M.  
 PA (RAIT/) RAITANO A B.  
 PA (FARI/) PARIS M.  
 PA (HUBE/) HUBERT R S.  
 PA (MORR/) MORRISON R K.  
 PA (GEWM/) GE W.

PA (JAKO/) JAKOBOVITS A.  
 XX  
 PI Cha11ita-B1d PM, Raitano AB, Paris M, Hubert RS, Morrison RK;  
 PI Ge W, Jakobovits A;  
 XX WPI, 2004-132240/13.  
 XX  
 PT Now composition comprising a substance that modulates the status of  
 PT 213P1F11, or a molecule that is modulated by 213P1F11, useful for  
 PT detecting or treating cancer, e.g. pancreatic or rectal cancer.  
 XX  
 PS Example 13, Page 161, 334pp; English.  
 XX

CC The invention describes a composition comprising a substance that  
 CC modulates the status of 213P1F11, or a molecule that is modulated by  
 CC 213P1F11, where the status of the cell that expresses 213P1F11 is  
 CC modulated and 213P1F11 is a gene overexpressed in many cancers. Also  
 CC described are: a pharmaceutical composition comprising the composition  
 CC cited above in a unit dose form; an antibody or its fragment; a non-human  
 CC transgenic animal that produced the antibody; a hybridoma that produces  
 CC the antibody; delivering a cytotoxic agent or a diagnostic agent to the  
 CC cell that expresses 213P1F11; a polynucleotide that encodes the protein;  
 CC inhibiting growth of cancer cells that expresses 213P1F11; generating a  
 CC mammalian immune response; detecting the presence of 213P1F11-related  
 CC protein or polynucleotide in a sample; and detecting the presence of  
 CC cancer in an individual. The compositions, molecules and methods are  
 CC useful for detecting and treating cancer, e.g. pancreatic or rectal  
 CC cancer. This is the amino acid sequence of a human 213P1F11 peptide  
 CC epitope bearing a human leukocyte antigen (HLA) class I or class II motif  
 CC useful in the creation of an HLA vaccine to modulate 213P1F11.  
 XX

Query Match 29.5%; Score 31; DB 8; Length 9;  
 Best Local Similarity 62.5%; Pred. No. 2e+06;  
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 QY 10 GFIYGEBSG 17  
 ||: ||: ||:  
 Db 2 GFLKGRDQ 9

RESULT 55  
 ADO68890  
 ID ADO68890 standard; peptide; 9 AA.  
 XX  
 AC ADO68890;  
 XX  
 DT 15-JUL-2004 (first entry)  
 XX  
 DE Human 213P1F11 HLA motif bearing epitope #4980.  
 XX  
 KW cytostatic; gene therapy; 213P1F11; 213P1F11 modulation; cancer;  
 KW transgenic; cytotoxic agent delivery; diagnostic agent delivery;  
 KW immune response; pancreatic cancer; rectal cancer; bladder cancer; human;  
 KW human leukocyte antigen; HLA; class I; class II; epitope; HLA motif;  
 XX HLA vaccine.  
 OS Homo sapiens.  
 XX  
 PN US2004019915-A1.  
 XX  
 PD 29-JAN-2004.  
 XX  
 PF 01-APR-2002; 2002US-00114432.  
 XX  
 PR 01-APR-2002; 2002US-00114432.  
 XX  
 PA (CHAL/) CHALLITA-BID P M.  
 PA (RAIT/) RAITANO A B.  
 PA (FARI/) PARIS M.  
 PA (HUBE/) HUBERT R S.  
 PA (MORR/) MORRISON R K.

PA (GEMW/) GE W.  
PA (JAKO/) JAKOBOVITS A.  
XX  
PI Challita-Eid PM, Raitano AB, Paris M, Hubert RS, Morrison RK,  
PI Ge W, Jakobovits A;  
XX  
DR WPI; 2004-132240/13.  
XX  
PT New composition comprising a substance that modulates the status of  
PT 213p1f1, or a molecule that is modulated by 213p1f1, useful for  
PT detecting or treating cancer, e.g. pancreatic or rectal cancer.  
XX  
PS Example 13; Page 142; 334pp; English.  
XX  
CC The invention describes a composition comprising a substance that  
CC modulates the status of 213p1f1, or a molecule that is modulated by  
CC 213p1f1, where the status of the cell that expresses 213p1f1 is  
CC modulated, and 213p1f1 is a gene overexpressed in many cancers. Also  
CC described are: a pharmaceutical composition comprising the composition  
CC cited above in a unit dose form; an antibody or its fragment; a non-human  
CC transgenic animal that produced the antibody; a hybridoma that produces  
CC the antibody; delivering a cytotoxic agent or a diagnostic agent to the  
CC cell that expresses 213p1f1; a polynucleotide that encodes the protein;  
CC inhibiting growth of cancer cells that expresses 213p1f1; generating a  
CC mammalian immune response; detecting the presence of 213p1f1-related  
CC protein or polynucleotide in a sample; and detecting the presence of  
CC cancer in an individual. The compositions, molecules and methods are  
CC useful for detecting and treating cancer, e.g. pancreatic or rectal  
CC cancer. This is the amino acid sequence of a human 213p1f1 peptide  
CC epitope bearing a human leukocyte antigen (HLA) class I or class II motif  
CC useful in the creation of an HLA vaccine to modulate 213p1f1.  
XX  
SQ Sequence 9 AA;

Query Match 29.5%; Score 31; DB 8; Length 9;  
Best Local Similarity 62.5%; Pred. No. 2e+06;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 10 GFLVGEHG 17  
DB 1 GFLVGEHG 8

RESULT 56  
AD068347  
ID AD068347 standard; peptide; 9 AA.  
XX  
AC AD068347;  
XX  
DT 15-JUL-2004 (first entry)  
XX  
DB Human 213p1f1 HLA motif bearing epitope #4437.  
XX  
KW cytostatic; gene therapy; 213p1f1; 213p1f1 modulation; cancer;  
KW transgenic; cytotoxic agent delivery; diagnostic agent delivery;  
KW immune response; pancreatic cancer; rectal cancer; bladder cancer; human;  
KW human leukocyte antigen; HLA; class I; class II; epitope; HLA motif;  
KW HLA vaccine.  
XX  
OS Homo sapiens.  
XX  
PN US2004019915-A1.  
XX  
PD 29-JAN-2004.  
XX  
PF 01-APR-2002; 2002US-00114432.  
XX  
PR 01-APR-2002; 2002US-00114432.  
XX  
PA (CHAL/) CHALLITA-EID P M.  
PA (RAIT/) RAITANO A B.  
PA (FARI/) PARIS M.  
PA (HUBE/) HUBERT R S.

PA (MORR/) MORRISON R K.  
PA (GEMW/) GE W.  
PA (JAKO/) JAKOBOVITS A.  
XX  
PI Challita-Eid PM, Raitano AB, Paris M, Hubert RS, Morrison RK,  
PI Ge W, Jakobovits A;  
XX  
DR WPI; 2004-132240/13.  
XX  
PT New composition comprising a substance that modulates the status of  
PT 213p1f1, or a molecule that is modulated by 213p1f1, useful for  
PT detecting or treating cancer, e.g. pancreatic or rectal cancer.  
XX  
PS Example 13; Page 133; 334pp; English.  
XX

CC The invention describes a composition comprising a substance that  
CC modulates the status of 213p1f1, or a molecule that is modulated by  
CC 213p1f1, where the status of the cell that expresses 213p1f1 is  
CC modulated, and 213p1f1 is a gene overexpressed in many cancers. Also  
CC described are: a pharmaceutical composition comprising the composition  
CC cited above in a unit dose form; an antibody or its fragment; a non-human  
CC transgenic animal that produced the antibody; a hybridoma that produces  
CC the antibody; delivering a cytotoxic agent or a diagnostic agent to the  
CC cell that expresses 213p1f1; a polynucleotide that encodes the protein;  
CC inhibiting growth of cancer cells that expresses 213p1f1; generating a  
CC mammalian immune response; detecting the presence of 213p1f1-related  
CC protein or polynucleotide in a sample; and detecting the presence of  
CC cancer in an individual. The compositions, molecules and methods are  
CC useful for detecting and treating cancer, e.g. pancreatic or rectal  
CC cancer. This is the amino acid sequence of a human 213p1f1 peptide  
CC epitope bearing a human leukocyte antigen (HLA) class I or class II motif  
CC useful in the creation of an HLA vaccine to modulate 213p1f1.  
XX  
SQ Sequence 9 AA;

Query Match 29.5%; Score 31; DB 8; Length 9;  
Best Local Similarity 62.5%; Pred. No. 2e+06;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 10 GFLVGEHG 17  
DB 2 GFLVGEHG 9

RESULT 57  
AD068354  
ID AD068354 standard; peptide; 9 AA.  
XX  
AC AD068354;  
XX  
DT 15-JUL-2004 (first entry)  
XX  
DB Human 213p1f1 HLA motif bearing epitope #4444.  
XX  
KW cytostatic; gene therapy; 213p1f1; 213p1f1 modulation; cancer;  
KW transgenic; cytotoxic agent delivery; diagnostic agent delivery;  
KW immune response; pancreatic cancer; rectal cancer; bladder cancer; human;  
KW human leukocyte antigen; HLA; class I; class II; epitope; HLA motif;  
KW HLA vaccine.  
XX  
OS Homo sapiens.  
XX  
PN US2004019915-A1.  
XX  
PD 29-JAN-2004.  
XX  
PF 01-APR-2002; 2002US-00114432.  
XX  
PR 01-APR-2002; 2002US-00114432.  
XX  
PA (CHAL/) CHALLITA-EID P M.  
PA (RAIT/) RAITANO A B.  
PA (FARI/) PARIS M.

PA (HUBE/) HUBERT R S.  
PA (MORR/) MORRISON R K.  
PA (GEWM/) GE W.  
PA (JAKO/) JAKOBOVITS A.  
XX  
PI Challita-Eid PM, Raitano AB, Faris M, Hubert RS, Morrison RK;  
PI Ge W, Jakobovits A;  
XX  
DR WPI, 2004-132240/13.  
XX  
PT New composition comprising a substance that modulates the status of  
PT 213p1f1, or a molecule that is modulated by 213p1f1, useful for  
PT detecting or treating cancer, e.g. pancreatic or rectal cancer.  
XX  
PS Example 13, Page 133, 334pp; English.  
XX  
CC The invention describes a composition comprising a substance that  
CC modulates the status of 213p1f1, or a molecule that is modulated by  
CC 213p1f1, where the status of the cell that expresses 213p1f1 is  
CC modulated and 213p1f1 is a gene overexpressed in many cancers. Also  
CC described are: a pharmaceutical composition comprising the composition  
CC cited above in a unit dose form; an antibody or its fragment; a non-human  
CC transgenic animal that produces the antibody; a hybridoma that produces  
CC the antibody; delivering a cytotoxic agent or a diagnostic agent to the  
CC cell that expresses 213p1f1; a polynucleotide that encodes the protein;  
CC inhibiting growth of cancer cells that expresses 213p1f1; generating a  
CC mammalian immune response; detecting the presence of 213p1f1-related  
CC protein or polynucleotide in a sample; and detecting the presence of  
CC cancer in an individual. The compositions, molecules and methods are  
CC useful for detecting and treating cancer, e.g. pancreatic or rectal  
CC cancer. This is the amino acid sequence of a human 213p1f1 peptide  
CC epitope bearing a human leukocyte antigen (HLA) class I or class II motif  
CC useful in the creation of an HLA vaccine to modulate 213p1f1.  
XX  
SQ Sequence 9 AA;  
XX  
Query Match 29.5%; Score 31; DB 8; Length 9;  
Best Local Similarity 62.5%; Pred. No. 2e+06; 1; Indels 0; Gaps 0;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
QY 10 GFLVGEKG 17  
Db 1 GFLKGEKG 8  
XX  
RESULT 58  
AD068030  
ID AD068030 standard; peptide; 9 AA.  
XX  
AC AD068030;  
XX  
DT 15-JUL-2004 (first entry)  
XX  
DB Human 213p1f1 HLA motif bearing epitope #4120.  
XX  
KW cytostatic; gene therapy; 213p1f1, 213p1f1 modulation; cancer;  
KW transgenic; cytotoxic agent delivery; diagnostic agent delivery;  
KW immune response; pancreatic cancer; rectal cancer; bladder cancer; human;  
KW human leukocyte antigen; HLA; class I; class II; epitope; HLA motif;  
KW HLA vaccine.  
XX  
OS Homo sapiens.  
XX  
PN US2004019915-A1.  
XX  
PD 29-JAN-2004.  
XX  
PF 01-APR-2002; 2002US-00114432.  
XX  
PR 01-APR-2002; 2002US-00114432.  
XX  
PA (CHAL/) CHALLITA-EID P M.  
PA (RAIT/) RAITANO A B.

PA (FARI/) FARIS M.  
PA (HUBE/) HUBERT R S.  
PA (MORR/) MORRISON R K.  
PA (GEWM/) GE W.  
PA (JAKO/) JAKOBOVITS A.  
XX  
PI Challita-Eid PM, Raitano AB, Faris M, Hubert RS, Morrison RK;  
PI Ge W, Jakobovits A;  
XX  
DR WPI, 2004-132240/13.  
XX  
PT New composition comprising a substance that modulates the status of  
PT 213p1f1, or a molecule that is modulated by 213p1f1, useful for  
PT detecting or treating cancer, e.g. pancreatic or rectal cancer.  
XX  
PS Example 13, Page 128, 334pp; English.  
XX  
CC The invention describes a composition comprising a substance that  
CC modulates the status of 213p1f1, or a molecule that is modulated by  
CC 213p1f1, where the status of the cell that expresses 213p1f1 is  
CC modulated and 213p1f1 is a gene overexpressed in many cancers. Also  
CC described are: a pharmaceutical composition comprising the composition  
CC cited above in a unit dose form; an antibody or its fragment; a non-human  
CC transgenic animal that produces the antibody; a hybridoma that produces  
CC the antibody; delivering a cytotoxic agent or a diagnostic agent to the  
CC cell that expresses 213p1f1; a polynucleotide that encodes the protein;  
CC inhibiting growth of cancer cells that expresses 213p1f1; generating a  
CC mammalian immune response; detecting the presence of 213p1f1-related  
CC protein or polynucleotide in a sample; and detecting the presence of  
CC cancer in an individual. The compositions, molecules and methods are  
CC useful for detecting and treating cancer, e.g. pancreatic or rectal  
CC cancer. This is the amino acid sequence of a human 213p1f1 peptide  
CC epitope bearing a human leukocyte antigen (HLA) class I or class II motif  
CC useful in the creation of an HLA vaccine to modulate 213p1f1.  
XX  
SQ Sequence 9 AA;  
XX  
Query Match 29.5%; Score 31; DB 8; Length 9;  
Best Local Similarity 62.5%; Pred. No. 2e+06; 1; Indels 0; Gaps 0;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
QY 10 GFLVGEKG 17  
Db 2 GFLKGEKG 9  
XX  
RESULT 59  
AD068858  
ID AD068858 standard; peptide; 9 AA.  
XX  
AC AD068858;  
XX  
DT 15-JUL-2004 (first entry)  
XX  
DB Human 213p1f1 HLA motif bearing epitope #4948.  
XX  
KW cytostatic; gene therapy; 213p1f1, 213p1f1 modulation; cancer;  
KW transgenic; cytotoxic agent delivery; diagnostic agent delivery;  
KW immune response; pancreatic cancer; rectal cancer; bladder cancer; human;  
KW human leukocyte antigen; HLA; class I; class II; epitope; HLA motif;  
KW HLA vaccine.  
XX  
OS Homo sapiens.  
XX  
PN US2004019915-A1.  
XX  
PD 29-JAN-2004.  
XX  
PF 01-APR-2002; 2002US-00114432.  
XX  
PR 01-APR-2002; 2002US-00114432.  
XX  
PA (CHAL/) CHALLITA-EID P M.

PA (RAIT/) RAITANO A B.  
PA (FARI/) FARIS M.  
PA (HUBE/) HUBERT R S.  
PA (MORR/) MORRISON R K.  
PA (GEWM/) GE W.  
PA (JAKO/) JAKOBOVITS A.  
XX  
XX  
PI Challita-Rid PM, Raitano AB, Faris M, Hubert RS, Morrison RK,  
PI Ge W, Jakobovits A;  
XX  
XX WPI; 2004-132240/13.  
XX  
XX  
PT New composition comprising a substance that modulates the status of  
PT 213p1f1, or a molecule that is modulated by 213p1f1, useful for  
PT detecting or treating cancer, e.g. pancreatic or rectal cancer.  
XX  
XX  
PS Example 13; Page 141; 334pp; English.

XX  
XX The invention describes a composition comprising a substance that  
CC modulates the status of 213p1f1, or a molecule that is modulated by  
CC 213p1f1, where the status of the cell that expresses 213p1f1 is  
CC modulated and 213p1f1 is a gene overexpressed in many cancers. Also  
CC described are: a pharmaceutical composition comprising the composition  
CC cited above in a unit dose form; an antibody or its fragment; a non-human  
CC transgenic animal that produced the antibody; a hybridoma that produces  
CC the antibody; delivering a cytotoxic agent or a diagnostic agent to the  
CC cell that expresses 213p1f1; a polynucleotide that encodes the protein;  
CC inhibiting growth of cancer cells that expresses 213p1f1; generating a  
CC mammalian immune response; detecting the presence of 213p1f1-related  
CC protein or polynucleotide in a sample; and detecting the presence of  
CC cancer in an individual. The compositions, molecules and methods are  
CC useful for detecting and treating cancer, e.g. pancreatic or rectal  
CC cancer. This is the amino acid sequence of a human 213p1f1 peptide  
CC epitope bearing a human leukocyte antigen (HLA) class I or class II motif  
CC useful in the creation of an HLA vaccine to modulate 213p1f1.  
XX  
XX

SQ Sequence 9 AA;

Query Match 29.5%; Score 31; DB 8; Length 9;

Best Local Similarity 62.5%; Pred. No. 2e+06; 1; Indels 0; Gaps 0;

Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 10 GFIYGEEG 17  
||: ||:|  
Db 2 GFIKGEDG 9

RESULT 60

AD069100 standard; peptide; 9 AA.

XX  
XX ADO69100;  
AC

XX 15-JUL-2004 (first entry)

DE Human 213p1f1 HLA motif bearing epitope #5190.

XX cytostatic; gene therapy; 213p1f1, 213p1f1 modulation; cancer;  
XX transgenic; cytotoxic agent delivery; diagnostic agent delivery;  
KW immune response; pancreatic cancer; rectal cancer; bladder cancer; human;  
KW human leukocyte antigen; HLA; class I; class II; epitope; HLA motif;  
KW HLA vaccine.  
XX  
XX

OS Homo sapiens.

XX US2004019915-A1.

XX 29-JAN-2004.

PD 01-APR-2002; 2002US-00114432.

XX 01-APR-2002; 2002US-00114432.

XX  
XX

PA (CHAL/) CHALLITA-RID P M.  
PA (RAIT/) RAITANO A B.  
PA (FARI/) FARIS M.  
PA (HUBE/) HUBERT R S.  
PA (MORR/) MORRISON R K.  
PA (GEWM/) GE W.  
PA (JAKO/) JAKOBOVITS A.  
XX  
XX

PI Challita-Rid PM, Raitano AB, Faris M, Hubert RS, Morrison RK,  
PI Ge W, Jakobovits A;  
XX  
XX

XX WPI; 2004-132240/13.

XX  
XX  
PT New composition comprising a substance that modulates the status of  
PT 213p1f1, or a molecule that is modulated by 213p1f1, useful for  
PT detecting or treating cancer, e.g. pancreatic or rectal cancer.  
XX  
XX

PS Example 13; Page 145; 334pp; English.

XX  
XX The invention describes a composition comprising a substance that  
CC modulates the status of 213p1f1, or a molecule that is modulated by  
CC 213p1f1, where the status of the cell that expresses 213p1f1 is  
CC modulated and 213p1f1 is a gene overexpressed in many cancers. Also  
CC described are: a pharmaceutical composition comprising the composition  
CC cited above in a unit dose form; an antibody or its fragment; a non-human  
CC transgenic animal that produced the antibody; a hybridoma that produces  
CC the antibody; delivering a cytotoxic agent or a diagnostic agent to the  
CC cell that expresses 213p1f1; a polynucleotide that encodes the protein;  
CC inhibiting growth of cancer cells that expresses 213p1f1; generating a  
CC mammalian immune response; detecting the presence of 213p1f1-related  
CC protein or polynucleotide in a sample; and detecting the presence of  
CC cancer in an individual. The compositions, molecules and methods are  
CC useful for detecting and treating cancer, e.g. pancreatic or rectal  
CC cancer. This is the amino acid sequence of a human 213p1f1 peptide  
CC epitope bearing a human leukocyte antigen (HLA) class I or class II motif  
CC useful in the creation of an HLA vaccine to modulate 213p1f1.  
XX  
XX

SQ Sequence 9 AA;

Query Match 29.5%; Score 31; DB 8; Length 9;

Best Local Similarity 62.5%; Pred. No. 2e+06; 1; Indels 0; Gaps 0;

Qy 10 GFIYGEEG 17  
||: ||:|  
Db 1 GFIKGEDG 8

RESULT 61

AD067954 standard; peptide; 9 AA.

XX  
XX ADO67954;  
AC

XX 15-JUL-2004 (first entry)

DE Human 213p1f1 HLA motif bearing epitope #4044.

XX cytostatic; gene therapy; 213p1f1, 213p1f1 modulation; cancer;  
XX transgenic; cytotoxic agent delivery; diagnostic agent delivery;  
KW immune response; pancreatic cancer; rectal cancer; bladder cancer; human;  
KW human leukocyte antigen; HLA; class I; class II; epitope; HLA motif;  
KW HLA vaccine.  
XX  
XX

OS Homo sapiens.

XX US2004019915-A1.

XX 29-JAN-2004.

PD 01-APR-2002; 2002US-00114432.

XX 01-APR-2002; 2002US-00114432.

XX  
XX

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XX (CHAL/) CHALLITA-BID P M.
PA (RAIT/) RAITANO A B.
PA (FARI/) FARIS M.
PA (HUBE/) HUBERT R S.
PA (MORR/) MORRISON R K.
PA (GEWM/) GE W.
PA (JAKO/) JAKOBOVITS A.
XX
PI Challita-Bid PM, Raitano AB, Faris M, Hubert RS, Morrison RK;
PI Ge W, Jakobovits A;
XX
DR WPI; 2004-132240/13.
XX
PT New composition comprising a substance that modulates the status of
PT 213p1f1, or a molecule that is modulated by 213p1f1, useful for
PT detecting or treating cancer, e.g. pancreatic or rectal cancer.
XX
PS Example 13; Page 127; 334pp; English.
XX
CC The invention describes a composition comprising a substance that
CC modulates the status of 213p1f1, or a molecule that is modulated by
CC 213p1f1, where the status of the cell that expresses 213p1f1 is
CC modulated and 213p1f1 is a gene overexpressed in many cancers. Also
CC described are: a pharmaceutical composition comprising the composition
CC cited above in a unit dose form; an antibody or its fragment; a non-human
CC transgenic animal that produced the antibody; a hybridoma that produces
CC the antibody; delivering a cytotoxic agent or a diagnostic agent to the
CC cell that expresses 213p1f1; a polynucleotide that encodes the protein;
CC inhibiting growth of cancer cells that expresses 213p1f1; generating a
CC mammalian immune response; detecting the presence of 213p1f1-related
CC protein or polynucleotide in a sample; and detecting the presence of
CC cancer in an individual. The compositions, molecules and methods are
CC useful for detecting and treating cancer, e.g. pancreatic or rectal
CC cancer. This is the amino acid sequence of a human 213p1f1 peptide
CC epitope bearing a human leukocyte antigen (HLA) class I or class II motif
CC useful in the creation of an HLA vaccine to modulate 213p1f1.
XX
SQ Sequence 9 AA;
XX
Query Match 29.5%; Score 31; DB 8; Length 9;
Best Local Similarity 62.5%; Pred. No. 2e+06;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 10 GPRVGEQ 17
DB 1 GFLKGRDG 8

```

RESULT 62

ADO66277

ID ADO66277 standard; peptide; 9 AA.

AC ADO66277;

XX

DT 15-JUL-2004 (first entry)

XX

DE Human 213p1f1 HLA motif bearing epitope #2367.

XX

KW cytotoxic; gene therapy; 213p1f1; 213p1f1 modulation; cancer;

KW transgenic; cytotoxic agent delivery; diagnostic agent delivery;

KW immune response; pancreatic cancer; rectal cancer; bladder cancer; human;

KW human leukocyte antigen; HLA; class I; class II; epitope; HLA motif;

KW HLA vaccine.

XX

OS Homo sapiens.

XX

PN US2004019915-A1.

XX

PD 29-JAN-2004.

XX

PF 01-APR-2002; 2002US-00114432.

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PR 01-APR-2002; 2002US-00114432.
XX
XX (CHAL/) CHALLITA-BID P M.
PA (RAIT/) RAITANO A B.
PA (FARI/) FARIS M.
PA (HUBE/) HUBERT R S.
PA (MORR/) MORRISON R K.
PA (GEWM/) GE W.
PA (JAKO/) JAKOBOVITS A.
XX
PI Challita-Bid PM, Raitano AB, Faris M, Hubert RS, Morrison RK;
PI Ge W, Jakobovits A;
XX
DR WPI; 2004-132240/13.
XX
PT New composition comprising a substance that modulates the status of
PT 213p1f1, or a molecule that is modulated by 213p1f1, useful for
PT detecting or treating cancer, e.g. pancreatic or rectal cancer.
XX
PS Example 13; Page 103; 334pp; English.
XX
CC The invention describes a composition comprising a substance that
CC modulates the status of 213p1f1, or a molecule that is modulated by
CC 213p1f1, where the status of the cell that expresses 213p1f1 is
CC modulated and 213p1f1 is a gene overexpressed in many cancers. Also
CC described are: a pharmaceutical composition comprising the composition
CC cited above in a unit dose form; an antibody or its fragment; a non-human
CC transgenic animal that produced the antibody; a hybridoma that produces
CC the antibody; delivering a cytotoxic agent or a diagnostic agent to the
CC cell that expresses 213p1f1; a polynucleotide that encodes the protein;
CC inhibiting growth of cancer cells that expresses 213p1f1; generating a
CC mammalian immune response; detecting the presence of 213p1f1-related
CC protein or polynucleotide in a sample; and detecting the presence of
CC cancer in an individual. The compositions, molecules and methods are
CC useful for detecting and treating cancer, e.g. pancreatic or rectal
CC cancer. This is the amino acid sequence of a human 213p1f1 peptide
CC epitope bearing a human leukocyte antigen (HLA) class I or class II motif
CC useful in the creation of an HLA vaccine to modulate 213p1f1.
XX
SQ Sequence 9 AA;
XX
Query Match 29.5%; Score 31; DB 8; Length 9;
Best Local Similarity 62.5%; Pred. No. 2e+06;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 10 GPRVGEQ 17
DB 1 GFLKGRDG 8

```

RESULT 63

ADO68944

ID ADO68944 standard; peptide; 9 AA.

AC ADO68944;

XX

DT 15-JUL-2004 (first entry)

XX

DE Human 213p1f1 HLA motif bearing epitope #5034.

XX

KW cytotoxic; gene therapy; 213p1f1; 213p1f1 modulation; cancer;

KW transgenic; cytotoxic agent delivery; diagnostic agent delivery;

KW immune response; pancreatic cancer; rectal cancer; bladder cancer; human;

KW human leukocyte antigen; HLA; class I; class II; epitope; HLA motif;

KW HLA vaccine.

XX

OS Homo sapiens.

XX

PN US2004019915-A1.

XX

PD 29-JAN-2004.

XX

PF 01-APR-2002; 2002US-00114432.

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XX 01-APR-2002; 2002US-00114432.
PR
XX (CHAL/) CHALLITA-EID P M.
PA (RAIT/) RAITANO A B.
PA (FARI/) FARI S.
PA (HUBE/) HUBERT R S.
PA (MORR/) MORRISON R K.
PA (GEWM/) GE W.
PA (JAKO/) JAKOBOVITS A.
XX
XX Chailita-Eid PM, Raitano AB, Farris M, Hubert RS, Morrison RK,
PI Ge W, Jakobovits A;
XX
XX WPI; 2004-132240/13.
DR
XX
XX New composition comprising a substance that modulates the status of
PT 213p1F1, or a molecule that is modulated by 213p1F1, useful for
PT detecting or treating cancer, e.g. pancreatic or rectal cancer.
XX
XX
XX Example 13; Page 143; 334pp; English.
XX
XX The invention describes a composition comprising a substance that
CC modulates the status of 213p1F1, or a molecule that is modulated by
CC 213p1F1, where the status of the cell that expresses 213p1F1 is
CC modulated and 213p1F1 is a gene overexpressed in many cancers. Also
CC described are: a pharmaceutical composition comprising the composition
CC cited above in a unit dose form, an antibody or its fragment, a non-human
CC transgenic animal that produced the antibody, a hydridoma that produces
CC the antibody, delivering a cytotoxic agent or a diagnostic agent to the
CC cell that expresses 213p1F1; a polynucleotide that encodes the protein;
CC inhibiting growth of cancer cells that expresses 213p1F1; generating a
CC mammalian immune response; detecting the presence of 213p1F1-related
CC protein or polynucleotide in a sample; and detecting the presence of
CC cancer in an individual. The compositions, molecules and methods are
CC useful for detecting and treating cancer, e.g. pancreatic or rectal
CC cancer. This is the amino acid sequence of a human 213p1F1 peptide
CC epitope bearing a human leukocyte antigen (HLA) class I or class II motif
CC useful in the creation of an HLA vaccine to modulate 213p1F1.
XX
XX Sequence 9 AA;
SQ
Query Match 29.5%; Score 31; DB 8; Length 9;
Best Local Similarity 62.5%; Pred. No. 2e+06;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 10 GFTVGEEG 17
DB 2 GFLKGEDG 9
RESULT 64
AD069211
ID AD069211 standard; peptide; 9 AA.
XX
XX AD069211;
AC
XX
XX 15-JUL-2004 (first entry)
DT
XX
XX Human 213p1F1 HLA motif bearing epitope #5301.
DE
XX
XX cytostatic; gene therapy; 213p1F1; 213p1F1 modulation; cancer;
KW transgenic; cytotoxic agent delivery; diagnostic agent delivery;
KW immune response; pancreatic cancer; rectal cancer; bladder cancer; human;
KW human leukocyte antigen; HLA; class I; class II; epitope; HLA motif;
KW HLA vaccine.
XX
XX Homo sapiens.
OS
XX
XX US2004019915-A1.
XX
XX 29-JAN-2004.
XX

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PF 01-APR-2002; 2002US-00114432.
XX
XX 01-APR-2002; 2002US-00114432.
PR
XX (CHAL/) CHALLITA-EID P M.
PA (RAIT/) RAITANO A B.
PA (FARI/) FARI S.
PA (HUBE/) HUBERT R S.
PA (MORR/) MORRISON R K.
PA (GEWM/) GE W.
PA (JAKO/) JAKOBOVITS A.
XX
XX Chailita-Eid PM, Raitano AB, Farris M, Hubert RS, Morrison RK,
PI Ge W, Jakobovits A;
XX
XX WPI; 2004-132240/13.
DR
XX
XX New composition comprising a substance that modulates the status of
PT 213p1F1, or a molecule that is modulated by 213p1F1, useful for
PT detecting or treating cancer, e.g. pancreatic or rectal cancer.
XX
XX
XX Example 13; Page 147; 334pp; English.
XX
XX The invention describes a composition comprising a substance that
CC modulates the status of 213p1F1, or a molecule that is modulated by
CC 213p1F1, where the status of the cell that expresses 213p1F1 is
CC modulated and 213p1F1 is a gene overexpressed in many cancers. Also
CC described are: a pharmaceutical composition comprising the composition
CC cited above in a unit dose form, an antibody or its fragment, a non-human
CC transgenic animal that produced the antibody, a hydridoma that produces
CC the antibody, delivering a cytotoxic agent or a diagnostic agent to the
CC cell that expresses 213p1F1; a polynucleotide that encodes the protein;
CC inhibiting growth of cancer cells that expresses 213p1F1; generating a
CC mammalian immune response; detecting the presence of 213p1F1-related
CC protein or polynucleotide in a sample; and detecting the presence of
CC cancer in an individual. The compositions, molecules and methods are
CC useful for detecting and treating cancer, e.g. pancreatic or rectal
CC cancer. This is the amino acid sequence of a human 213p1F1 peptide
CC epitope bearing a human leukocyte antigen (HLA) class I or class II motif
CC useful in the creation of an HLA vaccine to modulate 213p1F1.
XX
XX Sequence 9 AA;
SQ
Query Match 29.5%; Score 31; DB 8; Length 9;
Best Local Similarity 62.5%; Pred. No. 2e+06;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 10 GFTVGEEG 17
DB 1 GFLKGEDG 8
RESULT 65
AD068650
ID AD068650 standard; peptide; 9 AA.
XX
XX AD068650;
AC
XX
XX 15-JUL-2004 (first entry)
DT
XX
XX Human 213p1F1 HLA motif bearing epitope #4740.
DE
XX
XX cytostatic; gene therapy; 213p1F1; 213p1F1 modulation; cancer;
KW transgenic; cytotoxic agent delivery; diagnostic agent delivery;
KW immune response; pancreatic cancer; rectal cancer; bladder cancer; human;
KW human leukocyte antigen; HLA; class I; class II; epitope; HLA motif;
KW HLA vaccine.
XX
XX Homo sapiens.
OS
XX
XX US2004019915-A1.
XX
XX 29-JAN-2004.
XX

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XX 01-APR-2002; 2002US-00114432.
XX PF
XX 01-APR-2002; 2002US-00114432.
XX PR
XX 01-APR-2002; 2002US-00114432.
XX PA
XX (CHAL/) CHALLITA-BID P M.
XX PA (RAIT/) RAITANO A B.
XX PA (PART/) PARTS M.
XX PA (HUBB/) HUBERT R S.
XX PA (MORR/) MORRISON R K.
XX PA (GEWA/) GE W.
XX PA (JAKO/) JAKOBOVITS A.
XX XX
XX Challita-Bid PM, Raitano AB, Parts M, Hubert RS, Morrison RK,
XX PI Ge W, Jakobovits A;
XX DR
XX WPI, 2004-132240/13.
XX XX
XX New composition comprising a substance that modulates the status of
XX PT 213P1F1, or a molecule that is modulated by 213P1F1, useful for
XX PT detecting or treating cancer, e.g. pancreatic or rectal cancer.
XX XX
XX Example 13; Page 138; 334pp; English.
XX PS
XX The invention describes a composition comprising a substance that
XX CC modulates the status of 213P1F1, or a molecule that is modulated by
XX CC 213P1F1, where the status of the cell that expresses 213P1F1 is
XX CC modulated and 213P1F1 is a gene overexpressed in many cancers. Also
XX CC described are: a pharmaceutical composition comprising the composition
XX CC cited above in a unit dose form; an antibody or its fragment; a non-human
XX CC transgenic animal that produced the antibody; a hybridoma that produces
XX CC the antibody; delivering a cytotoxic agent or a diagnostic agent to the
XX CC cell that expresses 213P1F1; a polynucleotide that encodes the protein;
XX CC inhibiting growth of cancer cells that expresses 213P1F1; generating a
XX CC mammalian immune response; detecting the presence of 213P1F1-related
XX CC protein or polynucleotide in a sample; and detecting the presence of
XX CC cancer in an individual. The compositions, molecules and methods are
XX CC useful for detecting and treating cancer, e.g. pancreatic or rectal
XX CC cancer. This is the amino acid sequence of a human 213P1F1 peptide
XX CC epitope bearing a human leukocyte antigen (HLA) class I or class II motif
XX CC useful in the creation of an HLA vaccine to modulate 213P1F1.
XX CC
XX Sequence 9 AA:
XX SQ
XX
XX Query Match 29.5%; Score 31; DB 8; Length 9;
XX Best Local Similarity 62.5%; Pred. NO. 2e+06;
XX Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 10 GFIVGDEG 17
XX ||: ||:|
XX Db 1 GFLKGEDG 8
XX
XX RESULT 66
XX ADO69433
XX ID ADO69433 standard; peptide; 9 AA.
XX XX
XX ADO69433,
XX
XX 15-JUN-2004 (first entry)
XX DT
XX XX
XX Human 213P1F1 HLA motif bearing epitope #5523.
XX DE
XX cytostatic; gene therapy; 213P1F1, 213P1F1 modulation; cancer;
XX KW transgenic; cytotoxic agent delivery; diagnostic agent delivery;
XX KW immune response; pancreatic cancer; rectal cancer; bladder cancer; human;
XX KW human leukocyte antigen; HLA; class I; class II; epitope; HLA motif;
XX KW HLA vaccine.
XX XX
XX Homo sapiens.
XX OS
XX US2004019915-A1.
XX PN
XX

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PD	29-JAN-2004.
XX	
PF	01-APR-2002; 2002US-00114432.
PR	01-APR-2002; 2002US-00114432.
XX	
PA	(CHAL/) CHALLITA-BID P M.
PA	(RAIT/) RAITANO A B.
PA	(FARI/) PARIS M.
PA	(HUBB/) HUBERT R S.
PA	(MORR/) MORRISON R K.
PA	(GEWM/) GE W.
PA	(JAKO/) JAKOBOVITS A.
XX	
PI	Challita-Bid PM, Raitano AB, Farris M, Hubert RS, Morrison RK;
PI	Ge W, Jakobovits A;
XX	
DR	WPI; 2004-132240/13.
XX	
PT	New composition comprising a substance that modulates the status of
PT	213P1F1, or a molecule that is modulated by 213P1F1, useful for
PT	detecting or treating cancer, e.g. pancreatic or rectal cancer.
XX	
PS	Example 13; Page 151; 334pp; English.
XX	
CC	The invention describes a composition comprising a substance that
CC	modulates the status of 213P1F1, or a molecule that is modulated by
CC	213P1F1, where the status of the cell that expresses 213P1F1 is
CC	modulated and 213P1F1 is a gene overexpressed in many cancers. Also
CC	described are: a pharmaceutical composition comprising the composition
CC	cited above in a unit dose form; an antibody or its fragment; a non-human
CC	transgenic animal that produced the antibody; a hybridoma that produces
CC	the antibody; delivering a cytotoxic agent or a diagnostic agent to the
CC	cell that expresses 213P1F1; a polynucleotide that encodes the protein;
CC	inhibiting growth of cancer cells that expresses 213P1F1; generating a
CC	mammalian immune response; detecting the presence of 213P1F1-related
CC	protein or polynucleotide in a sample; and detecting the presence of
CC	cancer in an individual. The compositions, molecules and methods are
CC	useful for detecting and treating cancer, e.g. pancreatic or rectal
CC	cancer. This is the amino acid sequence of a human 213P1F1 peptide
CC	epitope bearing a human leukocyte antigen (HLA) class I or class II motif
CC	useful in the creation of an HLA vaccine to modulate 213P1F1.
XX	
SQ	Sequence 9 AA;
XX	
Query Match	29.5%; Score 31; DB 8; Length 9;
Best Local Similarity	62.5%; Pred. No. 2e+06;
Matches	5; Conservative 2; Mismatches 1; Indels 0; Gaps 0
OY	10 GPIVGEEG 17
	:   :
Db	1 GFLKGEQG 8
RESULT 67	
ADO69643	
ID	ADO69643 standard; peptide; 9 AA.
AC	ADO69643;
XX	
DT	15-JUL-2004 (first entry)
XX	
DE	Human 213P1F1 HLA motif bearing epitope #5733.
XX	
KW	cytostatic; gene therapy; 213P1F1; 213P1F1 modulation; cancer;
KW	transgenic; cytotoxic agent delivery; diagnostic agent delivery;
KW	immune response; pancreatic cancer; rectal cancer; bladder cancer; human;
KW	human leukocyte antigen; HLA; class I; class II; epitope; HLA motif;
KW	HLA vaccine.
XX	
OS	Homo sapiens.
XX	
PN	US2004019915-A1.

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XX 29-JAN-2004.
XX 01-APR-2002; 2002US-00114432.
XX 01-APR-2002; 2002US-00114432.
XX 01-APR-2002; 2002US-00114432.
XX (CHAL/) CHALLITA-EID P M.
XX (RAIT/) RAITANO A B.
XX (FARI/) FARIS M.
XX (HUBE/) HUBERT R S.
XX (MORR/) MORRISON R K.
XX (GEWM/) GE W.
XX (JAKO/) JAKOBOVITS A.
XX Chailita-Eid PM, Raitano AB, Faris M, Hubert RS, Morrison RK,
XX Ge W, Jakobovits A;
XX WPI; 2004-132240/13.
XX
XX New composition comprising a substance that modulates the status of
XX 213P1F1, or a molecule that is modulated by 213P1F1, useful for
XX detecting or treating cancer, e.g. pancreatic or rectal cancer.
XX
XX Example 13; Page 154; 334pp; English.
XX
XX The invention describes a composition comprising a substance that
XX modulates the status of 213P1F1, or a molecule that is modulated by
XX 213P1F1, where the status of the cell that expresses 213P1F1 is
XX modulated and 213P1F1 is a gene overexpressed in many cancers. Also
XX described are: a pharmaceutical composition comprising the composition
XX cited above in a unit dose form; an antibody or its fragment; a non-human
XX transgenic animal that produced the antibody; a hybridoma that produces
XX the antibody; delivering a cytotoxic agent or a diagnostic agent to the
XX cell that expresses 213P1F1; a polynucleotide that encodes the protein;
XX inhibiting growth of cancer cells that expresses 213P1F1; generating a
XX mammalian immune response; detecting the presence of 213P1F1-related
XX protein or polynucleotide in a sample; and detecting the presence of
XX cancer in an individual. The compositions, molecules and methods are
XX useful for detecting and treating cancer, e.g. pancreatic or rectal
XX cancer. This is the amino acid sequence of a human 213P1F1 peptide
XX epitope bearing a human leukocyte antigen (HLA) class I or class II motif
XX useful in the creation of an HLA vaccine to modulate 213P1F1.
XX
XX Sequence 9 AA;
XX
XX Query Match 29.5%; Score 31; DB 8; Length 9;
XX Best Local Similarity 62.5%; Pred. No. 2e+06;
XX Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 10 GFLVGEEG 17
XX ||: ||:|
XX 1 GFLKGEDEG 8
XX
XX Db
XX
XX RESULT 68
XX ADO71860
XX ID ADO71860 standard; peptide; 9 AA.
XX
XX AC ADO71860;
XX
XX DT 15-JUL-2004 (first entry)
XX
XX DE Human 213P1F1 HLA motif bearing epitope #5959.
XX
XX KW cytostatic; gene therapy; 213P1F1; 213P1F1 modulation; cancer;
XX transgenic; cytotoxic agent delivery; diagnostic agent delivery;
XX immune response; pancreatic cancer; rectal cancer; bladder cancer; human;
XX human leukocyte antigen; HLA; class I; class II; epitope; HLA motif;
XX HLA vaccine.
XX
XX KW Homo sapiens.
XX
XX OS
```

```
PN US2004019915-A1.
XX 29-JAN-2004.
XX 01-APR-2002; 2002US-00114432.
XX 01-APR-2002; 2002US-00114432.
XX 01-APR-2002; 2002US-00114432.
XX (CHAL/) CHALLITA-EID P M.
XX (RAIT/) RAITANO A B.
XX (FARI/) FARIS M.
XX (HUBE/) HUBERT R S.
XX (MORR/) MORRISON R K.
XX (GEWM/) GE W.
XX (JAKO/) JAKOBOVITS A.
XX Chailita-Eid PM, Raitano AB, Faris M, Hubert RS, Morrison RK,
XX Ge W, Jakobovits A;
XX WPI; 2004-132240/13.
XX
XX New composition comprising a substance that modulates the status of
XX 213P1F1, or a molecule that is modulated by 213P1F1, useful for
XX detecting or treating cancer, e.g. pancreatic or rectal cancer.
XX
XX Example 13; Page 158; 334pp; English.
XX
XX The invention describes a composition comprising a substance that
XX modulates the status of 213P1F1, or a molecule that is modulated by
XX 213P1F1, where the status of the cell that expresses 213P1F1 is
XX modulated and 213P1F1 is a gene overexpressed in many cancers. Also
XX described are: a pharmaceutical composition comprising the composition
XX cited above in a unit dose form; an antibody or its fragment; a non-human
XX transgenic animal that produced the antibody; a hybridoma that produces
XX the antibody; delivering a cytotoxic agent or a diagnostic agent to the
XX cell that expresses 213P1F1; a polynucleotide that encodes the protein;
XX inhibiting growth of cancer cells that expresses 213P1F1; generating a
XX mammalian immune response; detecting the presence of 213P1F1-related
XX protein or polynucleotide in a sample; and detecting the presence of
XX cancer in an individual. The compositions, molecules and methods are
XX useful for detecting and treating cancer, e.g. pancreatic or rectal
XX cancer. This is the amino acid sequence of a human 213P1F1 peptide
XX epitope bearing a human leukocyte antigen (HLA) class I or class II motif
XX useful in the creation of an HLA vaccine to modulate 213P1F1.
XX
XX Sequence 9 AA;
XX
XX Query Match 29.5%; Score 31; DB 8; Length 9;
XX Best Local Similarity 62.5%; Pred. No. 2e+06;
XX Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 10 GFLVGEEG 17
XX ||: ||:|
XX 2 GFLKGEDEG 9
XX
XX Db
XX
XX RESULT 69
XX ADO72141
XX ID ADO72141 standard; peptide; 9 AA.
XX
XX AC ADO72141;
XX
XX DT 15-JUL-2004 (first entry)
XX
XX DE Human 213P1F1 HLA motif bearing epitope #6240.
XX
XX KW cytostatic; gene therapy; 213P1F1; 213P1F1 modulation; cancer;
XX transgenic; cytotoxic agent delivery; diagnostic agent delivery;
XX immune response; pancreatic cancer; rectal cancer; bladder cancer; human;
XX human leukocyte antigen; HLA; class I; class II; epitope; HLA motif;
XX HLA vaccine.
XX
XX KW Homo sapiens.
XX
XX OS
```



XX	US2004019915-A1.
PN	
XX	
PD	29-JAN-2004.
XX	
XX	
PF	01-APR-2002; 2002US-00114432.
PP	
PR	01-APR-2002; 2002US-00114432.
XX	
PA	(CHAL/) CHALLITA-BID P M.
PA	(RAIT/) RAITANO A B.
PA	(FARI/) PARIS M.
PA	(HUBE/) HUBERT R S.
PA	(MORR/) MORRISON R K.
PA	(GEWU/) GE W.
PA	(JAKO/) JAKOBOVITS A.
PI	
PI	Challita-Bid PM, Raitano AB, Paris M, Hubert RS, Morrison RK,
DR	Ge W, Jakobovits A;
XX	
XX	WPI; 2004-132240/13.
XX	
PT	New composition comprising a substance that modulates the status of
PT	213P1F1, or a molecule that is modulated by 213P1F1, useful for
PT	detecting or treating cancer, e.g. pancreatic or rectal cancer.
XX	
PS	Example 13; Page 162; 334pp; English.
XX	
CC	The invention describes a composition comprising a substance that
CC	modulates the status of 213P1F1, or a molecule that is modulated by
CC	213P1F1, where the status of the cell that expresses 213P1F1 is
CC	modulated, and 213P1F1 is a gene overexpressed in many cancers. Also
CC	described are: a pharmaceutical composition comprising the composition
CC	cited above in a unit dose form; an antibody or its fragment; a non-human
CC	transgenic animal that produced the antibody; a hydridoma that produces
CC	the antibody; delivering a cytotoxic agent or a diagnostic agent to the
CC	cell that expresses 213P1F1; a polynucleotide that encodes the protein;
CC	Inhibiting growth of cancer cells that expresses 213P1F1; generating a
CC	mammalian immune response; detecting the presence of 213P1F1-related
CC	protein or polynucleotide in a sample; and detecting the presence of
CC	cancer in an individual. The compositions, molecules and methods are
CC	useful for detecting and treating cancer, e.g. pancreatic or rectal
CC	cancer. This is the amino acid sequence of a human 213P1F1 peptide
CC	epitope bearing a human leukocyte antigen (HLA) class I or class II motif
CC	useful in the creation of an HLA vaccine to modulate 213P1F1.
XX	
SO	Sequence 9 AA;
Query Match	29.5%; Score 31; DB #; Length 9;
Best Local Similarity	62.5%; Pred. No. 2e+06;
Matches 5; Conservative	2; Mismatches 1; Indels 0; Gaps 0
OY	10 GPVGEEG 17
DB	::
	1 GPLKGEDG 8
RESULT 70	
ADO74908	
ID	ADO74908 standard; peptide; 10 AA.
XX	
AC	ADO74908;
XX	
DT	15-JUL-2004 (first entry)
XX	
DE	Human 213P1F1 HLA motif bearing epitope #9007.
XX	
KW	Cycostatic; gene therapy; 213P1F1; 213P1F1 modulation; cancer;
KW	transgenic; cytotoxic agent delivery; diagnostic agent delivery;
KW	immune response; pancreatic cancer; rectal cancer; bladder cancer; human;
KW	human leukocyte antigen; HLA; class I; class II; epitope; HLA motif;
XX	HLA vaccine.
XX	

OS Homo sapiens.  
XX  
PN US2004019915-A1.  
XX  
PD 29-JAN-2004.  
XX  
PF 01-APR-2002; 2002US-00114432.  
XX  
PR 01-APR-2002; 2002US-00114432.  
XX  
PA (CHAL/) CHALILITA-BID P M.  
PA (RAIT/) RAITANO A B.  
PA (FARI/) FARIIS M.  
PA (HUBB/) HUBERT R S.  
PA (MORR/) MORRISON R K.  
PA (GEMW/) GE W.  
PA (JAKO/) JAKOBOVITS A.  
XX  
PI Chalilita-Bid PM, Raitano AB, Fariis M, Hubert RS, Morrison RK,  
PI Ge W, Jakobovits A;  
XX  
DR WPI: 2004-132240/13.  
XX  
XX  
PT New composition comprising a substance that modulates the status of  
PT 213P1F11, or a molecule that is modulated by 213P1F11, useful for  
PT detecting or treating cancer, e.g. pancreatic or rectal cancer.  
XX  
XX  
PS Example 13; Page 207; 334pp; English.  
XX  
XX  
CC The invention describes a composition comprising a substance that  
CC modulates the status of 213P1F11, or a molecule that is modulated by  
CC 213P1F11, where the status of the cell that expresses 213P1F11 is  
CC modulated and 213P1F11 is a gene overexpressed in many cancers. Also  
CC described are: a pharmaceutical composition comprising the composition  
CC cited above in a unit dose form; an antibody or its fragment; a non-human  
CC transgenic animal that produced the antibody; a hybridoma that produces  
CC the antibody; delivering a cytotoxic agent or a diagnostic agent to the  
CC cell that expresses 213P1F11; a polynucleotide that encodes the protein;  
CC inhibiting growth of cancer cells that expresses 213P1F11; generating a  
CC mammalian immune response; detecting the presence of 213P1F11-related  
CC protein or polynucleotide in a sample; and detecting the presence of  
CC cancer in an individual. The compositions, molecules and methods are  
CC useful for detecting and treating cancer, e.g. pancreatic or rectal  
CC cancer. This is the amino acid sequence of a human 213P1F11 peptide  
CC epitope bearing a human leukocyte antigen (HLA) class I or class II motif  
CC useful in the creation of an HLA vaccine to modulate 213P1F11.  
XX  
XX  
SQ Sequence 10 AA;  
XX  
XX  
Query Match 29.5%; Score 31; DB 8; Length 10;  
Best Local Similarity 62.5%; Pred. No. 6.8e-02;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0  
XX  
QY 10 GFIIVEEG 17  
||: ||:  
||: ||:  
Db 1 GFLKGEDG 8  
XX  
RESULT 71  
ADO67058  
ID ADO67058 standard; peptide; 10 AA.  
XX  
AC ADO67058;  
XX  
DT 15-JUL-2004 (first entry)  
XX  
XX  
DE Human 213P1F11 HLA motif bearing epitope #3148.  
XX  
XX  
KW cytoskeletal; gene therapy; 213P1F11; 213P1F11 modulation; cancer;  
KW transgenic; cytotoxic agent delivery; diagnostic agent delivery;  
KW immune response; pancreatic cancer; rectal cancer; bladder cancer; human;  
KW human leukocyte antigen; HLA; class I; class II; epitope; HLA motif;  
KW HLA vaccine.

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XX OS Homo sapiens.
XX PN US2004019915-A1.
XX PD 29-JAN-2004.
XX PF 01-APR-2002; 2002US-00114432.
XX PR 01-APR-2002; 2002US-00114432.
XX (CHAL/) CHALLITA-EID P M.
XX PA (RAIT/) RAITANO A B.
XX PA (FARI/) FARIS M.
XX PA (HUBE/) HUBERT R S.
XX PA (MORR/) MORRISON R K.
XX PA (GEWW/) GE W.
XX PA (JAKO/) JAKOBOVITS A.
XX PI Challita-Eid PM, Raitano AB, Faris M, Hubert RS, Morrison RK,
XX PI Ge W, Jakobovits A;
XX DR WPI; 2004-132240/13.
XX PT New composition comprising a substance that modulates the status of
XX PT 213p1f1, or a molecule that is modulated by 213p1f1, useful for
XX PT detecting or treating cancer, e.g. pancreatic or rectal cancer.
XX PS Example 13; Page 114; 334pp; English.
XX CC The invention describes a composition comprising a substance that
XX CC modulates the status of 213p1f1, or a molecule that is modulated by
XX CC 213p1f1, where the status of the cell that expresses 213p1f1 is
XX CC modulated and 213p1f1 is a gene overexpressed in many cancers. Also
XX CC described are: a pharmaceutical composition comprising the composition
XX CC cited above in a unit dose form; an antibody or its fragment; a non-human
XX CC transgenic animal that produced the antibody; a hybridoma that produces
XX CC the antibody; delivering a cytotoxic agent or a diagnostic agent to the
XX CC cell that expresses 213p1f1; a polynucleotide that encodes the protein;
XX CC inhibiting growth of cancer cells that expresses 213p1f1; generating a
XX CC mammalian immune response; detecting the presence of 213p1f1-related
XX CC protein or polynucleotide in a sample; and detecting the presence of
XX CC cancer in an individual. The compositions, molecules and methods are
XX CC useful for detecting and treating cancer, e.g. pancreatic or rectal
XX CC cancer. This is the amino acid sequence of a human 213p1f1 peptide
XX CC epitope bearing a human leukocyte antigen (HLA) class I or class II motif
XX CC useful in the creation of an HLA vaccine to modulate 213p1f1.
XX SQ Sequence 10 AA;
XX
XX Query Match 29.5%; Score 31; DB 8; Length 10;
XX Best Local Similarity 62.5%; Pred. No. 6.8e+02;
XX Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 10 GPTVGEBG 17
XX ||: ||:|
XX Db 1 GPTKGBDG 8
XX
XX RESULT 72
XX ADO74471
XX ID ADO74471 standard; peptide; 10 AA.
XX AC ADO74471;
XX AC 15-JUL-2004 (first entry)
XX DT Human 213p1f1 HLA motif bearing epitope #8570.
XX XX cytostatic; gene therapy; 213p1f1; 213p1f1 modulation; cancer;
XX KW transgenic; cytotoxic agent delivery; diagnostic agent delivery;
XX KW immune response; pancreatic cancer; rectal cancer; bladder cancer; human;
XX KW human leukocyte antigen; HLA; class I; class II; epitope; HLA motif;

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```

KW HLA vaccine.
XX OS Homo sapiens.
XX PN US2004019915-A1.
XX PD 29-JAN-2004.
XX PF 01-APR-2002; 2002US-00114432.
XX PR 01-APR-2002; 2002US-00114432.
XX (CHAL/) CHALLITA-EID P M.
XX PA (RAIT/) RAITANO A B.
XX PA (FARI/) FARIS M.
XX PA (HUBE/) HUBERT R S.
XX PA (MORR/) MORRISON R K.
XX PA (GEWW/) GE W.
XX PA (JAKO/) JAKOBOVITS A.
XX PI Challita-Eid PM, Raitano AB, Faris M, Hubert RS, Morrison RK,
XX PI Ge W, Jakobovits A;
XX DR WPI; 2004-132240/13.
XX PT New composition comprising a substance that modulates the status of
XX PT 213p1f1, or a molecule that is modulated by 213p1f1, useful for
XX PT detecting or treating cancer, e.g. pancreatic or rectal cancer.
XX PS Example 13; Page 200; 334pp; English.
XX CC The invention describes a composition comprising a substance that
XX CC modulates the status of 213p1f1, or a molecule that is modulated by
XX CC 213p1f1, where the status of the cell that expresses 213p1f1 is
XX CC modulated and 213p1f1 is a gene overexpressed in many cancers. Also
XX CC described are: a pharmaceutical composition comprising the composition
XX CC cited above in a unit dose form; an antibody or its fragment; a non-human
XX CC transgenic animal that produced the antibody; a hybridoma that produces
XX CC the antibody; delivering a cytotoxic agent or a diagnostic agent to the
XX CC cell that expresses 213p1f1; a polynucleotide that encodes the protein;
XX CC inhibiting growth of cancer cells that expresses 213p1f1; generating a
XX CC mammalian immune response; detecting the presence of 213p1f1-related
XX CC protein or polynucleotide in a sample; and detecting the presence of
XX CC cancer in an individual. The compositions, molecules and methods are
XX CC useful for detecting and treating cancer, e.g. pancreatic or rectal
XX CC cancer. This is the amino acid sequence of a human 213p1f1 peptide
XX CC epitope bearing a human leukocyte antigen (HLA) class I or class II motif
XX CC useful in the creation of an HLA vaccine to modulate 213p1f1.
XX SQ Sequence 10 AA;
XX
XX Query Match 29.5%; Score 31; DB 8; Length 10;
XX Best Local Similarity 62.5%; Pred. No. 6.8e+02;
XX Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 10 GPTVGEBG 17
XX ||: ||:|
XX Db 3 GPTKGBDG 10
XX
XX RESULT 73
XX ADO74828
XX ID ADO74828 standard; peptide; 10 AA.
XX AC ADO74828;
XX AC 15-JUL-2004 (first entry)
XX DT Human 213p1f1 HLA motif bearing epitope #8927.
XX XX cytostatic; gene therapy; 213p1f1; 213p1f1 modulation; cancer;
XX KW transgenic; cytotoxic agent delivery; diagnostic agent delivery;
XX KW immune response; pancreatic cancer; rectal cancer; bladder cancer; human;

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KM human leukocyte antigen; HLA; class I; class II; epitope; HLA motif;  
 KM HLA vaccine.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2004019915-A1.  
 XX  
 PD 29-JAN-2004.  
 XX  
 PF 01-APR-2002; 2002US-00114432.  
 XX  
 PR 01-APR-2002; 2002US-00114432.  
 XX  
 PA (CHAL/) CHALLITA-BID P M.  
 PA (RAIT/) RAITANO A B.  
 PA (PARI/) PARIS M.  
 PA (HUBE/) HUBERT R S.  
 PA (MORR/) MORRISON R K.  
 PA (GERM/) GE W.  
 PA (JAKO/) JAKOBOVITS A.  
 XX  
 PI Chailita-Bid PM, Raitano AB, Faris M, Hubert RS, Morrison RK;  
 PI Ge W, Jakobovits A;  
 XX  
 DR WPI; 2004-132240/13.  
 XX  
 PT New composition comprising a substance that modulates the status of  
 PT 213P1F1, or a molecule that is modulated by 213P1F1, useful for  
 PT detecting or treating cancer, e.g. pancreatic or rectal cancer.  
 XX  
 PS Example 13; Page 205; 334pp; English.  
 XX  
 CC The invention describes a composition comprising a substance that  
 CC modulates the status of 213P1F1, or a molecule that is modulated by  
 CC 213P1F1, where the status of the cell that expresses 213P1F1 is  
 CC modulated and 213P1F1 is a gene overexpressed in many cancers. Also  
 CC described are: a pharmaceutical composition comprising the composition  
 CC cited above in a unit dose form; an antibody or its fragment; a non-human  
 CC transgenic animal that produces the antibody; a hybridoma that produces  
 CC the antibody; delivering a cytotoxic agent or a diagnostic agent to the  
 CC cell that expresses 213P1F1; a polynucleotide that encodes the protein;  
 CC inhibiting growth of cancer cells that expresses 213P1F1; generating a  
 CC mammalian immune response; detecting the presence of 213P1F1-related  
 CC protein or polynucleotide in a sample; and detecting the presence of  
 CC cancer in an individual. The compositions, molecules and methods are  
 CC useful for detecting and treating cancer, e.g. pancreatic or rectal  
 CC cancer. This is the amino acid sequence of a human 213P1F1 peptide  
 CC epitope bearing a human leukocyte antigen (HLA) class I or class II motif  
 CC useful in the creation of an HLA vaccine to modulate 213P1F1.  
 CC  
 XX  
 SQ Sequence 10 AA;  
 XX

Query Match 29.5%; Score 31; DB 8; Length 10;  
 Best Local Similarity 62.5%; Pred. No. 6,8e+02;  
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 10 GFLVGEHG 17  
 ||: ||:|  
 Db 3 GFLKGEHG 10

RESULT 74  
 ADO66467 standard; peptide; 10 AA.  
 XX  
 AC ADO66467;  
 XX  
 DT 15-JUL-2004 (first entry)  
 XX  
 DE Human 213P1F1 HLA motif bearing epitope #2557.  
 XX  
 KM cytotoxic; gene therapy; 213P1F1; 213P1F1 modulation; cancer;  
 KM transgenic; cytotoxic agent delivery; diagnostic agent delivery;

KM immune response; pancreatic cancer; rectal cancer; bladder cancer; human;  
 KM human leukocyte antigen; HLA; class I; class II; epitope; HLA motif;  
 KM HLA vaccine.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2004019915-A1.  
 XX  
 PD 29-JAN-2004.  
 XX  
 PF 01-APR-2002; 2002US-00114432.  
 XX  
 PR 01-APR-2002; 2002US-00114432.  
 XX  
 PA (CHAL/) CHALLITA-BID P M.  
 PA (RAIT/) RAITANO A B.  
 PA (PARI/) PARIS M.  
 PA (HUBE/) HUBERT R S.  
 PA (MORR/) MORRISON R K.  
 PA (GERM/) GE W.  
 PA (JAKO/) JAKOBOVITS A.  
 XX  
 PI Chailita-Bid PM, Raitano AB, Faris M, Hubert RS, Morrison RK;  
 PI Ge W, Jakobovits A;  
 XX  
 DR WPI; 2004-132240/13.  
 XX  
 PT New composition comprising a substance that modulates the status of  
 PT 213P1F1, or a molecule that is modulated by 213P1F1, useful for  
 PT detecting or treating cancer, e.g. pancreatic or rectal cancer.  
 XX  
 PS Example 13; Page 105; 334pp; English.  
 XX  
 CC The invention describes a composition comprising a substance that  
 CC modulates the status of 213P1F1, or a molecule that is modulated by  
 CC 213P1F1, where the status of the cell that expresses 213P1F1 is  
 CC modulated and 213P1F1 is a gene overexpressed in many cancers. Also  
 CC described are: a pharmaceutical composition comprising the composition  
 CC cited above in a unit dose form; an antibody or its fragment; a non-human  
 CC transgenic animal that produces the antibody; a hybridoma that produces  
 CC the antibody; delivering a cytotoxic agent or a diagnostic agent to the  
 CC cell that expresses 213P1F1; a polynucleotide that encodes the protein;  
 CC inhibiting growth of cancer cells that expresses 213P1F1; generating a  
 CC mammalian immune response; detecting the presence of 213P1F1-related  
 CC protein or polynucleotide in a sample; and detecting the presence of  
 CC cancer in an individual. The compositions, molecules and methods are  
 CC useful for detecting and treating cancer, e.g. pancreatic or rectal  
 CC cancer. This is the amino acid sequence of a human 213P1F1 peptide  
 CC epitope bearing a human leukocyte antigen (HLA) class I or class II motif  
 CC useful in the creation of an HLA vaccine to modulate 213P1F1.  
 CC  
 XX  
 SQ Sequence 10 AA;  
 XX

Query Match 29.5%; Score 31; DB 8; Length 10;  
 Best Local Similarity 62.5%; Pred. No. 6,8e+02;  
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 10 GFLVGEHG 17  
 ||: ||:|  
 Db 1 GFLKGEHG 8

RESULT 75  
 ADO75227 standard; peptide; 10 AA.  
 XX  
 AC ADO75227;  
 XX  
 DT 15-JUL-2004 (first entry)  
 XX  
 DE Human 213P1F1 HLA motif bearing epitope #9326.  
 XX  
 KM cytotoxic; gene therapy; 213P1F1; 213P1F1 modulation; cancer;

KW transgenic; cytotoxic agent delivery; diagnostic agent delivery;  
KW immune response; pancreatic cancer; rectal cancer; bladder cancer; human;  
KW human leukocyte antigen; HLA; class I; class II; epitope; HLA motif;  
KW HLA vaccine.  
XX  
OS Homo sapiens.  
XX  
PN US2004019915-A1.  
XX  
PD 29-JAN-2004.  
XX  
PF 01-APR-2002; 2002US-00114432.  
XX  
PR 01-APR-2002; 2002US-00114432.  
XX  
PR 01-APR-2002; 2002US-00114432.  
XX  
PA (CHAL/) CHALLITA-BID P M.  
PA (RAIT/) RAITANO A B.  
PA (FARI/) FARIS M.  
PA (HUBB/) HUBERT R S.  
PA (MORR/) MORRISON R K.  
PA (GEWW/) GE W.  
PA (JAKO/) JAKOBOVITS A.  
XX  
XX  
XX Challita-Bid PM, Raitano AB, Faris M, Hubert RS, Morrison RK;  
PI Ge W, Jakobovits A;  
XX  
DR WPI, 2004-132240/13.  
XX  
XX New composition comprising a substance that modulates the status of  
PT 213P1F1, or a molecule that is modulated by 213P1F1, useful for  
PT detecting or treating cancer, e.g. pancreatic or rectal cancer.  
XX  
XX  
PS Example 13; Page 211; 334pp; English.  
XX  
XX The invention describes a composition comprising a substance that  
CC modulates the status of 213P1F1, or a molecule that is modulated by  
CC 213P1F1, where the status of the cell that expresses 213P1F1 is  
CC modulated and 213P1F1 is a gene overexpressed in many cancers. Also  
CC described are: a pharmaceutical composition comprising the composition  
CC cited above in a unit dose form; an antibody or its fragment; a non-human  
CC transgenic animal that produced the antibody; a hybridoma that produces  
CC the antibody; delivering a cytotoxic agent or a diagnostic agent to the  
CC cell that expresses 213P1F1; a polynucleotide that encodes the protein;  
CC inhibiting growth of cancer cells that expresses 213P1F1; generating a  
CC mammalian immune response; detecting the presence of 213P1F1-related  
CC protein or polynucleotide in a sample; and detecting the presence of  
CC cancer in an individual. The compositions, molecules and methods are  
CC useful for detecting and treating cancer, e.g. pancreatic or rectal  
CC cancer. This is the amino acid sequence of a human 213P1F1 peptide  
CC epitope bearing a human leukocyte antigen (HLA) class I or class II motif  
CC useful in the creation of an HLA vaccine to modulate 213P1F1.  
XX  
SQ Sequence 10 AA;  
XX

Query Match 29.5%; Score 31; DB 8; Length 10;  
Best Local Similarity 62.5%; Pred. No. 6.8e+02;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 10 GFTVGEEG 17  
||: ||: |  
DB 3 GFLKGEDG 10

RESULT 76  
AD074526  
ID AD074526 standard; peptide; 10 AA.  
XX  
AC AD074526;  
XX  
DT 15-JUL-2004 (first entry)  
XX  
DE Human 213P1F1 HLA motif bearing epitope #8625.  
XX

KW cytostatic; gene therapy; 213P1F1; 213P1F1 modulation; cancer;  
KW transgenic; cytotoxic agent delivery; diagnostic agent delivery;  
KW immune response; pancreatic cancer; rectal cancer; bladder cancer; human;  
KW human leukocyte antigen; HLA; class I; class II; epitope; HLA motif;  
KW HLA vaccine.  
XX  
OS Homo sapiens.  
XX  
PN US2004019915-A1.  
XX  
PD 29-JAN-2004.  
XX  
PF 01-APR-2002; 2002US-00114432.  
XX  
PR 01-APR-2002; 2002US-00114432.  
XX  
PR 01-APR-2002; 2002US-00114432.  
XX  
PA (CHAL/) CHALLITA-BID P M.  
PA (RAIT/) RAITANO A B.  
PA (FARI/) FARIS M.  
PA (HUBB/) HUBERT R S.  
PA (MORR/) MORRISON R K.  
PA (GEWW/) GE W.  
PA (JAKO/) JAKOBOVITS A.  
XX  
XX  
XX Challita-Bid PM, Raitano AB, Faris M, Hubert RS, Morrison RK;  
PI Ge W, Jakobovits A;  
XX  
DR WPI, 2004-132240/13.  
XX  
XX New composition comprising a substance that modulates the status of  
PT 213P1F1, or a molecule that is modulated by 213P1F1, useful for  
PT detecting or treating cancer, e.g. pancreatic or rectal cancer.  
XX  
XX  
PS Example 13; Page 201; 334pp; English.  
XX  
XX The invention describes a composition comprising a substance that  
CC modulates the status of 213P1F1, or a molecule that is modulated by  
CC 213P1F1, where the status of the cell that expresses 213P1F1 is  
CC modulated and 213P1F1 is a gene overexpressed in many cancers. Also  
CC described are: a pharmaceutical composition comprising the composition  
CC cited above in a unit dose form; an antibody or its fragment; a non-human  
CC transgenic animal that produced the antibody; a hybridoma that produces  
CC the antibody; delivering a cytotoxic agent or a diagnostic agent to the  
CC cell that expresses 213P1F1; a polynucleotide that encodes the protein;  
CC inhibiting growth of cancer cells that expresses 213P1F1; generating a  
CC mammalian immune response; detecting the presence of 213P1F1-related  
CC protein or polynucleotide in a sample; and detecting the presence of  
CC cancer in an individual. The compositions, molecules and methods are  
CC useful for detecting and treating cancer, e.g. pancreatic or rectal  
CC cancer. This is the amino acid sequence of a human 213P1F1 peptide  
CC epitope bearing a human leukocyte antigen (HLA) class I or class II motif  
CC useful in the creation of an HLA vaccine to modulate 213P1F1.  
XX  
SQ Sequence 10 AA;  
XX

Query Match 29.5%; Score 31; DB 8; Length 10;  
Best Local Similarity 62.5%; Pred. No. 6.8e+02;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 10 GFTVGEEG 17  
||: ||: |  
DB 1 GFLKGEDG 8

RESULT 77  
AD075022  
ID AD075022 standard; peptide; 10 AA.  
XX  
AC AD075022;  
XX  
DT 15-JUL-2004 (first entry)  
XX  
DE Human 213P1F1 HLA motif bearing epitope #9121.  
XX

XX cytostatic; gene therapy; 213P1F11; 213P1F11 modulation; cancer;  
 KM transgenic; cytotoxic agent delivery; 213P1F11 modulation; cancer;  
 KM immune response; pancreatic cancer; rectal cancer; bladder cancer; human;  
 KM human leukocyte antigen; HLA; class I; class II; epitope; HLA motif;  
 KM HLA vaccine.  
 XX Homo sapiens.  
 OS  
 PN US2004019915-A1.  
 XX  
 PD 29-JAN-2004.  
 XX  
 PF 01-APR-2002; 2002US-00114432.  
 XX  
 PR 01-APR-2002; 2002US-00114432.  
 XX  
 PA (CHAL/) CHALLITA-ELD P M.  
 PA (RAIT/) RAITANO A B.  
 PA (FARI/) FARIS M.  
 PA (HUBE/) HUBERT R S.  
 PA (MORR/) MORRISON R K.  
 PA (GEMW/) GE W.  
 PA (JAKO/) JAKOBOVITS A.  
 XX  
 PI Chailita-Elid PM, Raitano AB, Faris M, Hubert RS, Morrison RK;  
 PI Ge W, Jakobovits A;  
 XX  
 DR WPI; 2004-132240/13.  
 XX  
 PT New composition comprising a substance that modulates the status of  
 PT 213P1F11, or a molecule that is modulated by 213P1F11, useful for  
 PT detecting or treating cancer, e.g. pancreatic or rectal cancer.  
 XX  
 PS Example 13; Page 208; 334pp; English.  
 XX  
 CC The invention describes a composition comprising a substance that  
 CC modulates the status of 213P1F11, or a molecule that is modulated by  
 CC 213P1F11, where the status of the cell that expresses 213P1F11 is  
 CC modulated, and 213P1F11 is a gene overexpressed in many cancers. Also  
 CC described are: a pharmaceutical composition comprising the composition  
 CC cited above in a unit dose form; an antibody or its fragment; a non-human  
 CC transgenic animal that produced the antibody; a hybridoma that produces  
 CC the antibody; delivering a cytotoxic agent or a diagnostic agent to the  
 CC cell that expresses 213P1F11; a polynucleotide that encodes the protein;  
 CC inhibiting growth of cancer cells that expresses 213P1F11; generating a  
 CC mammalian immune response; detecting the presence of 213P1F11-related  
 CC protein or polynucleotide in a sample; and detecting the presence of  
 CC cancer in an individual. The compositions, molecules and methods are  
 CC useful for detecting and treating cancer, e.g. pancreatic or rectal  
 CC cancer. This is the amino acid sequence of a human 213P1F11 peptide  
 CC epitope bearing a human leukocyte antigen (HLA) class I or class II motif  
 CC useful in the creation of an HLA vaccine to modulate 213P1F11.  
 CC  
 XX  
 SQ Sequence 10 AA;  
 Query Match 29.5%; Score 31; DB 8; Length 10;  
 Best Local Similarity 62.5%; Pred. No. 6.8e+02;  
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 QY 10 GFLVGEEG 17  
 DB 1 GFLVGEEDG 8  
 RESULT 78  
 ADO65940  
 ID ADO65940 standard; peptide; 10 AA.  
 XX  
 AC ADO65940;  
 XX  
 DT 15-JUL-2004 (first entry)  
 XX

DE Human 213P1F11 HLA motif bearing epitope #2030.  
 XX  
 KM cytostatic; gene therapy; 213P1F11; 213P1F11 modulation; cancer;  
 KM transgenic; cytotoxic agent delivery; 213P1F11 modulation; cancer;  
 KM immune response; pancreatic cancer; rectal cancer; bladder cancer; human;  
 KM human leukocyte antigen; HLA; class I; class II; epitope; HLA motif;  
 KM HLA vaccine.  
 XX Homo sapiens.  
 OS  
 PN US2004019915-A1.  
 XX  
 PD 29-JAN-2004.  
 XX  
 PF 01-APR-2002; 2002US-00114432.  
 XX  
 PR 01-APR-2002; 2002US-00114432.  
 XX  
 PA (CHAL/) CHALLITA-ELD P M.  
 PA (RAIT/) RAITANO A B.  
 PA (FARI/) FARIS M.  
 PA (HUBE/) HUBERT R S.  
 PA (MORR/) MORRISON R K.  
 PA (GEMW/) GE W.  
 PA (JAKO/) JAKOBOVITS A.  
 XX  
 PI Chailita-Elid PM, Raitano AB, Faris M, Hubert RS, Morrison RK;  
 PI Ge W, Jakobovits A;  
 XX  
 DR WPI; 2004-132240/13.  
 XX  
 PT New composition comprising a substance that modulates the status of  
 PT 213P1F11, or a molecule that is modulated by 213P1F11, useful for  
 PT detecting or treating cancer, e.g. pancreatic or rectal cancer.  
 XX  
 PS Example 13; Page 98; 334pp; English.  
 XX  
 CC The invention describes a composition comprising a substance that  
 CC modulates the status of 213P1F11, or a molecule that is modulated by  
 CC 213P1F11, where the status of the cell that expresses 213P1F11 is  
 CC modulated, and 213P1F11 is a gene overexpressed in many cancers. Also  
 CC described are: a pharmaceutical composition comprising the composition  
 CC cited above in a unit dose form; an antibody or its fragment; a non-human  
 CC transgenic animal that produced the antibody; a hybridoma that produces  
 CC the antibody; delivering a cytotoxic agent or a diagnostic agent to the  
 CC cell that expresses 213P1F11; a polynucleotide that encodes the protein;  
 CC inhibiting growth of cancer cells that expresses 213P1F11; generating a  
 CC mammalian immune response; detecting the presence of 213P1F11-related  
 CC protein or polynucleotide in a sample; and detecting the presence of  
 CC cancer in an individual. The compositions, molecules and methods are  
 CC useful for detecting and treating cancer, e.g. pancreatic or rectal  
 CC cancer. This is the amino acid sequence of a human 213P1F11 peptide  
 CC epitope bearing a human leukocyte antigen (HLA) class I or class II motif  
 CC useful in the creation of an HLA vaccine to modulate 213P1F11.  
 CC  
 XX  
 SQ Sequence 10 AA;  
 Query Match 29.5%; Score 31; DB 8; Length 10;  
 Best Local Similarity 62.5%; Pred. No. 6.8e+02;  
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 QY 10 GFLVGEEG 17  
 DB 1 GFLVGEEDG 8  
 RESULT 79  
 ADO74212  
 ID ADO74212 standard; peptide; 10 AA.  
 XX  
 AC ADO74212;  
 XX  
 DT 15-JUL-2004 (first entry)  
 XX

```
XX Human 213P1F11 HLA motif bearing epitope #8311.
DE
XX
XX cytostatic; gene therapy; 213P1F11; 213P1F11 modulation; cancer;
KM transgenic; cytotoxic agent delivery; diagnostic agent delivery;
KM immune response; pancreatic cancer; rectal cancer; bladder cancer; human;
KM human leukocyte antigen; HLA; class I; class II; epitope; HLA motif;
XX HLA vaccine.
XX
OS Homo sapiens.
XX
XX US2004019915-A1.
XX
XX 29-JAN-2004.
XX
XX 01-APR-2002; 2002US-00114432.
XX
XX 01-APR-2002; 2002US-00114432.
XX
XX 01-APR-2002; 2002US-00114432.
XX
XX (CHAL/) CHALLITA-ElD P M.
XX
XX (RAIT/) RAITANO A B.
XX
XX (FARI/) FARI S M.
XX
XX (HUBE/) HUBERT R S.
XX
XX (MORR/) MORRISON R K.
XX
XX (GEWM/) GE W.
XX
XX (JAKO/) JAKOBOVITS A.
XX
XX
XX Chailita-ElD PM, Raitano AB, Fari S, Hubert RS, Morrison RK;
PI Ge W, Jakobovits A;
XX
XX WPI; 2004-132240/13.
XX
XX
XX New composition comprising a substance that modulates the status of
PT 213P1F11, or a molecule that is modulated by 213P1F11, useful for
PT detecting or treating cancer, e.g. pancreatic or rectal cancer.
XX
XX
XX Example 13; Page 197; 334pp; English.
XX
XX The invention describes a composition comprising a substance that
CC modulates the status of 213P1F11, or a molecule that is modulated by
CC 213P1F11, where the status of the cell that expresses 213P1F11 is
CC modulated and 213P1F11 is a gene overexpressed in many cancers. Also
CC described are: a pharmaceutical composition comprising the composition
CC cited above in a unit dose form; an antibody or its fragment; a non-human
CC transgenic animal that produced the antibody; a hybridoma that produces
CC the antibody; delivering a cytotoxic agent or a diagnostic agent to the
CC cell that expresses 213P1F11; a polynucleotide that encodes the protein;
CC inhibiting growth of cancer cells that expresses 213P1F11; generating a
CC mammalian immune response; detecting the presence of 213P1F11-related
CC protein or polynucleotide in a sample; and detecting the presence of
CC cancer in an individual. The compositions, molecules and methods are
CC useful for detecting and treating cancer, e.g. pancreatic or rectal
CC cancer. This is the amino acid sequence of a human 213P1F11 peptide
CC epitope bearing a human leukocyte antigen (HLA) class I or class II motif
CC useful in the creation of an HLA vaccine to modulate 213P1F11.
XX
XX
XX Sequence 10 AA;
SQ
Query Match 29.5%; Score 31; DB 8; Length 10;
Best Local Similarity 62.5%; Pred. No. 6.8e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 10 GFLVGEKG 17
DB 3 GFLVGEKG 10
RESULT 80
AD075255
ID AD075255 standard; peptide; 10 AA.
XX
XX AD075255;
XX
```

```
DT 15-JUL-2004 (first entry)
XX
XX Human 213P1F11 HLA motif bearing epitope #9354.
XX
XX cytostatic; gene therapy; 213P1F11; 213P1F11 modulation; cancer;
KM transgenic; cytotoxic agent delivery; diagnostic agent delivery;
KM immune response; pancreatic cancer; rectal cancer; bladder cancer; human;
KM human leukocyte antigen; HLA; class I; class II; epitope; HLA motif;
XX HLA vaccine.
XX
OS Homo sapiens.
XX
XX US2004019915-A1.
XX
XX 29-JAN-2004.
XX
XX 01-APR-2002; 2002US-00114432.
XX
XX 01-APR-2002; 2002US-00114432.
XX
XX 01-APR-2002; 2002US-00114432.
XX
XX (CHAL/) CHALLITA-ElD P M.
XX
XX (RAIT/) RAITANO A B.
XX
XX (FARI/) FARI S M.
XX
XX (HUBE/) HUBERT R S.
XX
XX (MORR/) MORRISON R K.
XX
XX (GEWM/) GE W.
XX
XX (JAKO/) JAKOBOVITS A.
XX
XX
XX Chailita-ElD PM, Raitano AB, Fari S, Hubert RS, Morrison RK;
PI Ge W, Jakobovits A;
XX
XX WPI; 2004-132240/13.
XX
XX
XX New composition comprising a substance that modulates the status of
PT 213P1F11, or a molecule that is modulated by 213P1F11, useful for
PT detecting or treating cancer, e.g. pancreatic or rectal cancer.
XX
XX
XX Example 13; Page 212; 334pp; English.
XX
XX The invention describes a composition comprising a substance that
CC modulates the status of 213P1F11, or a molecule that is modulated by
CC 213P1F11, where the status of the cell that expresses 213P1F11 is
CC modulated and 213P1F11 is a gene overexpressed in many cancers. Also
CC described are: a pharmaceutical composition comprising the composition
CC cited above in a unit dose form; an antibody or its fragment; a non-human
CC transgenic animal that produced the antibody; a hybridoma that produces
CC the antibody; delivering a cytotoxic agent or a diagnostic agent to the
CC cell that expresses 213P1F11; a polynucleotide that encodes the protein;
CC inhibiting growth of cancer cells that expresses 213P1F11; generating a
CC mammalian immune response; detecting the presence of 213P1F11-related
CC protein or polynucleotide in a sample; and detecting the presence of
CC cancer in an individual. The compositions, molecules and methods are
CC useful for detecting and treating cancer, e.g. pancreatic or rectal
CC cancer. This is the amino acid sequence of a human 213P1F11 peptide
CC epitope bearing a human leukocyte antigen (HLA) class I or class II motif
CC useful in the creation of an HLA vaccine to modulate 213P1F11.
XX
XX
XX Sequence 10 AA;
SQ
Query Match 29.5%; Score 31; DB 8; Length 10;
Best Local Similarity 62.5%; Pred. No. 6.8e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 10 GFLVGEKG 17
DB 2 GFLVGEKG 9
RESULT 81
AD067592
ID AD067592 standard; peptide; 10 AA.
XX
XX AD067592;
XX
```

```

XX 15-JUL-2004 (first entry)
DT
XX
XX
XX Human 213P1F11 HLA motif bearing epitope #3682.
DE
XX
XX cytostatic; gene therapy; 213P1F11, 213P1F11 modulation; cancer;
XX transgenic; cytotoxic agent delivery; diagnostic agent delivery;
XX immune response; pancreatic cancer; rectal cancer; bladder cancer; human;
XX human leukocyte antigen/ HLA; class I; class II; epitope; HLA motif;
XX HLA vaccine.
XX
XX Homo sapiens.
XX
XX US2004019915-A1.
XX
XX 29-JAN-2004.
XX
XX 01-APR-2002; 2002US-00114432.
XX
XX 01-APR-2002; 2002US-00114432.
XX
XX (CHAL/) CHALLITA-EID P M.
XX (RAIT/) RAITANO A B.
XX (FARI/) PARIS M.
XX (HUBE/) HUBERT R S.
XX (MORR/) MORRISON R K.
XX (GEWM/) GE W.
XX (JAKO/) JAKOBOVITS A.
XX
XX Challita-Eid PM, Raitano AB, Paris M, Hubert RS, Morrison RK,
XX Ge W, Jakobovits A;
XX WPI, 2004-132240/13.
XX
XX New composition comprising a substance that modulates the status of
XX 213P1F11, or a molecule that is modulated by 213P1F11, useful for
XX detecting or treating cancer, e.g. pancreatic or rectal cancer.
XX
XX Example 13; Page 121, 334pp; English.
XX
XX The invention describes a composition comprising a substance that
XX modulates the status of 213P1F11, or a molecule that is modulated by
XX 213P1F11, where the status of the cell that expresses 213P1F11 is
XX modulated and 213P1F11 is a gene overexpressed in many cancers. Also
XX described are: a pharmaceutical composition comprising the composition
XX cited above in a unit dose form; an antibody or its fragment; a non-human
XX transgenic animal that produced the antibody; a hybridoma that produces
XX the antibody; delivering a cytotoxic agent or a diagnostic agent to the
XX cell that expresses 213P1F11; a polynucleotide that encodes the protein;
XX inhibiting growth of cancer cells that express 213P1F11, generating a
XX mammalian immune response; detecting the presence of 213P1F11-related
XX protein or polynucleotide in a sample; and detecting the presence of
XX cancer in an individual. The compositions, molecules and methods are
XX useful for detecting and treating cancer, e.g. pancreatic or rectal
XX cancer. This is the amino acid sequence of a human 213P1F11 peptide
XX epitope bearing a human leukocyte antigen (HLA) class I or class II motif
XX useful in the creation of an HLA vaccine to modulate 213P1F11.
XX
XX Sequence 10 AA;
XX
XX
XX Query Match 29.5%; Score 31; DB 8; Length 10;
XX Best Local Similarity 62.5%; Pred. No. 6.8e+02;
XX Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
XX
XX 10 GYGVGEEG 17
XX ||: ||: ||
XX Db 1 GFLKGEDEG 8
XX
XX
XX RESULT 82
XX ADO74085
XX ID ADO74085 standard; peptide; 10 AA.
XX

```

```

AC AD074085;
XX 15-JUL-2004 (first entry)
XX
XX
DE Human 213P1F11 HLA motif bearing epitope #8184.
XX
XX cytotoxic; gene therapy; 213P1F11; 213P1F11 modulation; cancer;
XX transgenic; cytotoxic agent delivery; diagnostic agent delivery;
KW human leukocyte antigen; HLA; class I; class II; epitope; HLA motif;
KW HLA vaccine.
XX
XX Homo sapiens.
XX
XX US2004019915-A1.
XX
XX 29-JAN-2004.
XX
XX 01-APR-2002; 2002US-00114432.
XX
XX 01-APR-2002; 2002US-00114432.
XX
XX 01-APR-2002; 2002US-00114432.
XX
XX (CHAL/) CHALLITA-BID P M.
XX (RAIT/) RAITANO A B.
XX (FARI/) FARIS M.
XX (HUBE/) HUBERT R S.
XX (MORR/) MORRISON R K.
XX (GEWA/) GE W.
XX (JAKO/) JAKOBOVITS A.
XX
XX Challita-Bid PM, Raitano AB, Faris M, Hubert RS, Morrison RK,
XX Ge W, Jakobovits A;
XX
XX WPI: 2004-132240/13.
XX
XX
XX New composition comprising a substance that modulates the status of
XX 213P1F11, or a molecule that is modulated by 213P1F11, useful for
XX detecting or treating cancer, e.g. pancreatic or rectal cancer.
XX
XX
XX Example 13; Page 195, 334pp; English.
XX
XX
XX The invention describes a composition comprising a substance that
XX modulates the status of 213P1F11, or a molecule that is modulated by
XX 213P1F11, where the status of the cell that expresses 213P1F11 is
XX modulated and 213P1F11 is a gene overexpressed in many cancers. Also
XX described are: a pharmaceutical composition comprising the composition
XX cited above in a unit dose form; an antibody or its fragment; a non-human
XX transgenic animal that produced the antibody; a hybridoma that produces
XX the antibody; delivering a cytotoxic agent or a diagnostic agent to the
XX cell that expresses 213P1F11; a polynucleotide that encodes the protein;
XX inhibiting growth of cancer cells that expresses 213P1F11; generating a
XX mammalian immune response; detecting the presence of 213P1F11-related
XX protein or polynucleotide in a sample; and detecting the presence of
XX cancer in an individual. The compositions, molecules and methods are
XX useful for detecting and treating cancer, e.g. pancreatic or rectal
XX cancer. This is the amino acid sequence of a human 213P1F11 peptide
XX epitope bearing a human leukocyte antigen (HLA) class I or class II motif
XX useful in the creation of an HLA vaccine to modulate 213P1F11.
XX
XX
XX Sequence 10 AA;
XX
XX Query Match 29.5%; Score 31; DB 8; Length 10;
XX Best Local Similarity 62.5%; Pred. NO. 6.8e-02;
XX Match 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0
XX
XX 10 GPIVGEEG 17
XX ||: ||:|
XX 1 GFLKGEDG 8
XX
XX RESULT 83
XX ID AD074939
XX AD074939 standard; peptide; 10 AA.

```

XX AD074939;  
 AC 15-JUL-2004 (first entry)  
 XX  
 DT  
 XX  
 DE Human 213P1F11 HLA motif bearing epitope #9038.  
 XX  
 KW cytotoxic; gene therapy; 213P1F11; 213P1F11 modulation; cancer;  
 KW transgenic; cytotoxic agent delivery; diagnostic agent delivery;  
 KW immune response; pancreatic cancer; rectal cancer; bladder cancer; human;  
 KW human leukocyte antigen; HLA; class I; class II; epitope; HLA motif;  
 KW HLA vaccine.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2004019915-A1.  
 XX  
 PD 29-JAN-2004.  
 XX  
 PF 01-APR-2002; 2002US-00114432.  
 XX  
 PR 01-APR-2002; 2002US-00114432.  
 XX  
 PR 01-APR-2002; 2002US-00114432.  
 XX  
 PA (CHAL/) CHALLITA-BID P M.  
 PA (RAIT/) RAITANO A B.  
 PA (FARI/) FARIS M.  
 PA (HUBB/) HUBERT R S.  
 PA (MORR/) MORRISON R K.  
 PA (GEWW/) GE W.  
 PA (JAKO/) JAKOBOVITS A.  
 XX  
 PI Challita-Bid PM, Raitano AB, Faris M, Hubert RS, Morrison RK;  
 PI Ge W, Jakobovits A;  
 XX  
 DR WPI; 2004-132240/13.  
 XX  
 PT New composition comprising a substance that modulates the status of  
 PT 213P1F11, or a molecule that is modulated by 213P1F11, useful for  
 PT detecting or treating cancer, e.g. pancreatic or rectal cancer.  
 XX  
 PS Example 13; Page 207, 334pp; English.  
 XX  
 CC The invention describes a composition comprising a substance that  
 CC modulates the status of 213P1F11, or a molecule that is modulated by  
 CC 213P1F11, where the status of the cell that expresses 213P1F11 is  
 CC modulated and 213P1F11 is a gene overexpressed in many cancers. Also  
 CC described are: a pharmaceutical composition comprising the composition  
 CC cited above in a unit dose form; an antibody or its fragment; a non-human  
 CC transgenic animal that produced the antibody; a hybridoma that produces  
 CC the antibody; delivering a cytotoxic agent or a diagnostic agent to the  
 CC cell that expresses 213P1F11; a polynucleotide that encodes the protein;  
 CC inhibiting growth of cancer cells that expresses 213P1F11; generating a  
 CC mammalian immune response; detecting the presence of 213P1F11-related  
 CC protein or polynucleotide in a sample; and detecting the presence of  
 CC cancer in an individual. The compositions, molecules and methods are  
 CC useful for detecting and treating cancer, e.g. pancreatic or rectal  
 CC cancer. This is the amino acid sequence of a human 213P1F11 peptide  
 CC epitope bearing a human leukocyte antigen (HLA) class I or class II motif  
 CC useful in the creation of an HLA vaccine to modulate 213P1F11.  
 CC  
 XX  
 SQ Sequence 10 AA;

Query Match 29.5%; Score 31; DB 8; Length 10;  
 Best Local Similarity 62.5%; Pred. No. 6.8e+02;  
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 10 GRTVEEG 17  
 ||: ||: ||:  
 Db 2 GFLKGEDE 9

RESULT 84  
 AD075094

ID AD075094 standard; peptide; 10 AA.  
 XX  
 AC AD075094;  
 XX  
 DT 15-JUL-2004 (first entry)  
 XX  
 DE Human 213P1F11 HLA motif bearing epitope #9193.  
 XX  
 KW cytotoxic; gene therapy; 213P1F11; 213P1F11 modulation; cancer;  
 KW transgenic; cytotoxic agent delivery; diagnostic agent delivery;  
 KW immune response; pancreatic cancer; rectal cancer; bladder cancer; human;  
 KW human leukocyte antigen; HLA; class I; class II; epitope; HLA motif;  
 KW HLA vaccine.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2004019915-A1.  
 XX  
 PD 29-JAN-2004.  
 XX  
 PF 01-APR-2002; 2002US-00114432.  
 XX  
 PR 01-APR-2002; 2002US-00114432.  
 XX  
 PR 01-APR-2002; 2002US-00114432.  
 XX  
 PA (CHAL/) CHALLITA-BID P M.  
 PA (RAIT/) RAITANO A B.  
 PA (FARI/) FARIS M.  
 PA (HUBB/) HUBERT R S.  
 PA (MORR/) MORRISON R K.  
 PA (GEWW/) GE W.  
 PA (JAKO/) JAKOBOVITS A.  
 XX  
 PI Challita-Bid PM, Raitano AB, Faris M, Hubert RS, Morrison RK;  
 PI Ge W, Jakobovits A;  
 XX  
 DR WPI; 2004-132240/13.  
 XX  
 PT New composition comprising a substance that modulates the status of  
 PT 213P1F11, or a molecule that is modulated by 213P1F11, useful for  
 PT detecting or treating cancer, e.g. pancreatic or rectal cancer.  
 XX  
 PS Example 13; Page 209, 334pp; English.  
 XX  
 CC The invention describes a composition comprising a substance that  
 CC modulates the status of 213P1F11, or a molecule that is modulated by  
 CC 213P1F11, where the status of the cell that expresses 213P1F11 is  
 CC modulated and 213P1F11 is a gene overexpressed in many cancers. Also  
 CC described are: a pharmaceutical composition comprising the composition  
 CC cited above in a unit dose form; an antibody or its fragment; a non-human  
 CC transgenic animal that produced the antibody; a hybridoma that produces  
 CC the antibody; delivering a cytotoxic agent or a diagnostic agent to the  
 CC cell that expresses 213P1F11; a polynucleotide that encodes the protein;  
 CC inhibiting growth of cancer cells that expresses 213P1F11; generating a  
 CC mammalian immune response; detecting the presence of 213P1F11-related  
 CC protein or polynucleotide in a sample; and detecting the presence of  
 CC cancer in an individual. The compositions, molecules and methods are  
 CC useful for detecting and treating cancer, e.g. pancreatic or rectal  
 CC cancer. This is the amino acid sequence of a human 213P1F11 peptide  
 CC epitope bearing a human leukocyte antigen (HLA) class I or class II motif  
 CC useful in the creation of an HLA vaccine to modulate 213P1F11.  
 CC  
 XX  
 SQ Sequence 10 AA;

Query Match 29.5%; Score 31; DB 8; Length 10;  
 Best Local Similarity 62.5%; Pred. No. 6.8e+02;  
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 10 GRTVEEG 17  
 ||: ||: ||:  
 Db 3 GFLKGEDE 10

RESULT 85



AD075374  
ID AD075374 standard; peptide; 10 AA.  
XX  
AC AD075374,  
XX  
DT 15-JUL-2004 (first entry)  
XX  
DE Human 213P1P11 HLA motif bearing epitope #9473.  
XX  
KW cytotoxic; gene therapy; 213P1P11, 213P1P11 modulation; cancer;  
transgenic; cytotoxic agent delivery; diagnostic agent delivery;  
KW immune response; pancreatic cancer; rectal cancer; bladder cancer; human;  
human leukocyte antigen; HLA; class I; class II; epitope; HLA motif;  
KW HLA vaccine.  
XX  
OS Homo sapiens.  
XX  
PN US2004019915-A1.  
XX  
PD 29-JAN-2004.  
XX  
PF 01-APR-2002; 2002US-00114432.  
XX  
PR 01-APR-2002; 2002US-00114432.  
XX  
PA (CHAL/) CHALLITA-RID P M.  
PA (RAIT/) RAITANO A B.  
PA (FARI/) FARIS M.  
PA (HUBE/) HUBERT R S.  
PA (MORR/) MORRISON R K.  
PA (GEMW/) GE W.  
PA (JAKO/) JAKOBOVITS A.  
XX  
PI Chalita-Rid PM, Raitano AB, Faris M, Hubert RS, Morrison RK;  
PI Ge W, Jakobovits A;  
XX  
DR WPI; 2004-132240/13.  
XX  
PT New composition comprising a substance that modulates the status of  
PT 213P1P11, or a molecule that is modulated by 213P1P11, useful for  
PT detecting or treating cancer, e.g. pancreatic or rectal cancer.  
XX  
PS Example 13; Page 213; 334pp; English.  
XX  
CC The invention describes a composition comprising a substance that  
CC modulates the status of 213P1P11, or a molecule that is modulated by  
CC 213P1P11, where the status of the cell that expresses 213P1P11 is  
CC modulated and 213P1P11 is a gene overexpressed in many cancers. Also  
CC described are: a pharmaceutical composition comprising the composition  
CC cited above in a unit dose form; an antibody or its fragment; a non-human  
CC transgenic animal that produced the antibody; a hybridoma that produces  
CC the antibody; delivering a cytotoxic agent or a diagnostic agent to the  
CC cell that expresses 213P1P11; a polynucleotide that encodes the protein;  
CC inhibiting growth of cancer cells that expresses 213P1P11; generating a  
CC mammalian immune response; detecting the presence of 213P1P11-related  
CC protein or polynucleotide in a sample; and detecting the presence of  
CC cancer in an individual. The compositions, molecules and methods are  
CC useful for detecting and treating cancer, e.g. pancreatic or rectal  
CC cancer. This is the amino acid sequence of a human 213P1P11 peptide  
CC epitope bearing a human leukocyte antigen (HLA) class I or class II motif  
CC useful in the creation of an HLA vaccine to modulate 213P1P11.  
XX  
SQ Sequence 10 AA;  
SQ

Query Match 29.5%; Score 31; DB 8; Length 10;  
Best Local Similarity 62.5%; Pred. No. 6.8e+02;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 10 GFLVGEEG 17  
||: ||: |  
DB 1 GFLKGEDG 8

RESULT 86  
AD074213  
ID AD074213 standard; peptide; 10 AA.  
XX  
AC AD074213,  
XX  
DT 15-JUL-2004 (first entry)  
XX  
DE Human 213P1P11 HLA motif bearing epitope #8312.  
XX  
KW cytotoxic; gene therapy; 213P1P11, 213P1P11 modulation; cancer;  
transgenic; cytotoxic agent delivery; diagnostic agent delivery;  
KW immune response; pancreatic cancer; rectal cancer; bladder cancer; human;  
human leukocyte antigen; HLA; class I; class II; epitope; HLA motif;  
KW HLA vaccine.  
XX  
OS Homo sapiens.  
XX  
PN US2004019915-A1.  
XX  
PD 29-JAN-2004.  
XX  
PF 01-APR-2002; 2002US-00114432.  
XX  
PR 01-APR-2002; 2002US-00114432.  
XX  
PA (CHAL/) CHALLITA-RID P M.  
PA (RAIT/) RAITANO A B.  
PA (FARI/) FARIS M.  
PA (HUBE/) HUBERT R S.  
PA (MORR/) MORRISON R K.  
PA (GEMW/) GE W.  
PA (JAKO/) JAKOBOVITS A.  
XX  
PI Chalita-Rid PM, Raitano AB, Faris M, Hubert RS, Morrison RK;  
PI Ge W, Jakobovits A;  
XX  
DR WPI; 2004-132240/13.  
XX  
PT New composition comprising a substance that modulates the status of  
PT 213P1P11, or a molecule that is modulated by 213P1P11, useful for  
PT detecting or treating cancer, e.g. pancreatic or rectal cancer.  
XX  
PS Example 13; Page 197; 334pp; English.  
XX  
CC The invention describes a composition comprising a substance that  
CC modulates the status of 213P1P11, or a molecule that is modulated by  
CC 213P1P11, where the status of the cell that expresses 213P1P11 is  
CC modulated and 213P1P11 is a gene overexpressed in many cancers. Also  
CC described are: a pharmaceutical composition comprising the composition  
CC cited above in a unit dose form; an antibody or its fragment; a non-human  
CC transgenic animal that produced the antibody; a hybridoma that produces  
CC the antibody; delivering a cytotoxic agent or a diagnostic agent to the  
CC cell that expresses 213P1P11; a polynucleotide that encodes the protein;  
CC inhibiting growth of cancer cells that expresses 213P1P11; generating a  
CC mammalian immune response; detecting the presence of 213P1P11-related  
CC protein or polynucleotide in a sample; and detecting the presence of  
CC cancer in an individual. The compositions, molecules and methods are  
CC useful for detecting and treating cancer, e.g. pancreatic or rectal  
CC cancer. This is the amino acid sequence of a human 213P1P11 peptide  
CC epitope bearing a human leukocyte antigen (HLA) class I or class II motif  
CC useful in the creation of an HLA vaccine to modulate 213P1P11.  
XX  
SQ Sequence 10 AA;  
SQ

Query Match 29.5%; Score 31; DB 8; Length 10;  
Best Local Similarity 62.5%; Pred. No. 6.8e+02;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 10 GFLVGEEG 17  
||: ||: |  
DB 2 GFLKGEDG 9

RESULT 87  
 ADO75134  
 ID ADO75134 standard; peptide; 10 AA.  
 AC ADO75134;  
 DT 15-JUL-2004 (first entry)  
 DE Human 213P1F11 HLA motif bearing epitope #9213.  
 XX  
 XX cytostatic; gene therapy; 213P1F11; 213P1F11 modulation; cancer;  
 KW transgenic; cytotoxic agent delivery; diagnostic agent delivery;  
 KW immune response; pancreatic cancer; rectal cancer; bladder cancer; human;  
 KW human leukocyte antigen; HLA; class I; class II; epitope; HLA motif;  
 KW HLA vaccine.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2004019915-A1.  
 XX  
 PD 29-JAN-2004.  
 XX  
 PF 01-APR-2002; 2002US-00114432.  
 XX  
 PR 01-APR-2002; 2002US-00114432.  
 XX  
 PA (CHAL/) CHALLITA-BID P M.  
 PA (RAIT/) RAITANO A B.  
 PA (FARI/) FARIS M.  
 PA (HUBE/) HUBERT R S.  
 PA (MORR/) MORRISON R K.  
 PA (GEWM/) GE W.  
 PA (JAKO/) JAKOBOVITS A.  
 XX  
 PI Chalita-Bid PM, Raitano AB, Faris M, Hubert RS, Morrison RK,  
 PI Ge W, Jakobovits A;  
 XX  
 DR WPI; 2004-132240/13.  
 XX  
 PT New composition comprising a substance that modulates the status of  
 PT 213P1F11, or a molecule that is modulated by 213P1F11, useful for  
 PT detecting or treating cancer, e.g. pancreatic or rectal cancer.  
 XX  
 PS Example 13; Page 210; 334pp; English.  
 XX  
 CC The invention describes a composition comprising a substance that  
 CC modulates the status of 213P1F11, or a molecule that is modulated by  
 CC 213P1F11, where the status of the cell that expresses 213P1F11 is  
 CC modulated and 213P1F11 is a gene overexpressed in many cancers. Also  
 CC described are: a pharmaceutical composition comprising the composition  
 CC cited above in a unit dose form; an antibody or its fragment; a non-human  
 CC transgenic animal that produced the antibody; a hybridoma that produces  
 CC the antibody; delivering a cytotoxic agent or a diagnostic agent to the  
 CC cell that expresses 213P1F11; a polynucleotide that encodes the protein;  
 CC inhibiting growth of cancer cells that expresses 213P1F11; generating a  
 CC mammalian immune response; detecting the presence of 213P1F11-related  
 CC protein or polynucleotide in a sample; and detecting the presence of  
 CC cancer in an individual. The compositions, molecules and methods are  
 CC useful for detecting and treating cancer, e.g. pancreatic or rectal  
 CC cancer. This is the amino acid sequence of a human 213P1F11 peptide  
 CC epitope bearing a human leukocyte antigen (HLA) class I or class II motif  
 CC useful in the creation of an HLA vaccine to modulate 213P1F11.  
 CC  
 XX  
 SQ Sequence 10 AA;  
 Query Match 29.5%; Score 31; DB 8; Length 10;  
 Best Local Similarity 62.5%; Pred. No. 6.8e+02;  
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

RESULT 88  
 ADO74599  
 ID ADO74599 standard; peptide; 10 AA.  
 AC ADO74599;  
 DT 15-JUL-2004 (first entry)  
 DE Human 213P1F11 HLA motif bearing epitope #8698.  
 XX  
 XX cytostatic; gene therapy; 213P1F11; 213P1F11 modulation; cancer;  
 KW transgenic; cytotoxic agent delivery; diagnostic agent delivery;  
 KW immune response; pancreatic cancer; rectal cancer; bladder cancer; human;  
 KW human leukocyte antigen; HLA; class I; class II; epitope; HLA motif;  
 KW HLA vaccine.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2004019915-A1.  
 XX  
 PD 29-JAN-2004.  
 XX  
 PF 01-APR-2002; 2002US-00114432.  
 XX  
 PR 01-APR-2002; 2002US-00114432.  
 XX  
 PA (CHAL/) CHALLITA-BID P M.  
 PA (RAIT/) RAITANO A B.  
 PA (FARI/) FARIS M.  
 PA (HUBE/) HUBERT R S.  
 PA (MORR/) MORRISON R K.  
 PA (GEWM/) GE W.  
 PA (JAKO/) JAKOBOVITS A.  
 XX  
 PI Chalita-Bid PM, Raitano AB, Faris M, Hubert RS, Morrison RK,  
 PI Ge W, Jakobovits A;  
 XX  
 DR WPI; 2004-132240/13.  
 XX  
 PT New composition comprising a substance that modulates the status of  
 PT 213P1F11, or a molecule that is modulated by 213P1F11, useful for  
 PT detecting or treating cancer, e.g. pancreatic or rectal cancer.  
 XX  
 PS Example 13; Page 202; 334pp; English.  
 XX  
 CC The invention describes a composition comprising a substance that  
 CC modulates the status of 213P1F11, or a molecule that is modulated by  
 CC 213P1F11, where the status of the cell that expresses 213P1F11 is  
 CC modulated and 213P1F11 is a gene overexpressed in many cancers. Also  
 CC described are: a pharmaceutical composition comprising the composition  
 CC cited above in a unit dose form; an antibody or its fragment; a non-human  
 CC transgenic animal that produced the antibody; a hybridoma that produces  
 CC the antibody; delivering a cytotoxic agent or a diagnostic agent to the  
 CC cell that expresses 213P1F11; a polynucleotide that encodes the protein;  
 CC inhibiting growth of cancer cells that expresses 213P1F11; generating a  
 CC mammalian immune response; detecting the presence of 213P1F11-related  
 CC protein or polynucleotide in a sample; and detecting the presence of  
 CC cancer in an individual. The compositions, molecules and methods are  
 CC useful for detecting and treating cancer, e.g. pancreatic or rectal  
 CC cancer. This is the amino acid sequence of a human 213P1F11 peptide  
 CC epitope bearing a human leukocyte antigen (HLA) class I or class II motif  
 CC useful in the creation of an HLA vaccine to modulate 213P1F11.  
 CC  
 XX  
 SQ Sequence 10 AA;  
 Query Match 29.5%; Score 31; DB 8; Length 10;  
 Best Local Similarity 62.5%; Pred. No. 6.8e+02;  
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 2 GFLKGEDG 9

RESULT 89  
ID ABP62415 standard; peptide; 11 AA.  
XX  
XX ABP62415;  
AC  
XX  
DT 10-OCT-2002 (first entry)  
XX  
XX Human immunopeptide to HCV E2 glycoprotein light chain CDR #92.  
DE  
XX  
XX Vlnuclide; human; immunopolypeptide; immunopeptide; envelope glycoprotein;  
KM nonstructural protein; hepatitis C virus; HCV; E2 glycoprotein;  
KM NS3 protein; viral infection.  
XX  
XX Homo sapiens.  
OS  
XX MO200259340-A1.  
PN  
XX 01-AUG-2002.  
PD  
XX  
XX 25-JAN-2002; 2002MO-US002303.  
PF  
XX  
XX 26-JAN-2001; 2001US-0264451P.  
PR  
XX  
XX (BCRI ) SCRIpps RES INST.  
PA  
XX  
XX Maruyama T, Jones IM, Burton DR, Fox RI,  
PI  
XX WPI; 2002-599801/64.  
DR  
XX  
XX New human immunopolypeptide with binding specificity for certain envelope  
PT glycoproteins and nonstructural proteins of hepatitis C virus (HCV), for  
PT diagnosing or treating patients having or suspected of having HCV  
PT infection.  
XX  
XX Claim 1; Fig 17; 308bp; English.  
PS  
XX  
XX The present invention relates to human immunopolypeptides, produced by a  
CC phase transfected cell library. The present sequence is one such  
CC immunopolypeptide. The immunopolypeptides have binding specificity for  
CC envelope glycoprotein E2 and nonstructural protein NS3 of hepatitis C  
CC virus (HCV). E2 glycoprotein is believed to be responsible for target  
CC cell binding and contains neutralizing epitopes, while NS3 is thought to  
CC be involved in the replication of HCV. The immunopolypeptides are useful  
CC for diagnosing and treating a patient having or suspected to be having  
CC HCV infection  
CC  
XX  
SQ Sequence 11 AA;

Query Match 29.5%; Score 31; DB 5; Length 11;  
Best Local Similarity 71.4%; Pred. No. 7.5e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 GMSPPGFG 11  
| | | | |  
| | | | |  
DB 4 GSPSPGFG 10

RESULT 90  
ID AAR13452 standard; peptide; 13 AA.  
XX  
XX AAR13452;  
AC  
XX  
XX 25-MAR-2003 (revised)  
DT 28-OCT-1991 (first entry)  
XX  
XX Residues 145-157 of 152(I) bovine factor VII.  
DE  
XX  
XX Thrombosis; tissue factor; heparin.  
KM

XX OS Bos taurus.  
XX  
XX Key Location/Qualifiers  
XX Cleavage-site 8..9  
XX Region 8  
XX FT /label= mutation  
XX FT /note= "Arg -> Leu"  
XX  
XX MO9111514-A.  
PN  
XX  
XX 08-AUG-1991.  
PD  
XX  
XX 29-JAN-1990; 90US-00471313.  
PF  
XX  
XX 29-JAN-1990; 90US-00471313.  
PR  
XX  
XX (ZYMO ) ZYMOGENETICS INC.  
PA  
XX  
XX Berkner KL;  
PI  
XX  
XX WPI; 1991-252647/34.  
DR  
XX  
XX New modified factor VII to treat and prevent coagulation disorders - has  
PT a reduced susceptibility to activation by plasma factor Xa and inhibits  
PT clotting activity of wild type factor VIIa.  
PT  
XX  
XX Claim 1; Fig 1; 40bp; English.  
PS  
XX  
XX The Arg-11e cleavage site is modified to reduce susceptibility to  
CC activation by plasma factor Xa. It therefore has a longer plasma half-  
CC life and a correspondingly longer period of anticoagulative activity. The  
CC modified factor VII binds tissue factor, and competes with wild type  
CC factor VIIa. It is more selective than heparin, being active only in the  
CC presence of tissue factor, and because it does not destroy other  
CC coagulation proteins it is likely to be more effective and cause less  
CC bleeding complications. See also AAR13446-R13455. (Updated on 25-MAR-2003  
CC to correct PA field.)  
CC  
XX  
SQ Sequence 13 AA;

Query Match 29.5%; Score 31; DB 2; Length 13;  
Best Local Similarity 60.0%; Pred. No. 9e+02;  
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 GMSPPGFG 14  
| | | | |  
| | | | |  
DB 2 GSKPGGLVIG 11

RESULT 91  
ID AAR13455 standard; peptide; 13 AA.  
XX  
XX AAR13455;  
AC  
XX  
XX 25-MAR-2003 (revised)  
DT 28-OCT-1991 (first entry)  
XX  
XX Residues 145-157 of 152(I) bovine factor VII.  
DE  
XX  
XX Thrombosis; tissue factor; heparin.  
KM  
XX  
XX Bos taurus.  
OS  
XX  
XX Key Location/Qualifiers  
XX Cleavage-site 8..9  
XX Region 8  
XX FT /label= mutation  
XX FT /note= "Arg -> Ile"  
XX  
XX MO9111514-A.  
PN  
XX

PD 08-AUG-1991.  
 XX  
 PF 29-JAN-1990; 90US-00471313.  
 XX  
 PR 29-JAN-1990; 90US-00471313.  
 XX  
 PA (ZYMO ) ZYMOGENETICS INC.  
 XX  
 PI Berkner KL;  
 XX  
 DR WPI; 1991-252647/34.  
 XX  
 PT New modified factor VII to treat and prevent coagulation disorders - has  
 PT a reduced susceptibility to activation by plasma factor Xa and inhibits  
 PT clotting activity of wild type factor VIIa.  
 XX  
 PS Claim 1; Fig 1; 40pp; English.  
 XX  
 CC The Arg-116 cleavage site is modified to reduce susceptibility to  
 CC activation by plasma factor Xa. It therefore has a longer plasma half-  
 CC life and a correspondingly longer period of anticoagulative activity. The  
 CC modified factor VII binds tissue factor, and competes with wild type  
 CC factor VIIa. It is more selective than heparin, being active only in the  
 CC presence of tissue factor, and because it does not destroy other  
 CC coagulation proteins it is likely to be more effective and cause less  
 CC bleeding complications. See also AAR13446-R13454. (Updated on 25-MAR-2003  
 CC to correct PA field.)  
 XX  
 SQ Sequence 13 AA;

Query Match 29.5%; Score 31; DB 2; Length 13;  
 Best Local Similarity 60.0%; Pred. No. 9e+02;  
 Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 GMSPPGFIVG 14  
 | | | | |  
 DB 2 GSKPGGIIVG 11

RESULT 92  
 AAB83040  
 ID AAB83040 standard; peptide; 14 AA.  
 XX  
 AC AAB83040;  
 XX  
 DT 25-JUN-2001 (first entry)  
 XX  
 DS Human Smad PY motif #6.  
 XX  
 KW Human; HECT; homologous to E6 carboxyl terminus; ubiquitination;  
 KW HECT E3 ubiquitin ligase; antiinflammatory; cytosolic; osteopapic;  
 KW antimicrobial; neuroprotective; transforming growth factor beta;  
 KW TGF-beta; bone morphogenic protein; BMP; Smad; cell signalling;  
 KW inflammation; ageing; cancer; infection; bone anabolism; osteoporosis;  
 KW renal failure; neurodegeneration; fibrosis; PY motif.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200116604-A1.  
 XX  
 PD 08-MAR-2001.  
 XX  
 PF 29-AUG-2000; 2000WO-US023729.  
 XX  
 PR 30-AUG-1999; 99US-00385918.  
 XX  
 PA (SIGN-) SIGNAL PHARM INC.  
 XX  
 PI Hoekstra MF, Xie W, Murray BW, Mercurio FM;  
 XX  
 DR WPI; 2001-327913/34.  
 XX  
 PT Screening for modulators of TGF-beta and/or bone morphogenic protein

PT (BMP) mediated signalling useful for treating cancer and osteoporosis by  
 PT evaluating the ability of agents to modulate Smad protein degradation.  
 XX  
 PS Example 2; Page 31; 75pp; English.  
 XX

CC The present sequence is a Smad PY motif. The PY motif binds to the WW  
 CC domain of HECT (homologous to E6 carboxyl terminus) E3 ubiquitin ligase,  
 CC resulting in ubiquitination of Smad by the E3 ubiquitin ligase. The  
 CC sequence is provided in a specification relating to a method for  
 CC screening for agents that modulate transforming growth factor (TGF)-beta  
 CC and/or bone morphogenic protein (BMP)-mediated signalling. The method  
 CC involves evaluating the effect of an agent on binding of HECT E3  
 CC ubiquitin ligase WW domain to Smad PY motif, on ubiquitination of Smad  
 CC protein by E3 ubiquitin ligase, or on the cellular levels of Smad protein  
 CC HECT E3 ubiquitin ligase activity. The method is useful for stimulating  
 CC bone formation in a patient or treating a condition associated with  
 CC insufficient TGF-beta and/or BMP-mediated cell signalling. Agents that  
 CC inhibit BMP-mediated signalling are useful for treating inflammation,  
 CC ageing, cancer and infectious diseases. Agents that augment BMP-mediated  
 CC signalling are useful for stimulating bone anabolism as well as treating  
 CC broken bones, osteoporosis, and acute or chronic renal failure. Agents  
 CC that inhibit TGF-mediated signalling and fibrosis  
 CC inflammation, neurodegeneration and fibrosis

Query Match 29.5%; Score 31; DB 4; Length 14;  
 Best Local Similarity 38.5%; Pred. No. 9.7e+02;  
 Matches 5; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 5 GMSPPGFIVGSEG 17  
 | : | : | : | : | : |  
 DB 2 GTRPPGYLSDDG 14

RESULT 93  
 ADC22507  
 ID ADC22507 standard; peptide; 15 AA.  
 XX  
 AC ADC22507;  
 XX  
 DT 18-DEC-2003 (first entry)  
 XX  
 DS Protein binding domain amino acid sequence SEQ ID NO:356.  
 XX  
 KW recombinant fusion protein; fusion protein; binding; detection;  
 KW localization domain; binding domain;  
 KW subcellular compartment localisation.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2003012068-A2.  
 XX  
 PD 13-FEB-2003.  
 XX  
 PF 01-AUG-2002; 2002WO-US024572.  
 XX  
 PR 01-AUG-2001; 2001US-0309395P.  
 XX  
 PR 13-DEC-2001; 2001US-0341589P.  
 XX  
 PA (CELL-) CELLWICS INC.  
 XX  
 PI Bright G, Premkumar DR, Chen Y;  
 XX  
 DR WPI; 2003-248174/24.  
 XX  
 DR N-PSDB; ADC22506.  
 XX  
 PT New recombinant fusion protein comprising detection and first  
 PT localization domains and a binding domain for the molecule of interest,  
 PT useful for detecting binding of a molecule of interest.  
 XX  
 PS Claim 8; SEQ ID NO 356; 101pp; English.  
 XX

CC The present invention describes a recombinant fusion protein (1) for  
CC detecting binding of a molecule of interest. (1) comprises: (a) a  
CC detection domain; (b) a first localisation domain; and (c) a binding  
CC domain for the molecule of interest. The detection domain, the first  
CC localisation domain and the binding domain for the molecule of interest  
CC constituting the recombinant fusion protein for detecting binding of a  
CC molecule of interest are operably linked. The binding domain for the  
CC -20 amino acid residues. The first localisation domain and the binding  
CC domain for the molecule of interest both do not occur in a single non-  
CC recombinant protein with the same spacing as in the recombinant fusion  
CC protein for detecting binding of a molecule of interest. Also described:  
CC (1) a recombinant nucleic acid encoding the recombinant fusion protein;  
CC (2) a recombinant expression vector comprising the nucleic acid control  
CC sequences operably linked to the recombinant nucleic acid molecule; (3) a  
CC genetically engineered host cell transfected with the recombinant  
CC expression vector; (4) a kit for detecting binding of the molecule of  
CC interest; and (5) a method for identifying compounds that alter the  
CC binding of the molecule of interest. The recombinant fusion protein is  
CC useful for detecting binding of a molecule of interest. The recombinant  
CC fusion protein eliminates the need to construct two or more chimeric  
CC proteins and enables the monitoring of biochemical events in live, intact  
CC or fixed cells. The present sequence is used in the exemplification of  
CC the present invention.

SQ Sequence 15 AA;

Query Match 29.5%; Score 31; DB 7; Length 15;  
Best Local Similarity 55.6%; Pred. NO. 1e+03;  
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 2 PAKGMSPPG 10  
| | | | |  
Db 2 PGKGVKSPG 10

RESULT 94

ADP89482  
ID ADF89482 standard; peptide; 15 AA.

AC ADF89482;

DT 26-FEB-2004 (first entry)

DE Human E2F1-derived P49 peptide.

KM histone-deacetylase; inhibitor; subtype; human; E2F1.

OS Homo sapiens.

PN JP2003221399-A.

PD 05-AUG-2003.

PF 19-NOV-2002; 2002JP-00335851.

PR 22-NOV-2001; 2001JP-00358583.

CC (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.

PA WPI; 2003-883175/82.

PT Novel peptide substrate or its salt, useful for measuring histone-  
deacetylase activity and screening of histone-deacetylase inhibitors.

PS Disclosure; SEQ ID NO 57; 40pp; Japanese.

CC The invention relates to a novel compound or its salt. The compound of  
CC the invention may be useful for measuring the activity of histone-  
CC deacetylase, screening for a histone-deacetylase inhibitor and  
CC identifying the subtypes of histone-deacetylase. The current sequence is  
CC that of the human E2F1-derived peptide of the invention.

SQ Sequence 15 AA;

Query Match 29.5%; Score 31; DB 7; Length 15;  
Best Local Similarity 55.6%; Pred. NO. 1e+03;  
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 2 PAKGMSPPG 10  
| | | | |  
Db 5 PGKGVKSPG 13

RESULT 95

ADK48864  
ID ADK48864 standard; peptide; 15 AA.

AC ADK48864;

DT 06-MAY-2004 (first entry)

DE C-terminal acetylated human EFLF derived peptide SeqID 57.

KM human; EFLF; erythroid Kruppel like factor; histone-deacetylase; HDAC;

KM fluorescence; colour developing substrate; histone deacetylase inhibitor;

KM cancer; cytostatic.

OS Homo sapiens.

PN JP2003221398-A.

PD 05-AUG-2003.

PF 19-NOV-2002; 2002JP-00335840.

PR 22-NOV-2001; 2001JP-00358583.

CC (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.

PA WPI; 2004-102668/11.

PT Novel peptide substrate or its salt, useful for measuring histone  
deacetylase activity.

PS Disclosure; SEQ ID NO 57; 39pp; Japanese.

CC This invention relates to a novel method for measuring the histone-  
CC deacetylase (HDAC) activity of a substrate using specific radioactivity,  
CC fluorescence or a colour developing substrate. Specifically, it refers to  
CC compound such as peptidyl-Lys(NAC)-WCA, which comprises a protecting group  
CC of a hydrogen atom or an amino terminus, a group in which deacetylation  
CC is carried out by the histone deacetylase linked to an acetylated lysine  
CC residue that in turn is linked to the fluorescent group MCA (7-amino 4-  
CC methylcoumarin). The present invention describes a method for measuring  
CC HDAC activity, as well as identifying the subtype of histone deacetylase.  
CC Furthermore, it can be used to screen for histone deacetylase inhibitors,  
CC such that they can be used to regulate gene expression. Accordingly,  
CC these compositions can be used to treat cancer and exhibit cytostatic  
CC activities. This peptide sequence is a C-terminal acetylated human  
CC peptide used to determine HDAC activity of the invention.

SQ Sequence 15 AA;

Query Match 29.5%; Score 31; DB 8; Length 15;  
Best Local Similarity 55.6%; Pred. NO. 1e+03;  
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 2 PAKGMSPPG 10  
| | | | |  
Db 5 PGKGVKSPG 13

RESULT 96

ADO76533  
ID ADO76533 standard; peptide; 15 AA.

XX AD076533;  
 XX 15-JUL-2004 (first entry)  
 XX Human 213P1F11 HLA motif bearing epitope #10632.  
 XX  
 XX cytotoxic; gene therapy; 213P1F11; 213P1F11 modulation; cancer;  
 XX transgenic; cytotoxic agent delivery; diagnostic agent delivery;  
 XX immune response; pancreatic cancer; rectal cancer; bladder cancer; human;  
 XX human leukocyte antigen; HLA; class I; class II; epitope; HLA motif;  
 XX HLA vaccine.  
 XX  
 XX Homo sapiens.  
 XX US2004019915-A1.  
 XX 29-JAN-2004.  
 XX 01-APR-2002; 2002US-00114432.  
 XX 01-APR-2002; 2002US-00114432.  
 XX 01-APR-2002; 2002US-00114432.  
 XX  
 XX (CHAL/) CHALLITA-EID P M.  
 XX (RAIT/) RAITANO A B.  
 XX (FARI/) FARIS M.  
 XX (HUB/) HUBERT R S.  
 XX (MORR/) MORRISON R K.  
 XX (GEW/) GE W.  
 XX (JAKO/) JAKOBOVITS A.  
 XX  
 XX Challita-Eid PM, Raitano AB, Faris M, Hubert RS, Morrison RK;  
 XX Ge W, Jakobovits A;  
 XX WPI; 2004-132240/13.  
 XX  
 XX New composition comprising a substance that modulates the status of  
 XX 213P1F11, or a molecule that is modulated by 213P1F11, useful for  
 XX detecting or treating cancer, e.g. pancreatic or rectal cancer.  
 XX  
 XX Example 13; Page 231; 334pp; English.  
 XX  
 XX The invention describes a composition comprising a substance that  
 XX modulates the status of 213P1F11, or a molecule that is modulated by  
 XX 213P1F11, where the status of the cell that expresses 213P1F11 is  
 XX modulated and 213P1F11 is a gene overexpressed in many cancers. Also  
 XX described are: a pharmaceutical composition comprising the composition  
 XX cited above in a unit dose form; an antibody or its fragment; a non-human  
 XX transgenic animal that produced the antibody; a hybridoma that produces  
 XX the antibody; delivering a cytotoxic agent or a diagnostic agent to the  
 XX cell that expresses 213P1F11; a polynucleotide that encodes the protein;  
 XX inhibiting growth of cancer cells that expresses 213P1F11; generating a  
 XX mammalian immune response; detecting the presence of 213P1F11-related  
 XX protein or polynucleotide in a sample; and detecting the presence of  
 XX cancer in an individual. The compositions, molecules and methods are  
 XX useful for detecting and treating cancer, e.g. pancreatic or rectal  
 XX cancer. This is the amino acid sequence of a human 213P1F11 peptide  
 XX epitope bearing a human leukocyte antigen (HLA) class I or class II motif  
 XX useful in the creation of an HLA vaccine to modulate 213P1F11.  
 XX  
 XX Sequence 15 AA;  
 XX  
 XX Query Match 29.5%; Score 31; DB 8; Length 15;  
 XX Best Local Similarity 62.5%; Pred. No. 1e+03;  
 XX Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 10 GIVGEG 17  
 ||: ||: ||:  
 Db 4 GFLKGE 11

RESULT 97  
 AD076718

ID AD076718 standard; peptide; 15 AA.  
 XX  
 XX AD076718;  
 XX 15-JUL-2004 (first entry)  
 XX Human 213P1F11 HLA motif bearing epitope #10817.  
 XX  
 XX cytotoxic; gene therapy; 213P1F11; 213P1F11 modulation; cancer;  
 XX transgenic; cytotoxic agent delivery; diagnostic agent delivery;  
 XX immune response; pancreatic cancer; rectal cancer; bladder cancer; human;  
 XX human leukocyte antigen; HLA; class I; class II; epitope; HLA motif;  
 XX HLA vaccine.  
 XX  
 XX Homo sapiens.  
 XX US2004019915-A1.  
 XX 29-JAN-2004.  
 XX 01-APR-2002; 2002US-00114432.  
 XX 01-APR-2002; 2002US-00114432.  
 XX 01-APR-2002; 2002US-00114432.  
 XX  
 XX (CHAL/) CHALLITA-EID P M.  
 XX (RAIT/) RAITANO A B.  
 XX (FARI/) FARIS M.  
 XX (HUB/) HUBERT R S.  
 XX (MORR/) MORRISON R K.  
 XX (GEW/) GE W.  
 XX (JAKO/) JAKOBOVITS A.  
 XX  
 XX Challita-Eid PM, Raitano AB, Faris M, Hubert RS, Morrison RK;  
 XX Ge W, Jakobovits A;  
 XX WPI; 2004-132240/13.  
 XX  
 XX New composition comprising a substance that modulates the status of  
 XX 213P1F11, or a molecule that is modulated by 213P1F11, useful for  
 XX detecting or treating cancer, e.g. pancreatic or rectal cancer.  
 XX  
 XX Example 13; Page 234; 334pp; English.  
 XX  
 XX The invention describes a composition comprising a substance that  
 XX modulates the status of 213P1F11, or a molecule that is modulated by  
 XX 213P1F11, where the status of the cell that expresses 213P1F11 is  
 XX modulated and 213P1F11 is a gene overexpressed in many cancers. Also  
 XX described are: a pharmaceutical composition comprising the composition  
 XX cited above in a unit dose form; an antibody or its fragment; a non-human  
 XX transgenic animal that produced the antibody; a hybridoma that produces  
 XX the antibody; delivering a cytotoxic agent or a diagnostic agent to the  
 XX cell that expresses 213P1F11; a polynucleotide that encodes the protein;  
 XX inhibiting growth of cancer cells that expresses 213P1F11; generating a  
 XX mammalian immune response; detecting the presence of 213P1F11-related  
 XX protein or polynucleotide in a sample; and detecting the presence of  
 XX cancer in an individual. The compositions, molecules and methods are  
 XX useful for detecting and treating cancer, e.g. pancreatic or rectal  
 XX cancer. This is the amino acid sequence of a human 213P1F11 peptide  
 XX epitope bearing a human leukocyte antigen (HLA) class I or class II motif  
 XX useful in the creation of an HLA vaccine to modulate 213P1F11.  
 XX  
 XX Sequence 15 AA;  
 XX  
 XX Query Match 29.5%; Score 31; DB 8; Length 15;  
 XX Best Local Similarity 62.5%; Pred. No. 1e+03;  
 XX Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 10 GIVGEG 17  
 ||: ||: ||:  
 Db 8 GFLKGE 15

RESULT 98

AD076801  
ID ADO76801 standard; peptide; 15 AA.  
XX  
AC ADO76801;  
XX  
DT 15-JUL-2004 (first entry)  
XX  
DE Human 213P1F11 HLA motif bearing epitope #10900.  
XX  
KW cytostatic; gene therapy; 213P1F11; 213P1F11 modulation; cancer;  
transgenic; cytotoxic agent delivery; diagnostic agent delivery;  
immune response; pancreatic cancer; rectal cancer; bladder cancer; human;  
human leukocyte antigen; HLA; class I; class II; epitope; HLA motif;  
HLA vaccine.  
KM  
XX Homo sapiens.  
OS  
XX US2004019915-A1.  
PN  
XX 29-JAN-2004.  
PD  
XX  
PF 01-APR-2002; 2002US-00114432.  
PR  
XX 01-APR-2002; 2002US-00114432.  
XX  
XX (CHAL/) CHALLITA-BID P M.  
PA (RAIT/) RAITANO A B.  
PA (FARI/) PARIS M.  
PA (HUBE/) HUBERT R S.  
PA (MORR/) MORRISON R K.  
PA (GEMW/) GE W.  
PA (JAKO/) JAKOBOVITS A.  
XX  
PI Challita-Eld PM, Raitano AB, Farris M, Hubert RS, Morrison RK;  
PI Ge W, Jakobovits A;  
PI WPI; 2004-132240/13.  
XX  
XX New composition comprising a substance that modulates the status of  
PT 213P1F11, or a molecule that is modulated by 213P1F11, useful for  
PT detecting or treating cancer, e.g. pancreatic or rectal cancer.  
XX  
XX Example 13; Page 235; 334pp; English.  
XX  
PS The invention describes a composition comprising a substance that  
CC modulates the status of 213P1F11, or a molecule that is modulated by  
CC 213P1F11, where the status of the cell that expresses 213P1F11 is  
CC modulated and 213P1F11 is a gene overexpressed in many cancers. Also  
CC described are: a pharmaceutical composition comprising the composition  
CC cited above in a unit dose form; an antibody or its fragment; a non-human  
CC transgenic animal that produced the antibody; a hybridoma that produces  
CC the antibody; delivering a cytotoxic agent or a diagnostic agent to the  
CC cell that expresses 213P1F11; a polynucleotide that encodes the protein;  
CC inhibiting growth of cancer cells that expresses 213P1F11; generating a  
CC mammalian immune response; detecting the presence of 213P1F11-related  
CC protein or polynucleotide in a sample; and detecting the presence of  
CC cancer in an individual. The compositions, molecules and methods are  
CC useful for detecting and treating cancer, e.g. pancreatic or rectal  
CC cancer. This is the amino acid sequence of a human 213P1F11 peptide  
CC epitope bearing a human leukocyte antigen (HLA) class I or class II motif  
CC useful in the creation of an HLA vaccine to modulate 213P1F11.  
XX  
SQ Sequence 15 AA;  
XX

Query Match 29.5%; Score 31; DB 8; Length 15;  
Best Local Similarity 62.5%; Pred. No. 1e+03;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
QY 10 GFLVGEKG 17  
DB 2 GFLKGBDG 9

RESULT 99  
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XX ADO77052 standard; peptide; 15 AA.  
XX  
AC ADO77052;  
XX  
DT 15-JUL-2004 (first entry)  
XX  
DE Human 213P1F11 HLA motif bearing epitope #11151.  
XX  
KW cytostatic; gene therapy; 213P1F11; 213P1F11 modulation; cancer;  
transgenic; cytotoxic agent delivery; diagnostic agent delivery;  
immune response; pancreatic cancer; rectal cancer; bladder cancer; human;  
human leukocyte antigen; HLA; class I; class II; epitope; HLA motif;  
HLA vaccine.  
KM  
XX Homo sapiens.  
OS  
XX US2004019915-A1.  
PN  
XX 29-JAN-2004.  
PD  
XX  
PF 01-APR-2002; 2002US-00114432.  
PR  
XX 01-APR-2002; 2002US-00114432.  
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XX (CHAL/) CHALLITA-BID P M.  
PA (RAIT/) RAITANO A B.  
PA (FARI/) PARIS M.  
PA (HUBE/) HUBERT R S.  
PA (MORR/) MORRISON R K.  
PA (GEMW/) GE W.  
PA (JAKO/) JAKOBOVITS A.  
XX  
PI Challita-Eld PM, Raitano AB, Farris M, Hubert RS, Morrison RK;  
PI Ge W, Jakobovits A;  
PI WPI; 2004-132240/13.  
XX  
XX New composition comprising a substance that modulates the status of  
PT 213P1F11, or a molecule that is modulated by 213P1F11, useful for  
PT detecting or treating cancer, e.g. pancreatic or rectal cancer.  
XX  
XX Example 13; Page 239; 334pp; English.  
XX  
PS The invention describes a composition comprising a substance that  
CC modulates the status of 213P1F11, or a molecule that is modulated by  
CC 213P1F11, where the status of the cell that expresses 213P1F11 is  
CC modulated and 213P1F11 is a gene overexpressed in many cancers. Also  
CC described are: a pharmaceutical composition comprising the composition  
CC cited above in a unit dose form; an antibody or its fragment; a non-human  
CC transgenic animal that produced the antibody; a hybridoma that produces  
CC the antibody; delivering a cytotoxic agent or a diagnostic agent to the  
CC cell that expresses 213P1F11; a polynucleotide that encodes the protein;  
CC inhibiting growth of cancer cells that expresses 213P1F11; generating a  
CC mammalian immune response; detecting the presence of 213P1F11-related  
CC protein or polynucleotide in a sample; and detecting the presence of  
CC cancer in an individual. The compositions, molecules and methods are  
CC useful for detecting and treating cancer, e.g. pancreatic or rectal  
CC cancer. This is the amino acid sequence of a human 213P1F11 peptide  
CC epitope bearing a human leukocyte antigen (HLA) class I or class II motif  
CC useful in the creation of an HLA vaccine to modulate 213P1F11.  
XX  
SQ Sequence 15 AA;  
XX

Query Match 29.5%; Score 31; DB 8; Length 15;  
Best Local Similarity 62.5%; Pred. No. 1e+03;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
QY 10 GFLVGEKG 17  
DB 3 GFLKGBDG 10

Search completed: January 20, 2006, 19:05:17  
Job time : 78.5769 secs

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RESULT 100
AD076676
ID AD076676 standard; peptide; 15 AA.
XX
AC AD076676,
XX
DT 15-JUL-2004 (first entry)
XX
DE Human 213P1F1 HLA motif bearing epitope #10775.
XX
KW cytostatic; gene therapy; 213P1F1; 213P1F1 modulation; cancer;
KW transgenic; cytotoxic agent delivery; diagnostic agent delivery;
KW immune response; pancreatic cancer; rectal cancer; bladder cancer; human;
KW human leukocyte antigen; HLA; class I; class II; epitope; HLA motif;
KW HLA vaccine.
XX
OS Homo sapiens.
XX
PN US2004019915-A1.
XX
PD 29-JAN-2004.
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PF 01-APR-2002; 2002US-00114432.
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PR 01-APR-2002; 2002US-00114432.
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PA (FARI/) FARIS M.
PA (HUBE/) HUBERT R S.
PA (MORR/) MORRISON R K.
PA (GEMW/) GE W.
PA (JAKO/) JAKOBOVITS A.
XX
PI Challita-Elid PM, Raitano AB, Faris M, Hubert RS, Morrison RK;
PI Ge W, Jakobovits A;
XX
DR WPI; 2004-132240/13.
XX
PT New composition comprising a substance that modulates the status of
PT 213P1F1, or a molecule that is modulated by 213P1F1, useful for
PT detecting or treating cancer, e.g. pancreatic or rectal cancer.
XX
PS Example 13; Page 233; 334pp; English.
XX
CC The invention describes a composition comprising a substance that
CC modulates the status of 213P1F1, or a molecule that is modulated by
CC 213P1F1, where the status of the cell that expresses 213P1F1 is
CC modulated and 213P1F1 is a gene overexpressed in many cancers. Also
CC described are: a pharmaceutical composition comprising the composition
CC cited above in a unit dose form; an antibody or its fragment; a non-human
CC transgenic animal that produced the antibody; a hybridoma that produces
CC the antibody; delivering a cytotoxic agent or a diagnostic agent to the
CC cell that expresses 213P1F1; a polynucleotide that encodes the protein;
CC inhibiting growth of cancer cells that expresses 213P1F1; generating a
CC mammalian immune response; detecting the presence of 213P1F1-related
CC protein or polynucleotide in a sample; and detecting the presence of
CC cancer in an individual. The compositions, molecules and methods are
CC useful for detecting and treating cancer, e.g. pancreatic or rectal
CC cancer. This is the amino acid sequence of a human 213P1F1 peptide
CC epitope bearing a human leukocyte antigen (HLA) class I or class II motif
CC useful in the creation of an HLA vaccine to modulate 213P1F1.
XX
SQ Sequence 15 AA;
Query Match 29.5%; Score 31; DB 8; Length 15;
Best Local Similarity 62.5%; Pred. No. 1e+03;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 10 GRTVGEEG 17
DB 4 GPLKGEDG 11

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OM protein - protein search, using sw model

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(without alignments)  
78.883 Million cell updates/sec

Title: US-09-662-293-4

Perfect score: 105

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Scoring table: BLOSUM62

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 223517

Minimum DB seq length: 0  
Maximum DB seq length: 20

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 100 summaries

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- 3: /cgn2\_6/ptodata/1/1aa/H\_COMB.pep:\*
- 4: /cgn2\_6/ptodata/1/1aa/PCFUS\_COMB.pep:\*
- 5: /cgn2\_6/ptodata/1/1aa/RB\_COMB.pep:\*
- 6: /cgn2\_6/ptodata/1/1aa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	105	100.0	20	2 US-09-292-225-4	Sequence 4, Appl
2	105	100.0	20	2 US-09-292-225-13	Sequence 13, Appl
3	34	32.4	8	2 US-08-475-955-116	Sequence 116, App
4	34	32.4	9	2 US-07-867-819D-116	Sequence 116, App
5	34	32.4	9	2 US-08-475-955-100	Sequence 100, App
6	34	32.4	9	2 US-07-867-819D-100	Sequence 100, App
7	34	32.4	18	2 US-08-990-888-28	Sequence 28, Appl
8	33	31.4	15	2 US-09-157-689-67	Sequence 67, Appl
9	33	31.4	15	2 US-09-353-510-67	Sequence 67, Appl
10	33	31.4	20	2 US-09-667-857-397	Sequence 397, App
11	33	31.4	20	2 US-10-198-053-397	Sequence 397, App
12	33	31.4	20	2 US-10-198-053-603	Sequence 603, App
13	33	31.4	20	2 US-09-827-721-397	Sequence 397, App
14	31	29.5	16	1 US-08-482-142-185	Sequence 185, App
15	31	29.5	16	1 US-08-478-572-185	Sequence 185, App
16	31	29.5	16	1 US-08-484-396-185	Sequence 185, App
17	31	29.5	18	2 US-08-990-888-36	Sequence 36, Appl
18	31	29.5	18	2 US-09-570-022-13	Sequence 13, Appl
19	31	29.5	18	2 US-09-635-501-29	Sequence 29, Appl
20	31	29.5	20	2 US-10-007-700-463	Sequence 463, App
21	30	28.6	8	2 US-08-475-955-12	Sequence 12, Appl
22	30	28.6	8	2 US-08-475-955-205	Sequence 205, App
23	30	28.6	8	2 US-08-475-955-206	Sequence 206, App
24	30	28.6	8	2 US-07-867-819D-12	Sequence 12, Appl
25	30	28.6	8	2 US-07-867-819D-112	Sequence 112, App
26	30	28.6	8	2 US-07-867-819D-113	Sequence 113, App
27	30	28.6	10	2 US-08-476-509B-32	Sequence 32, Appl

28	30	28.6	10	2 US-08-476-509B-35	Sequence 35, Appl
29	30	28.6	10	2 US-08-988-742-11	Sequence 11, Appl
30	30	28.6	11	1 US-08-526-764-1	Sequence 1, Appl
31	30	28.6	12	2 US-08-988-242-10	Sequence 10, Appl
32	30	28.6	12	2 US-07-867-819D-14	Sequence 14, Appl
33	30	28.6	14	2 US-08-630-916A-53	Sequence 53, Appl
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35	30	28.6	14	2 US-09-509-958-20	Sequence 20, Appl
36	30	28.6	18	2 US-08-990-888-25	Sequence 25, Appl
37	30	28.6	18	2 US-08-990-888-65	Sequence 65, Appl
38	30	28.6	19	2 US-09-010-999-9	Sequence 9, Appl
39	30	28.6	19	2 US-09-470-830A-27	Sequence 27, Appl
40	30	28.6	20	2 US-08-928-213B-128	Sequence 128, App
41	30	28.6	20	2 US-08-928-213B-129	Sequence 129, App
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47	29.5	28.1	17	1 PCT-US91-0580A-10	Sequence 10, Appl
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50	29	27.6	8	2 US-09-718-693A-13	Sequence 3, Appl
51	29	27.6	8	2 US-07-867-819D-147	Sequence 147, App
52	29	27.6	8	2 US-07-867-819D-149	Sequence 149, App
53	29	27.6	8	2 US-07-867-819D-157	Sequence 157, App
54	29	27.6	11	2 US-08-475-955-10	Sequence 10, Appl
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56	29	27.6	12	2 US-08-475-955-14	Sequence 14, Appl
57	29	27.6	16	1 US-07-994-469A-21	Sequence 21, Appl
58	29	27.6	16	1 US-08-482-142-186	Sequence 186, App
59	29	27.6	16	1 US-08-478-572-186	Sequence 186, App
60	29	27.6	16	1 US-08-484-296-186	Sequence 186, App
61	29	27.6	18	2 US-08-990-888-24	Sequence 24, Appl
62	29	27.6	18	2 US-08-990-888-46	Sequence 46, Appl
63	29	27.6	19	2 US-08-990-888-62	Sequence 62, Appl
64	29	27.6	19	2 US-09-010-999-8	Sequence 8, Appl
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66	29	27.6	20	2 US-10-007-700-413	Sequence 413, App
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72	28	26.7	5	2 US-09-151-467-15	Sequence 15, Appl
73	28	26.7	5	2 US-09-078-403A-7	Sequence 7, Appl
74	28	26.7	5	2 US-09-256-838-15	Sequence 15, Appl
75	28	26.7	5	2 US-09-261-718-3	Sequence 3, Appl
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77	28	26.7	8	2 US-08-475-955-117	Sequence 117, App
78	28	26.7	8	2 US-07-867-819D-117	Sequence 117, App
79	28	26.7	9	2 US-09-769-180-31	Sequence 31, Appl
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81	28	26.7	11	2 US-08-915-498B-22	Sequence 22, Appl
82	28	26.7	12	2 US-10-394-980-15	Sequence 15, Appl
83	28	26.7	13	2 US-08-630-916A-6	Sequence 6, Appl
84	28	26.7	14	2 US-08-630-916A-85	Sequence 85, Appl
85	28	26.7	14	2 US-08-630-916A-141	Sequence 141, App
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87	28	26.7	15	6 5187078-4	Patent No. 5187078
88	28	26.7	18	2 US-08-630-916A-9	Sequence 9, Appl
89	28	26.7	18	2 US-08-990-888-30	Sequence 30, Appl
90	28	26.7	18	2 US-08-990-888-69	Sequence 69, Appl
91	28	26.7	18	2 US-09-292-225-12	Sequence 12, Appl
92	28	26.7	19	2 US-09-570-022-12	Sequence 12, Appl
93	28	26.7	19	2 US-09-068-624-2	Sequence 2, Appl
94	28	26.7	19	2 US-09-068-624-3	Sequence 3, Appl
95	28	26.7	20	1 US-07-956-848A-17	Sequence 17, Appl
96	28	26.7	20	1 US-08-468-514-7	Sequence 7, Appl
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98	28	26.7	20	2 US-08-786-455B-2	Sequence 2, Appl
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100	27	25.7	8	2 US-08-475-955-195	Sequence 195, App

## ALIGNMENTS

## RESULT 1

US-09-292-225-4  
; Sequence 4, Application US/09292225  
; Patent No. 6455686  
; GENERAL INFORMATION:  
; APPLICANT: McCall, Catherine A.  
; APPLICANT: Hunter, Shirley Wu  
; APPLICANT: Weber, Eric R.  
; TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS  
; TITLE OF INVENTION: AND USUS THEREOF  
; FILE REFERENCE: AL-2-C3  
; CURRENT APPLICATION NUMBER: US/09/292,225  
; EARLIER FILING DATE: 1999-04-15  
; EARLIER APPLICATION NUMBER: 60/098,909  
; EARLIER FILING DATE: 1998-09-02  
; EARLIER APPLICATION NUMBER: 60/085,295  
; EARLIER FILING DATE: 1998-05-13  
; EARLIER APPLICATION NUMBER: 60/098,565  
; EARLIER FILING DATE: 1998-04-17  
; EARLIER APPLICATION NUMBER: 09/062,013  
; EARLIER FILING DATE: 1998-04-17  
; NUMBER OF SEQ ID NOS: 49  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 4  
; LENGTH: 20  
; TYPE: PRT  
; ORGANISM: Dermatophagoides farinae  
US-09-292-225-4

Query Match 100.0%; Score 105; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e-10;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPAKMSPPGFVGEVGLS 20  
Db 1 DPAKMSPPGFVGEVGLS 20

## RESULT 2

US-09-292-225-13  
; Sequence 13, Application US/09292225  
; Patent No. 6455686  
; GENERAL INFORMATION:  
; APPLICANT: McCall, Catherine A.  
; APPLICANT: Hunter, Shirley Wu  
; APPLICANT: Weber, Eric R.  
; TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS  
; TITLE OF INVENTION: AND USUS THEREOF  
; FILE REFERENCE: AL-2-C3  
; CURRENT APPLICATION NUMBER: US/09/292,225  
; EARLIER FILING DATE: 1999-04-15  
; EARLIER APPLICATION NUMBER: 60/098,909  
; EARLIER FILING DATE: 1998-09-02  
; EARLIER APPLICATION NUMBER: 60/085,295  
; EARLIER FILING DATE: 1998-05-13  
; EARLIER APPLICATION NUMBER: 60/098,565  
; EARLIER FILING DATE: 1998-04-17  
; EARLIER APPLICATION NUMBER: 09/062,013  
; EARLIER FILING DATE: 1998-04-17  
; NUMBER OF SEQ ID NOS: 49  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 13  
; LENGTH: 20  
; TYPE: PRT  
; ORGANISM: Dermatophagoides farinae  
US-09-292-225-13

Query Match 100.0%; Score 105; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e-10;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPAKMSPPGFVGEVGLS 20  
Db 1 DPAKMSPPGFVGEVGLS 20

Best Local Similarity 100.0%; Pred. No. 1.8e-10;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPAKMSPPGFVGEVGLS 20  
Db 1 DPAKMSPPGFVGEVGLS 20

## RESULT 3

US-08-475-955-116  
; Sequence 116, Application US/08475955  
; Patent No. 6641813  
; GENERAL INFORMATION:  
; APPLICANT: Harley, John  
; TITLE OF INVENTION: METHODS AND REAGENTS FOR DIAGNOSIS OF  
; TITLE OF INVENTION: AUTOANTIBODIES  
; NUMBER OF SEQUENCES: 218  
; CORRESPONDENCE ADDRESS:  
; ADDRESSER: Patrea L. Pabst  
; STREET: 2800 One Atlantic Center, 1250 West Peachtree Street  
; CITY: Atlanta  
; STATE: GA  
; COUNTRY: USA  
; ZIP: 30309-3450  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/475,955  
; FILING DATE: June 7, 1995  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/648,205  
; FILING DATE: January 31, 1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/472,947  
; FILING DATE: January 31, 1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Pabst, Patrea L.  
; REGISTRATION NUMBER: 31,284  
; REFERENCE/DOCKET NUMBER: OMF114CIP (2) DIV  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (404) -873-8794  
; TELEFAX: (404) -873-8795  
; INFORMATION FOR SEQ ID NO: 116:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-475-955-116

Query Match 32.4%; Score 34; DB 2; Length 8;  
Best Local Similarity 75.0%; Pred. No. 4.6e+05;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PAKGMSPP 9  
Db 1 PAKGMSPP 8

## RESULT 4

US-07-867-819D-116  
; Sequence 116, Application US/07867819D  
; Patent No. 6897287  
; GENERAL INFORMATION:

APPLICANT: Harley, John  
TITLE OF INVENTION: Methods and Reagents for Diagnosis of Autoantibodies  
FILE REFERENCE: OMRP 114 CIP (2)  
CURRENT APPLICATION NUMBER: US/07/867,819D  
CURRENT FILING DATE: 1992-04-13  
PRIOR APPLICATION NUMBER: 07/472,947  
PRIOR FILING DATE: 1990-01-31  
PRIOR APPLICATION NUMBER: 07/648,205  
PRIOR FILING DATE: 1991-01-31  
NUMBER OF SEQ ID NOS: 161  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 116  
LENGTH: 8  
TYPE: PRT  
ORGANISM: homo sapien  
US-07-867-819D-116

Query Match 32.4%; Score 34; DB 2; Length 8;  
Best Local Similarity 75.0%; Pred. No. 4.6e+05;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PAKGMSP 9  
Db 1 PAKGMRP 8

RESULT 5  
US-08-475-955-100  
Sequence 100, Application US/08475955  
Patent No. 6641813  
GENERAL INFORMATION:  
APPLICANT: Harley, John  
TITLE OF INVENTION: METHODS AND REAGENTS FOR DIAGNOSIS OF  
NUMBER OF SEQUENCES: 218  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Patricia L. Pabst  
STREET: 2800 One Atlantic Center, 1250 West Peachtree Street  
City: Atlanta  
STATE: GA  
COUNTRY: USA  
ZIP: 30309-3450  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/475,955  
FILING DATE: June 7, 1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/867,819  
FILING DATE: April 13, 1992  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/648,205  
FILING DATE: January 31, 1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/472,947  
FILING DATE: January 31, 1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Pabst, Patricia L.  
REGISTRATION NUMBER: 31,284  
REFERENCE/DOCKET NUMBER: OMRP114CIP(2)DIV  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (404)-873-8794  
TELEFAX: (404)-873-8795  
INFORMATION FOR SEQ ID NO: 100:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
STRANDEDNESS: single

TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Binding-site  
LOCATION: 1..8  
US-08-475-955-100

Query Match 32.4%; Score 34; DB 2; Length 9;  
Best Local Similarity 75.0%; Pred. No. 4.6e+05;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PAKGMSP 9  
Db 2 PAKGMRP 9

RESULT 6  
US-07-867-819D-100  
Sequence 100, Application US/07867819D  
Patent No. 6897287  
GENERAL INFORMATION:  
APPLICANT: Harley, John  
TITLE OF INVENTION: Methods and Reagents for Diagnosis of Autoantibodies  
FILE REFERENCE: OMRP 114 CIP (2)  
CURRENT APPLICATION NUMBER: US/07/867,819D  
CURRENT FILING DATE: 1992-04-13  
PRIOR APPLICATION NUMBER: 07/472,947  
PRIOR FILING DATE: 1990-01-31  
PRIOR APPLICATION NUMBER: 07/648,205  
PRIOR FILING DATE: 1991-01-31  
NUMBER OF SEQ ID NOS: 161  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 100  
LENGTH: 9  
TYPE: PRT  
ORGANISM: homo sapien  
FEATURE:  
NAME/KEY: MISC FEATURE  
LOCATION: (1)..(8)  
OTHER INFORMATION: Binding site  
US-07-867-819D-100

Query Match 32.4%; Score 34; DB 2; Length 9;  
Best Local Similarity 75.0%; Pred. No. 4.6e+05;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PAKGMSP 9  
Db 2 PAKGMRP 9

RESULT 7  
US-08-990-888-28  
Sequence 28, Application US/08990888B  
Patent No. 6387879  
GENERAL INFORMATION:  
APPLICANT: Blume, Arthur J.  
APPLICANT: Brissette, Renee  
APPLICANT: Carcamo, Juan  
APPLICANT: Mandek, Wlodek S.  
TITLE OF INVENTION: Assays for Compounds which Bind Growth Hormone Receptor  
FILE REFERENCE: 2598-4002  
CURRENT APPLICATION NUMBER: US/08/990,888B  
CURRENT FILING DATE: 1997-12-15  
NUMBER OF SEQ ID NOS: 81  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 28  
LENGTH: 18  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: H5 peptide secondary library sequence

US-08-990-888-28

Query Match 32.4%; Score 34; DB 2; Length 18;  
Best Local Similarity 60.0%; Pred. No. 60;  
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 5 GMSPPGPIVG 14  
|:|:|:|:  
DB 6 GVSYPGWLVG 15

RESULT 8  
US-09-157-689-67  
; Sequence 67, Application US/09157689  
; Patent No. 6599510

GENERAL INFORMATION:  
APPLICANT: Horwitz, Marcus A.  
TITLE OF INVENTION: Abundant Extracellular Products and  
METHODS FOR THEIR PRODUCTION AND USE  
NUMBER OF SEQUENCES: 95  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Kurt A. Maclean  
STREET: 2029 Century Park East, Suite 3800  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90067

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09157,689  
FILING DATE:

CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/568,357  
FILING DATE: 06-DEC-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/551,149  
FILING DATE: 31-OCT-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/447,398  
FILING DATE: 23-MAY-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/289,667  
FILING DATE: 12-AUG-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/156,358  
FILING DATE: 23-NOV-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Maclean, Kurt A.  
REGISTRATION NUMBER: 31,118  
REFERENCE/DOCKET NUMBER: 118-119  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (310) 788-5000  
TELEFAX: (310) 277-1297

INFORMATION FOR SEQ ID NO: 67:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
STRANDEDNESS:

TOPOLOGY: linear  
MOLECULAR TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: internal  
ORIGINAL SOURCE:  
ORGANISM: Mycobacterium tuberculosis  
STRAIN: B7man

US-09-157-689-67

Query Match 31.4%; Score 33; DB 2; Length 15;  
Best Local Similarity 62.5%; Pred. No. 71;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 DPAKGMSP 8  
|:|:|:|:  
DB 4 DPGQGMGP 11

RESULT 9  
US-09-953-510-67  
; Sequence 67, Application US/09953510  
; Patent No. 6818223

GENERAL INFORMATION:  
APPLICANT: Horwitz, Marcus A.  
TITLE OF INVENTION: Abundant Extracellular  
Products and Methods for Their Production and Use  
NUMBER OF SEQUENCES: 91  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Kurt A. Maclean  
STREET: 2029 Century Park East, Suite 3800  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90067

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0,  
Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/953,510  
FILING DATE: 14-SEP-2001  
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/447,398  
FILING DATE: 23-MAY-1995  
APPLICATION NUMBER: US 08/289,667  
FILING DATE: 12-AUG-1994  
APPLICATION NUMBER: US 08/156,358  
FILING DATE: 23-NOV-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Maclean, Kurt A.  
REGISTRATION NUMBER: 31,118  
REFERENCE/DOCKET NUMBER: 112-272  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (310) 788-5000  
TELEFAX: (310) 277-1297  
INFORMATION FOR SEQ ID NO: 67:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>

TOPOLOGY: linear  
MOLECULAR TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: internal  
ORIGINAL SOURCE:  
ORGANISM: Mycobacterium tuberculosis  
STRAIN: B7man  
SEQUENCE DESCRIPTION: SEQ ID NO: 67:  
US-09-953-510-67

Query Match 31.4%; Score 33; DB 2; Length 15;  
Best Local Similarity 62.5%; Pred. No. 71;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 DPAKGMSP 8  
|:|:|:|:  
DB 4 DPGQGMGP 11

```
RESULT 10
US-09-667-857-397
; Sequence 397, Application US/09667857
; Patent No. 6699664
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: King, Gordon E.
; APPLICANT: Algate, Paul A.
; APPLICANT: Fling, Steven P.
; APPLICANT: Retter, Marc W.
; APPLICANT: Fanger, Gary Richard
; APPLICANT: Reed, Steven G.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darick
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.462C5
; CURRENT APPLICATION NUMBER: US/09/667,857
; CURRENT FILING DATE: 2000-09-20
; NUMBER OF SEQ ID NOS: 455
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 397
; LENGTH: 20
; TYPE: PRF
; ORGANISM: Homo sapiens
US-09-667-857-397
```

```
Query Match
Best Local Similarity 31.4%; Score 33; DB 2; Length 20;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
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```
Qy 13 VGESEGLS 20
: |||: |||
Db 3 IGEDGILS 10
```

```
RESULT 11
US-10-198-053-397
; Sequence 397, Application US/10198053
; Patent No. 6858710
; GENERAL INFORMATION:
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Retter, Marc W.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Hill, Paul
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.462C9
; CURRENT APPLICATION NUMBER: US/10/198,053
; CURRENT FILING DATE: 2002-07-17
; NUMBER OF SEQ ID NOS: 624
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 397
; LENGTH: 20
; TYPE: PRF
; ORGANISM: Homo sapiens
US-10-198-053-397
```

```
Query Match
Best Local Similarity 31.4%; Score 33; DB 2; Length 20;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 13 VGESEGLS 20
: |||: |||
Db 3 IGEDGILS 10
```

```
RESULT 12
US-10-198-053-603
; Sequence 603, Application US/10198053
; Patent No. 6858710
```

```
; GENERAL INFORMATION:
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Retter, Marc W.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Hill, Paul
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.462C9
; CURRENT APPLICATION NUMBER: US/10/198,053
; CURRENT FILING DATE: 2002-07-17
; NUMBER OF SEQ ID NOS: 624
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 603
; LENGTH: 20
; TYPE: PRF
; ORGANISM: Homo sapiens
US-10-198-053-603
```

```
Query Match
Best Local Similarity 31.4%; Score 33; DB 2; Length 20;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 13 VGESEGLS 20
: |||: |||
Db 3 IGEDGILS 10
```

```
RESULT 13
US-09-827-271-397
; Sequence 397, Application US/09827271
; Patent No. 6962980
; GENERAL INFORMATION:
; APPLICANT: Retter, Marc W.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.462C6
; CURRENT APPLICATION NUMBER: US/09/827,271
; CURRENT FILING DATE: 2001-04-04
; NUMBER OF SEQ ID NOS: 461
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 397
; LENGTH: 20
; TYPE: PRF
; ORGANISM: Homo sapiens
US-09-827-271-397
```

```
Query Match
Best Local Similarity 31.4%; Score 33; DB 2; Length 20;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 13 VGESEGLS 20
: |||: |||
Db 3 IGEDGILS 10
```

```
RESULT 14
US-08-482-142-185
; Sequence 185, Application US/08482142
; Patent No. 5820862
; GENERAL INFORMATION:
; APPLICANT: Garman, Richard
; APPLICANT: Greenstein, Julia
; APPLICANT: Kuo, Mei-chang
; APPLICANT: Rogers, Bruce
; APPLICANT: Pranzan, Henry
; APPLICANT: Chen, Xian
; APPLICANT: Evans, Sean
; APPLICANT: Shaked, Ze'ev
; TITLE OF INVENTION: T CELL EPITOPES OF THE MAJOR ALLERGENS
; NUMBER OF SEQUENCES: 207
; CORRESPONDENCE ADDRESS:
```

ADDRESSEE: IMMUNOLOGIC PHARMACEUTICAL CORPORATION  
STREET: 610 LINCOLN STREET  
CITY: WALTHAM  
STATE: MA  
COUNTRY: USA  
ZIP: 02154  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII TEXT  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/482,142  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/445,307  
FILING DATE: 07 June 1995  
ATTORNEY/AGENT INFORMATION:  
NAME: CRAIG, ANNE I.  
REGISTRATION NUMBER: 32,976  
REFERENCE/DOCKET NUMBER: 017.6US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 466-6000  
TELEFAX: (617) 466-6040  
INFORMATION FOR SEQ ID NO: 185:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: internal  
US-08-482-142-185

Query Match 29.5%; Score 31; DB 1; Length 16;  
Best Local Similarity 55.6%; Pred. No. 1.6e+02;  
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 12 IYVGEVGLS 20  
:|||||:  
Db 6 LVGDDGVLA 14

RESULT 15  
US-08-478-572-185  
; Sequence 185, Application US/08478572  
; Patent No. 5968526  
; GENERAL INFORMATION:  
; APPLICANT: Garman, Richard  
; APPLICANT: Greenstein, Julia  
; APPLICANT: Kuo, Mei-chang  
; APPLICANT: Rogers, Bruce  
; APPLICANT: Franzen, Henry  
; APPLICANT: Chen, Xian  
; APPLICANT: Evans, Sean  
; APPLICANT: Shaked, Ze'ev  
; TITLE OF INVENTION: T CELL EPITOPES OF THE MAJOR ALLERGENS  
; TITLE OF INVENTION: FROM DERMATOPHAGOIDES (HOUSE DUST MITE)  
; NUMBER OF SEQUENCES: 207  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: IMMUNOLOGIC PHARMACEUTICAL CORPORATION  
; STREET: 610 LINCOLN STREET  
; CITY: WALTHAM  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02154  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII TEXT  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/478,572

FILING DATE: 07-June-1995  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/445,307  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: CRAIG, ANNE I.  
REGISTRATION NUMBER: 32,976  
REFERENCE/DOCKET NUMBER: 017.6US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 466-6000  
TELEFAX: (617) 466-6040  
INFORMATION FOR SEQ ID NO: 185:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: internal  
US-08-478-572-185

Query Match 29.5%; Score 31; DB 1; Length 16;  
Best Local Similarity 55.6%; Pred. No. 1.6e+02;  
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 12 IYVGEVGLS 20  
:|||||:  
Db 6 LVGDDGVLA 14

RESULT 16  
US-08-484-296-185  
; Sequence 185, Application US/08484296  
; Patent No. 6268491  
; GENERAL INFORMATION:  
; APPLICANT: Garman, Richard  
; APPLICANT: Greenstein, Julia  
; APPLICANT: Kuo, Mei-chang  
; APPLICANT: Rogers, Bruce  
; APPLICANT: Franzen, Henry  
; APPLICANT: Chen, Xian  
; APPLICANT: Evans, Sean  
; APPLICANT: Shaked, Ze'ev  
; TITLE OF INVENTION: T CELL EPITOPES OF THE MAJOR ALLERGENS  
; TITLE OF INVENTION: FROM DERMATOPHAGOIDES (HOUSE DUST MITE)  
; NUMBER OF SEQUENCES: 207  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: IMMUNOLOGIC PHARMACEUTICAL CORPORATION  
; STREET: 610 LINCOLN STREET  
; CITY: WALTHAM  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02154  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII TEXT  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/484,296  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/445,307  
; FILING DATE: 07 June 1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: CRAIG, ANNE I.  
; REGISTRATION NUMBER: 32,976  
; REFERENCE/DOCKET NUMBER: 017.6US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 466-6000  
; TELEFAX: (617) 466-6040  
; INFORMATION FOR SEQ ID NO: 185:

SEQUENCE CHARACTERISTICS:  
LENGTH: 16 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: internal  
US-08-484-296-185

Query Match 29.5%; Score 31; DB 2; Length 16;  
Best Local Similarity 55.6%; Pred. No. 1.6e+02;  
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 12 IVGSEGVLS 20  
DB 6 LVGDDEVLV 14

RESULT 17  
US-08-990-888-36  
Sequence 36, Application US/08990888B  
Patent No. 6387879  
GENERAL INFORMATION:  
APPLICANT: Blume, Arthur J.  
APPLICANT: Brissette, Renee  
APPLICANT: Carcamo, Juan  
APPLICANT: Mandeckl, Wlodeck S.  
TITLE OF INVENTION: Assays For Compounds Which Bind Growth Hormone Receptor  
FILE REFERENCE: 2598-4002  
CURRENT APPLICATION NUMBER: US/08/990,888B  
CURRENT FILING DATE: 1997-12-15  
NUMBER OF SEQ ID NOS: 81  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 36  
LENGTH: 18  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: H5 peptide secondary library sequence  
US-08-990-888-36

Query Match 29.5%; Score 31; DB 2; Length 16;  
Best Local Similarity 50.0%; Pred. No. 1.9e+02;  
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 5 GMSPPGPIVG 14  
DB 6 GVTYPGMLVG 15

RESULT 18  
US-09-570-022-13  
Sequence 13, Application US/09570022  
Patent No. 6573244  
GENERAL INFORMATION:  
APPLICANT: GORDON, RICHARD K.  
APPLICANT: MOORAD, DEBORAH R.  
APPLICANT: DOCTOR, BHUPENDRA P.  
APPLICANT: GARCIA, GREGORY B.  
TITLE OF INVENTION: PREVING AS SPECIFIC INHIBITORS AND THERAPEUTIC AGENTS  
FILE REFERENCE: 38644-170531  
CURRENT APPLICATION NUMBER: US/09/570,022  
CURRENT FILING DATE: 2000-05-12  
PRIOR APPLICATION NUMBER: 60/134,446  
PRIOR FILING DATE: 1999-05-17  
NUMBER OF SEQ ID NOS: 26  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 13  
LENGTH: 18  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
OTHER INFORMATION: peptide  
US-09-570-022-13

Query Match 29.5%; Score 31; DB 2; Length 18;  
Best Local Similarity 54.5%; Pred. No. 1.9e+02;  
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 AKGMSPPGPIV 13  
DB 5 AKGIQPPGLMV 15

RESULT 19  
US-09-635-501-29  
Sequence 29, Application US/09635501  
Patent No. 6884771  
GENERAL INFORMATION:  
APPLICANT: Actor, Susan L. et al.  
TITLE OF INVENTION: ANGIOTENSIN CONVERTING ENZYME HOMOLOG AND THERAPEUTIC  
FILE REFERENCE: MNT-132CP3  
CURRENT APPLICATION NUMBER: US/09/635,501  
CURRENT FILING DATE: 2000-08-09  
PRIOR APPLICATION NUMBER: 09/407,427  
PRIOR FILING DATE: 1999-09-29  
PRIOR APPLICATION NUMBER: 09/163,648  
PRIOR FILING DATE: 1998-09-30  
PRIOR APPLICATION NUMBER: 08/989,299  
PRIOR FILING DATE: 1997-12-11  
NUMBER OF SEQ ID NOS: 107  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 29  
LENGTH: 18  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: motifs  
US-09-635-501-29

Query Match 29.5%; Score 31; DB 2; Length 18;  
Best Local Similarity 54.5%; Pred. No. 1.9e+02;  
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 DPAKMSPPGPF 11  
DB 1 DISKGNPPGF 11

RESULT 20  
US-10-007-700-463  
Sequence 463, Application US/10007700  
Patent No. 6960570  
GENERAL INFORMATION:  
APPLICANT: Wang, Tongtong  
APPLICANT: Wang, Aljun  
APPLICANT: Skelky, Yasir A.W.  
APPLICANT: Li, Samuel X.  
APPLICANT: Kalos, Michael D.  
APPLICANT: Henderson, Robert A.  
APPLICANT: McNeill, Patricia D.  
APPLICANT: Fanger, Neil  
APPLICANT: Retter, Marc W.  
APPLICANT: Durham, Margareta  
APPLICANT: Fanger, Gary R.  
APPLICANT: Vedvick, Thomas S.  
APPLICANT: Carter, Darrick  
APPLICANT: Watanabe, Yoshihiro  
APPLICANT: Beckman, David W.  
APPLICANT: Cai, Feng  
APPLICANT: Foy, Teresa M.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
AND DIAGNOSIS OF LUNG CANCER

FILE REFERENCE: 210121.455C17  
CURRENT APPLICATION NUMBER: US/10/007,700  
CURRENT FILING DATE: 2001-11-30  
NUMBER OF SEQ ID NOS: 469  
SOFTWARE: FASTSeq for Windows Version 4.0  
SEQ ID NO 463  
LENGTH: 20  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-007-700-463

Query Match 29.5%; Score 31; DB 2; Length 20;  
Best Local Similarity 62.5%; Pred. No. 2.1e+02;  
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 PAKGMSPP 9  
DB 9 PTSGMPP 16

## RESULT 21

US-08-475-955-12  
Sequence 12, Application US/08475955  
Patent No. 6641813  
GENERAL INFORMATION:  
APPLICANT: Harley, John  
TITLE OF INVENTION: METHODS AND REAGENTS FOR DIAGNOSIS OF  
NUMBER OF SEQUENCES: 218  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Patrea L. Pabst  
STREET: 2800 One Atlantic Center, 1250 West Peachtree Street  
CITY: Atlanta  
STATE: GA  
COUNTRY: USA  
ZIP: 30309-3450  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/475,955  
FILING DATE: June 7, 1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/867,819  
FILING DATE: April 13, 1992  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/648,205  
FILING DATE: January 31, 1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/472,947  
FILING DATE: January 31, 1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Pabst, Patrea L.  
REGISTRATION NUMBER: 31,284  
REFERENCE/DOCKET NUMBER: OMRF114CIP(2)DIV  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (404)-873-8794  
TELEFAX: (404)-873-8795  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Binding-site  
LOCATION: 1..8  
US-08-475-955-12

Query Match 28.6%; Score 30; DB 2; Length 8;  
Best Local Similarity 83.3%; Pred. No. 4.6e+05;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GMSPPG 10  
DB 3 GMPPPG 8

## RESULT 22

US-08-475-955-205  
Sequence 205, Application US/08475955  
Patent No. 6641813  
GENERAL INFORMATION:  
APPLICANT: Harley, John  
TITLE OF INVENTION: METHODS AND REAGENTS FOR DIAGNOSIS OF  
NUMBER OF SEQUENCES: 218  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Patrea L. Pabst  
STREET: 2800 One Atlantic Center, 1250 West Peachtree Street  
CITY: Atlanta  
STATE: GA  
COUNTRY: USA  
ZIP: 30309-3450  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/475,955  
FILING DATE: June 7, 1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/867,819  
FILING DATE: April 13, 1992  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/648,205  
FILING DATE: January 31, 1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/472,947  
FILING DATE: January 31, 1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Pabst, Patrea L.  
REGISTRATION NUMBER: 31,284  
REFERENCE/DOCKET NUMBER: OMRF114CIP(2)DIV  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (404)-873-8794  
TELEFAX: (404)-873-8795  
INFORMATION FOR SEQ ID NO: 205:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-475-955-205

Query Match 28.6%; Score 30; DB 2; Length 8;  
Best Local Similarity 83.3%; Pred. No. 4.6e+05;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GMSPPG 10  
DB 2 GMPPPG 7

RESULT 23  
US-08-475-955-206  
Sequence 206, Application US/08475955



Patent No. 6641813  
GENERAL INFORMATION:  
APPLICANT: Harley, John  
TITLE OF INVENTION: METHODS AND REAGENTS FOR DIAGNOSIS OF  
TITLE OF INVENTION: AUTOANTIBODIES  
NUMBER OF SEQUENCES: 218  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Patricia L. Pabst  
STREET: 2800 One Atlantic Center, 1250 West Peachtree Street  
CITY: Atlanta  
STATE: GA  
COUNTRY: USA  
ZIP: 30309-3450  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/475,955  
FILING DATE: June 7, 1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/867,819  
FILING DATE: April 13, 1992  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/648,205  
FILING DATE: January 31, 1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/472,947  
FILING DATE: January 31, 1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Pabst, Patricia L.  
REGISTRATION NUMBER: 31,284  
REFERENCE/DOCKET NUMBER: OMRP14CIP(2)DIV  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (404)-873-8794  
TELEFAX: (404)-873-8795  
INFORMATION FOR SEQ ID NO: 206:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULAR TYPE: peptide  
US-08-475-955-206

Query Match 28.6%; Score 30; DB 2; Length 8;  
Best Local Similarity 83.3%; Pred. No. 4.6e+05;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GMSPPG 10  
DB 1 GMPPPG 6

RESULT 24  
US-07-867-819D-12  
Sequence 12, Application US/07867819D  
Patent No. 6897287  
GENERAL INFORMATION:  
APPLICANT: Harley, John  
TITLE OF INVENTION: Methods and Reagents for Diagnosis of Autoantibodies  
FILE REFERENCE: OMRP 114 CIP (2)  
CURRENT APPLICATION NUMBER: US/07/867,819D  
CURRENT FILING DATE: 1992-04-13  
PRIOR APPLICATION NUMBER: 07/472,947  
PRIOR FILING DATE: 1990-01-31  
PRIOR APPLICATION NUMBER: 07/648,205  
PRIOR FILING DATE: 1991-01-31  
NUMBER OF SEQ ID NOS: 161  
SOFTWARE: PatentIn version 3.1

SEQ ID NO 12  
LENGTH: 8  
TYPE: PRT  
ORGANISM: homo sapien  
FEATURE:  
NAME/KEY: MISC FEATURE  
LOCATION: (1)-(8)  
OTHER INFORMATION: Binding site  
US-07-867-819D-12

Query Match 28.6%; Score 30; DB 2; Length 8;  
Best Local Similarity 83.3%; Pred. No. 4.6e+05;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GMSPPG 10  
DB 3 GMPPPG 8

RESULT 25  
US-07-867-819D-112  
Sequence 112, Application US/07867819D  
Patent No. 6897287  
GENERAL INFORMATION:  
APPLICANT: Harley, John  
TITLE OF INVENTION: Methods and Reagents for Diagnosis of Autoantibodies  
FILE REFERENCE: OMRP 114 CIP (2)  
CURRENT APPLICATION NUMBER: US/07/867,819D  
CURRENT FILING DATE: 1992-04-13  
PRIOR APPLICATION NUMBER: 07/472,947  
PRIOR FILING DATE: 1990-01-31  
PRIOR APPLICATION NUMBER: 07/648,205  
PRIOR FILING DATE: 1991-01-31  
NUMBER OF SEQ ID NOS: 161  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 112  
LENGTH: 8  
TYPE: PRT  
ORGANISM: homo sapien  
US-07-867-819D-112

Query Match 28.6%; Score 30; DB 2; Length 8;  
Best Local Similarity 83.3%; Pred. No. 4.6e+05;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GMSPPG 10  
DB 2 GMPPPG 7

RESULT 26  
US-07-867-819D-113  
Sequence 113, Application US/07867819D  
Patent No. 6897287  
GENERAL INFORMATION:  
APPLICANT: Harley, John  
TITLE OF INVENTION: Methods and Reagents for Diagnosis of Autoantibodies  
FILE REFERENCE: OMRP 114 CIP (2)  
CURRENT APPLICATION NUMBER: US/07/867,819D  
CURRENT FILING DATE: 1992-04-13  
PRIOR APPLICATION NUMBER: 07/472,947  
PRIOR FILING DATE: 1990-01-31  
PRIOR APPLICATION NUMBER: 07/648,205  
PRIOR FILING DATE: 1991-01-31  
NUMBER OF SEQ ID NOS: 161  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 113  
LENGTH: 8  
TYPE: PRT  
ORGANISM: homo sapien  
US-07-867-819D-113

Query Match 28.6%; Score 30; DB 2; Length 8;

Best Local Similarity 83.3%; Pred. No. 4.6e+05;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 GMSPPG 10  
Db 1 GMPPG 6

## RESULT 27

US-08-476-509B-32  
Sequence 32, Application US/08476509B  
Patent No. 6034212  
GENERAL INFORMATION:  
APPLICANT: SUDOL, MARIUS  
APPLICANT: PEER, BORK  
APPLICANT: HENRY, CHEN  
TITLE OF INVENTION: A SH2 DOMAIN ASSOCIATED PROTEIN, A  
TITLE OF INVENTION: SIGNALING DOMAIN THEREIN, NUCLEIC ACIDS ENCODING THE  
TITLE OF INVENTION: PROTEIN AND THE DOMAIN, AND DIAGNOSTIC AND THERAPEUTICS  
TITLE OF INVENTION: THEREOF  
NUMBER OF SEQUENCES: 50  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Klauber & Jackson  
STREET: 411 Hackensack Avenue  
CITY: Hackensack  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07601  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/476,509B  
FILING DATE: 01-DEC-1994  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Jackson Esq., David A.  
REGISTRATION NUMBER: 26,742  
REFERENCE/DOCKET NUMBER: 600-1-101 CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201 487-5800  
TELEFAX: 201 343-1684  
TELEX: 133521  
INFORMATION FOR SEQ. ID NO: 32:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
US-08-476-509B-32

Query Match 28.6%; Score 30; DB 2; Length 10;  
Best Local Similarity 50.0%; Pred. No. 1.4e+02;  
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 5 GMSPPG 14  
Db 1 GTAPPYTVG 10

RESULT 28  
US-08-476-509B-35  
Sequence 35, Application US/08476509B  
Patent No. 6034212  
GENERAL INFORMATION:  
APPLICANT: SUDOL, MARIUS  
APPLICANT: PEER, BORK  
APPLICANT: HENRY, CHEN  
TITLE OF INVENTION: A SH2 DOMAIN ASSOCIATED PROTEIN, A

TITLE OF INVENTION: SIGNALING DOMAIN THEREIN, NUCLEIC ACIDS ENCODING THE  
TITLE OF INVENTION: PROTEIN AND THE DOMAIN, AND DIAGNOSTIC AND THERAPEUTICS  
TITLE OF INVENTION: THEREOF  
NUMBER OF SEQUENCES: 50  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Klauber & Jackson  
STREET: 411 Hackensack Avenue  
CITY: Hackensack  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07601  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/476,509B  
FILING DATE: 01-DEC-1994  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Jackson Esq., David A.  
REGISTRATION NUMBER: 26,742  
REFERENCE/DOCKET NUMBER: 600-1-101 CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201 487-5800  
TELEFAX: 201 343-1684  
TELEX: 133521  
INFORMATION FOR SEQ. ID NO: 35:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
US-08-476-509B-35

Query Match 28.6%; Score 30; DB 2; Length 10;  
Best Local Similarity 50.0%; Pred. No. 1.4e+02;  
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 5 GMSPPG 14  
Db 1 GTAPPYTVG 10

## RESULT 29

US-08-988-242-11  
Sequence 11, Application US/08988242  
Patent No. 6403103  
GENERAL INFORMATION:  
APPLICANT: PARANHOS-BACCALA, GLAUCIA  
APPLICANT: LEBENECHAL, MYLENE  
APPLICANT: JOLIVET, MICHEL  
APPLICANT: MANDRAND, BERNARD  
TITLE OF INVENTION: NEW TYRANOSOMA CRUZI ANTIGEN, GENE  
TITLE OF INVENTION: ENCODING THEREFOR, AND METHODS OF DETECTING AND TREATING  
TITLE OF INVENTION: CHAGAS DISEASE  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: OLIFF & BERRIDGE, PLC  
STREET: P. O. BOX 19928  
CITY: Alexandria  
STATE: Virginia  
COUNTRY: U.S.A.  
ZIP: 22320  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:

```

: APPLICATION NUMBER: US/08/988,242
: FILING DATE: 10-DEC-1997
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Berridge, William P.
: REGISTRATION NUMBER: 30,024
: REFERENCE/DOCKET NUMBER: WPB 36400A
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 703-836-6400
: TELEFAX: 703-836-2787
: INFORMATION FOR SEQ ID NO: 11:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 10 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE:
: DESCRIPTION: /desc = "protein"
US-08-988-242-11

Query Match      28.6%; Score 30; DB 2; Length 10;
Best Local Similarity 62.5%; Pred. No. 1.4e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      2 PAKGMSPP 9
DB      1 PAKGAAP 8

RESULT 30
US-08-526-764-1
: Sequence 1, Application US/08526764
: Patent No. 5834431
: GENERAL INFORMATION:
: APPLICANT:
: TITLE OF INVENTION: DES-ARG9-BK ANTAGONISTS
: NUMBER OF SEQUENCES: 1
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/526,764
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 11 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
US-08-526-764-1

Query Match      28.6%; Score 30; DB 1; Length 11;
Best Local Similarity 71.4%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      5 GMSPPGF 11
DB      2 GKRPFGF 8

RESULT 31
US-08-988-242-10
: Sequence 10, Application US/08988242
: Patent No. 6403103
: GENERAL INFORMATION:
: APPLICANT: PARANHOS-BACCALA, GLAUCIA
: APPLICANT: LESBNECHAL, MYLENE
: APPLICANT: JOLIVET, MICHEL
: APPLICANT: MANDRAND, BERNARD
: TITLE OF INVENTION: NEW TRYFANOSOMA CRUZI ANTIGEN, GENE
: OTHER INFORMATION: ENCODING THEREFOR, AND METHODS OF DETECTING AND TREATING
US-07-867-819D-14
```

```

: TITLE OF INVENTION: CHAGAS DISEASE
: NUMBER OF SEQUENCES: 19
: CORRESPONDENCE ADDRESS:
: ADDRESSER: OLIF & BERRIDGE, PLC
: STREET: P.O. BOX 19928
: CITY: Alexandria
: STATE: Virginia
: COUNTRY: U.S.A.
: ZIP: 22320
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/988,242
: FILING DATE: 10-DEC-1997
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Berridge, William P.
: REGISTRATION NUMBER: 30,024
: REFERENCE/DOCKET NUMBER: WPB 36400A
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 703-836-6400
: TELEFAX: 703-836-2787
: INFORMATION FOR SEQ ID NO: 10:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 12 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE:
: DESCRIPTION: /desc = "protein"
US-08-988-242-10

Query Match      28.6%; Score 30; DB 2; Length 12;
Best Local Similarity 62.5%; Pred. No. 1.7e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      2 PAKGMSPP 9
DB      3 PAKGAAP 10

RESULT 32
US-07-867-819D-14
: Sequence 14, Application US/07867819D
: Patent No. 6897287
: GENERAL INFORMATION:
: APPLICANT: Harley, John
: TITLE OF INVENTION: Methods and Reagents for Diagnosis of Autoantibodies
: FILE REFERENCE: OMRP 114 CIP (2)
: CURRENT APPLICATION NUMBER: US/07/867,819D
: PRIOR FILING DATE: 1992-04-13
: PRIOR APPLICATION NUMBER: 07/472,947
: PRIOR FILING DATE: 1990-01-31
: PRIOR APPLICATION NUMBER: 07/648,205
: PRIOR FILING DATE: 1991-01-31
: NUMBER OF SEQ ID NOS: 161
: SOFTWARE: Patentin version 3.1
: SEQ ID NO 14
: LENGTH: 12
: TYPE: PRT
: ORGANISM: homo sapien
: FEATURE:
: NAME/KEY: MISC FEATURE
: LOCATION: (3)..(10)
: OTHER INFORMATION: Binding site
: FEATURE:
: NAME/KEY: VARIANT
: LOCATION: (9)..(9)
: OTHER INFORMATION: Can be R, F, G, H, I, K, S, T, V or Y
US-07-867-819D-14
```

Query Match 28.6%; Score 30; DB 2; Length 12;  
Best Local Similarity 62.5%; Pred. No. 1.7e+02;  
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 PAKGMSPP 9  
Db 4 PPGKXPP 11

## RESULT 33

US-08-630-916A-53  
Sequence 53, Application US/08630916A  
Patent No. 601137  
GENERAL INFORMATION:  
APPLICANT: Pirozzi, Gregorio  
APPLICANT: Kay, Brian K.  
TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL  
POLYPEPTIDES HAVING WW DOMAINS AND METHODS OF USING SAME  
NUMBER OF SEQUENCES: 124  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: United States  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/630,916A  
FILING DATE: 03-APR-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: MISROCK, S. LESLIE  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 1101-203  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 896-8864/9741  
INFORMATION FOR SEQ ID NO: 53:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-630-916A-53

Query Match 28.6%; Score 30; DB 2; Length 14;  
Best Local Similarity 50.0%; Pred. No. 2e+02;  
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 5 GMSPPFTVG 14  
Db 2 GTPPPYTVG 11

## RESULT 34

US-08-630-916A-54  
Sequence 54, Application US/08630916A  
Patent No. 601137  
GENERAL INFORMATION:  
APPLICANT: Pirozzi, Gregorio  
APPLICANT: Kay, Brian K.  
TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL  
POLYPEPTIDES HAVING WW DOMAINS AND METHODS OF USING SAME  
NUMBER OF SEQUENCES: 124

## CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: United States  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/630,916A  
FILING DATE: 03-APR-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: MISROCK, S. LESLIE  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 1101-203  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 896-8864/9741  
INFORMATION FOR SEQ ID NO: 54:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-630-916A-54

Query Match 28.6%; Score 30; DB 2; Length 14;  
Best Local Similarity 50.0%; Pred. No. 2e+02;  
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 5 GMSPPFTVG 14  
Db 2 GTPPPYTVG 11

## RESULT 35

US-09-509-595B-20  
Sequence 20, Application US/09509595B  
Patent No. 6951928  
GENERAL INFORMATION:  
APPLICANT: MAX-PLANCK-GESellschaft ZUR FORDERUNG DER WISSENSCHAFTEN E.V.  
APPLICANT: NATIONAL PUBLIC HEALTH INSTITUTE  
APPLICANT: PELTONEN, Leena  
APPLICANT: ALTONEN, Johanna  
APPLICANT: BJORSES, Petra  
APPLICANT: PERHENTUPA, Jaakko  
APPLICANT: PALOTIE, Aarno  
APPLICANT: HORELLI-KUITUNEN, Nina  
APPLICANT: VASPO, Marie-Laure  
APPLICANT: LEHACH, Hans  
TITLE OF INVENTION: NUCLEIC ACID MOLECULE ENCODING A (POLY)PEPTIDE CO-SEGREGATING IN  
FOAM WITH AUTOTMONE POLYENDOCRINOATRY CANDIDIASIS ECTODERMAL D  
TITLE OF INVENTION: (APBCED)  
FILE REFERENCE: VOS81130  
CURRENT APPLICATION NUMBER: US/09/509,595B  
PRIOR FILING DATE: 2000-07-05  
PRIOR APPLICATION NUMBER: EP 97117154.1  
PRIOR FILING DATE: 1997-10-02  
PRIOR APPLICATION NUMBER: EP 97117398.4  
PRIOR FILING DATE: 1997-10-08  
PRIOR APPLICATION NUMBER: EP 97119810.6  
PRIOR FILING DATE: 1997-11-12  
NUMBER OF SEQ ID NOS: 30  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 20  
LENGTH: 14  
TYPE: PRT

ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic peptide  
US-09-509-595B-20

Query Match 28.6% Score 30; DB 2; Length 14;  
Best Local Similarity 62.5% Pred. No. 2e+02;  
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 PAKGSP 9  
DB 3 PRKGRKP 10

RESULT 36  
US-08-990-888-25  
Sequence 25, Application US/08990888B  
Patent No. 6387879  
GENERAL INFORMATION:  
APPLICANT: Blume, Arthur J.  
APPLICANT: Brissette, Renee  
APPLICANT: Carcamo, Juan  
APPLICANT: Mandeckl, Wlodeck S.  
TITLE OF INVENTION: Assays For Compounds Which Bind Growth Hormone Receptor  
FILE REFERENCE: 2598-4002  
CURRENT APPLICATION NUMBER: US/08/990,888B  
CURRENT FILING DATE: 1997-12-15  
NUMBER OF SEQ ID NOS: 81  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 25  
LENGTH: 18  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: H5 peptide secondary library sequence  
US-08-990-888-25

Query Match 28.6% Score 30; DB 2; Length 18;  
Best Local Similarity 50.0% Pred. No. 2.7e+02;  
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 5 GMSPPGTVG 14  
DB 6 GVSYPGWLNG 15

RESULT 37  
US-08-990-888-65  
Sequence 65, Application US/08990888B  
Patent No. 6387879  
GENERAL INFORMATION:  
APPLICANT: Blume, Arthur J.  
APPLICANT: Brissette, Renee  
APPLICANT: Carcamo, Juan  
APPLICANT: Mandeckl, Wlodeck S.  
APPLICANT: Tang, Pauline M.  
TITLE OF INVENTION: Assays For Compounds Which Bind Growth Hormone Receptor  
FILE REFERENCE: 2598-4002  
CURRENT APPLICATION NUMBER: US/08/990,888B  
CURRENT FILING DATE: 1997-12-15  
NUMBER OF SEQ ID NOS: 81  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 65  
LENGTH: 18  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: H5 peptide secondary library sequence  
US-08-990-888-65

Query Match 28.6% Score 30; DB 2; Length 18;  
Best Local Similarity 50.0% Pred. No. 2.7e+02;

Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 5 GMSPPGTVG 14  
DB 6 GVSYPGWLNG 15

RESULT 38  
US-09-010-999-9  
Sequence 9, Application US/09010999  
Patent No. 6132976  
GENERAL INFORMATION:  
APPLICANT: Poole, Anthony R.  
APPLICANT: Hollander, Anthony P.  
APPLICANT: Billingham, R. C.  
TITLE OF INVENTION: IMMUNOASSAYS FOR THE MEASUREMENT OF  
COLLAGEN DENATURATION AND CLEAVAGE IN CARTILAGE  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/010,999  
FILING DATE: 22-JAN-1998  
CLASSIFICATION: 4335  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/448,501  
FILING DATE: 17-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/984,123  
FILING DATE: 04-DEC-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Bent, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 032931/0212  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 672-5300  
TELEFAX: (202) 672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-010-999-9

Query Match 28.6% Score 30; DB 2; Length 19;  
Best Local Similarity 41.2% Pred. No. 2.9e+02;  
Matches 7; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 3 AKGMSPPGTVGBEVL 19  
DB 2 APGTPPGGIAGORGIV 18

RESULT 39  
US-09-470-830A-27  
Sequence 27, Application US/09470830A  
Patent No. 6677139  
GENERAL INFORMATION:  
APPLICANT: Genencor International, Inc.  
TITLE OF INVENTION: Methods for Production of Proteins in

FILE OF INVENTION: Host Cells  
FILE REFERENCE: GC559-PCT  
CURRENT APPLICATION NUMBER: US/09/470,830A  
CURRENT FILING DATE: 1999-12-23  
PRIOR APPLICATION NUMBER: US 09/470,830  
PRIOR FILING DATE: 1999-12-23  
NUMBER OF SEQ ID NOS: 44  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 27  
LENGTH: 19  
TYPE: PRT  
ORGANISM: Mycobacterium leprae  
US-09-470-830A-27

Query Match 28.6%; Score 30; DB 2; Length 19;  
Best Local Similarity 38.5%; Pred. No. 2.9e+02;  
Matches 5; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 3 AKGSPPGFVGS 15  
| : | : | : |  
Db 2 AETMPSGLVPE 14

RESULT 40  
US-08-928-213B-128  
Sequence 128, Application US/089282138  
Patent No. 6238905  
GENERAL INFORMATION:  
APPLICANT: McHenry, Charles S.  
Seville, Mark  
Cull, Millard G.  
TITLE OF INVENTION: NOVEL THERMOPHILIC POLYMERASE III  
HOLENZYME  
NUMBER OF SEQUENCES: 195  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/928,213B  
FILING DATE: 12-Sep-1997  
CLASSIFICATION: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: MacKnight, Kamrin T.  
REGISTRATION/DOCKET NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: ENZYCO-02550  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-705-8410  
TELEFAX: 415-397-8338  
INFORMATION FOR SEQ ID NO: 128:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
MOLECULE TYPE: protein  
TOPOLOGY: not relevant  
SEQUENCE DESCRIPTION: SEQ ID NO: 128:  
US-08-928-213B-128

Query Match 28.6%; Score 30; DB 2; Length 20;  
Best Local Similarity 60.0%; Pred. No. 3e+02;  
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
Qy 9 PGFVGESEV 18  
| | | | | | :  
| : | : | : | : |

Db 1 PLFVGESEGL 10

RESULT 41  
US-08-928-213B-129  
Sequence 129, Application US/089282138  
Patent No. 6238905  
GENERAL INFORMATION:  
APPLICANT: McHenry, Charles S.  
Seville, Mark  
Cull, Millard G.  
TITLE OF INVENTION: NOVEL THERMOPHILIC POLYMERASE III  
HOLENZYME  
NUMBER OF SEQUENCES: 195  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/928,213B  
FILING DATE: 12-Sep-1997  
CLASSIFICATION: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: MacKnight, Kamrin T.  
REGISTRATION/DOCKET NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: ENZYCO-02550  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-705-8410  
TELEFAX: 415-397-8338  
INFORMATION FOR SEQ ID NO: 129:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
MOLECULE TYPE: protein  
TOPOLOGY: not relevant  
SEQUENCE DESCRIPTION: SEQ ID NO: 129:  
US-08-928-213B-129

Query Match 28.6%; Score 30; DB 2; Length 20;  
Best Local Similarity 60.0%; Pred. No. 3e+02;  
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 9 PGFVGESEV 18  
| | | | | | :  
Db 1 PLFVGESEGL 10

RESULT 42  
US-07-721-761A-17  
Sequence 17, Application US/07721761A  
Patent No. 5475099  
GENERAL INFORMATION:  
APPLICANT: Vic. C. Knauf  
APPLICANT: Gregory A. Thompson  
TITLE OF INVENTION: Plant Fatty Acid Synthases  
NUMBER OF SEQUENCES: 52  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Calgene, Inc.  
STREET: 1920 Fifth Street  
CITY: Davis  
STATE: CA  
COUNTRY: USA  
ZIP: 95616  
COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: Macintosh 6.0.7  
SOFTWARE: Microsoft Word 4.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/721,761A  
FILING DATE: 19910626  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/568,493  
FILING DATE: 15-AUGUST-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Elizabeth Lassen  
REGISTRATION NUMBER: 31,845  
NAME: Donna E. Scherer  
REGISTRATION NUMBER: 34,719  
REFERENCE/DOCKET NUMBER: CGNE 76-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (916) 753-6313  
TELEFAX: (916) 753-1510  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-07-721-761A-17

Query Match 28.1% Score 29.5; DB 1; Length 14;  
Best Local Similarity 63.6%; Pred. No. 2.4e+02;  
Matches 7; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

QY 10 GPRVR-BGYL 19  
DB 2 GFVMSGAGVL 12

RESULT 43  
US-07-978-687-17  
Sequence 17, Application US/07978687  
Patent No. 5510255  
GENERAL INFORMATION:  
APPLICANT: Vic. C. Knauf  
TITLE OF INVENTION: Plant Fatty Acid Synthases  
NUMBER OF SEQUENCES: 51  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Calgene, Inc.  
STREET: 1920 Fifth Street  
CITY: Davis  
STATE: CA  
COUNTRY: USA  
ZIP: 95616  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB  
OPERATING SYSTEM: Macintosh 6.0.7  
SOFTWARE: Microsoft Word 4.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/978,687  
FILING DATE: FEBRUARY 1, 1993  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US91/05801  
FILING DATE: 15-AUGUST-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/568,493  
FILING DATE: 15-AUGUST-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/721,761  
FILING DATE: 26-JUNE-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Elizabeth Lassen

REGISTRATION NUMBER: 31,845  
NAME: Donna E. Scherer  
REGISTRATION NUMBER: 34,719  
REFERENCE/DOCKET NUMBER: CGNE 76-2 WO  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (916) 753-6313  
TELEFAX: (916) 753-1510  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-07-978-687-17

Query Match 28.1% Score 29.5; DB 1; Length 14;  
Best Local Similarity 63.6%; Pred. No. 2.4e+02;  
Matches 7; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

QY 10 GPRVR-BGYL 19  
DB 2 GFVMSGAGVL 12

RESULT 44  
PCT-US91-05801-17  
Sequence 17, Application PC/TUS9105801  
GENERAL INFORMATION:  
APPLICANT: Vic. C. Knauf  
TITLE OF INVENTION: Plant Fatty Acid Synthases  
NUMBER OF SEQUENCES:  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Calgene, Inc.  
STREET: 1920 Fifth Street  
CITY: Davis  
STATE: CA  
COUNTRY: USA  
ZIP: 95616  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: Macintosh 6.0.7  
SOFTWARE: Microsoft Word 4.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US91/05801  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/568,493  
FILING DATE: 15-AUGUST-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/721,761  
FILING DATE: 26-JUNE-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Elizabeth Lassen  
REGISTRATION NUMBER: 31,845  
NAME: Donna E. Scherer  
REGISTRATION NUMBER: 34,719  
REFERENCE/DOCKET NUMBER: CGNE 76-2 WO  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (916) 753-6313  
TELEFAX: (916) 753-1510  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
PCT-US91-05801-17

Query Match 28.1% Score 29.5; DB 4; Length 14;  
Best Local Similarity 63.6%; Pred. No. 2.4e+02;

Matches 7; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

QY 10 GRIIVE-EGVL 19  
Db 2 GFVWEGAGVL 12

## RESULT 45

US-07-721-761A-10  
Sequence 10, Application US/07721761A  
Patent No. 5475099  
GENERAL INFORMATION:  
APPLICANT: Vlc. C. Knauf  
APPLICANT: Gregory A. Thompson  
TITLE OF INVENTION: Plant Fatty Acid Synthases  
NUMBER OF SEQUENCES: 52  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Calgene, Inc.  
STREET: 1920 Fifth Street  
CITY: Davis  
STATE: CA  
COUNTRY: USA  
ZIP: 95616  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: Macintosh 6.0.7  
SOFTWARE: Microsoft Word 4.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/721,761A  
FILING DATE: 19910626  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/568,493  
FILING DATE: 15-AUGUST-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Elizabeth Lassen  
REGISTRATION NUMBER: 31,845  
NAME: Donna E. Scherer  
REGISTRATION NUMBER: 34,719  
REFERENCE/DOCKET NUMBER: CGNE 76-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (916) 753-6313  
TELEFAX: (916) 753-1510  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-07-721-761A-10

Query Match 28.1%; Score 29.5; DB 1; Length 17;  
Best Local Similarity 63.6%; Pred. No. 3.1e+02;  
Matches 7; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

QY 10 GRIIVE-EGVL 19  
Db 2 GFVWEGAGVL 12

## RESULT 46

US-07-978-687-10  
Sequence 10, Application US/07978687  
Patent No. 5510255  
GENERAL INFORMATION:  
APPLICANT: Vlc. C. Knauf  
APPLICANT: Gregory A. Thompson  
TITLE OF INVENTION: Plant Fatty Acid Synthases  
NUMBER OF SEQUENCES: 51  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Calgene, Inc.  
STREET: 1920 Fifth Street

CITY: Davis  
STATE: CA  
COUNTRY: USA  
ZIP: 95616

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: Macintosh 6.0.7  
SOFTWARE: Microsoft Word 4.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/978,687  
FILING DATE: FEBRUARY 1, 1993  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US91/05801  
FILING DATE: 15-AUGUST-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/568,493  
FILING DATE: 15-AUGUST-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/721,761  
FILING DATE: 26-JUNE-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Elizabeth Lassen  
REGISTRATION NUMBER: 31,845  
NAME: Donna E. Scherer  
REGISTRATION NUMBER: 34,719  
REFERENCE/DOCKET NUMBER: CGNE 76-2 WO  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (916) 753-6313  
TELEFAX: (916) 753-1510  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-07-978-687-10

Query Match 28.1%; Score 29.5; DB 1; Length 17;  
Best Local Similarity 63.6%; Pred. No. 3.1e+02;  
Matches 7; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

QY 10 GRIIVE-EGVL 19  
Db 2 GFVWEGAGVL 12

## RESULT 47

PCT-US91-05801-10  
Sequence 10, Application PC/TUS9105801  
GENERAL INFORMATION:  
APPLICANT: Vlc. C. Knauf  
APPLICANT: Gregory A. Thompson  
TITLE OF INVENTION: Plant Fatty Acid Synthases  
NUMBER OF SEQUENCES:  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Calgene, Inc.  
STREET: 1920 Fifth Street  
CITY: Davis  
STATE: CA  
COUNTRY: USA  
ZIP: 95616  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: Macintosh 6.0.7  
SOFTWARE: Microsoft Word 4.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US91/05801  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:



APPLICATION NUMBER: 07/568,493  
FILING DATE: 15-AUGUST-1990  
PRIOR APPLICATION DATA: 07/721,761  
APPLICATION NUMBER: 07/721,761  
FILING DATE: 26-JUNE-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Elizabeth Laessen  
REGISTRATION NUMBER: 31,845  
NAME: Donna E. Scherer  
REGISTRATION NUMBER: 34,719  
REFERENCE/DOCKET NUMBER: CGNE 76-2 WO  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (916) 753-6313  
TELEFAX: (916) 753-1510  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
PCT-US91-05801-10

Query Match 28.1%; Score 29.5; DB 4; Length 17;  
Best Local Similarity 63.6%; Pred. No. 3.1e+02;  
Matches 7; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

QY 10 GPRVE-EGYL 19  
DB 2 GPRVGGAGVL 12

RESULT 48  
US-08-160-604-1  
Sequence 1, Application US/08160604  
Patent No. 6232522  
GENERAL INFORMATION:  
APPLICANT: Harley, John  
APPLICANT: James, Judith A.  
TITLE OF INVENTION: PEPTIDE INDUCTION OF AUTOIMMUNITY AND CLINICAL SYMPTOMATOLOGY  
NUMBER OF SEQUENCES: 127  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Patrea L. Pabat  
STREET: 1100 Peachtree Street, Suite 2800  
CITY: Atlanta  
STATE: Georgia  
COUNTRY: USA  
ZIP: 30309-4530  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/160,604  
FILING DATE: 30-NOV-1993  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/867,819  
FILING DATE: 13-APR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/648,205  
FILING DATE: 31-JAN-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/472,947  
FILING DATE: 31-JAN-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Pabst, Patrea L.  
REGISTRATION NUMBER: 31,284  
REFERENCE/DOCKET NUMBER: OMRF114CIP(3)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (404)-815-6508  
TELEFAX: (404)-815-6555

INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: N-terminal  
US-08-160-604-1

Query Match 27.6%; Score 29; DB 2; Length 8;  
Best Local Similarity 62.5%; Pred. No. 4.6e+05;  
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 PAKGMSPP 9  
DB 1 PPGWRPP 8

RESULT 49  
US-08-475-955-123  
Sequence 123, Application US/08475955  
Patent No. 6641813  
GENERAL INFORMATION:  
APPLICANT: Harley, John  
TITLE OF INVENTION: METHODS AND REAGENTS FOR DIAGNOSIS OF  
NUMBER OF SEQUENCES: 218  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Patrea L. Pabat  
STREET: 2800 One Atlantic Center, 1250 West Peachtree Street  
CITY: Atlanta  
STATE: GA  
COUNTRY: USA  
ZIP: 30309-3450  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/475,955  
FILING DATE: June 7, 1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/867,819  
FILING DATE: April 13, 1992  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/648,205  
FILING DATE: January 31, 1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/472,947  
FILING DATE: January 31, 1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Pabst, Patrea L.  
REGISTRATION NUMBER: 31,284  
REFERENCE/DOCKET NUMBER: OMRF114CIP(2) DIV  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (404)-873-8794  
TELEFAX: (404)-873-8795  
INFORMATION FOR SEQ ID NO: 123:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-475-955-123

Query Match 27.6%; Score 29; DB 2; Length 8;

Best Local Similarity 62.5%; Pred. No. 4.6e+05;  
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 PAKGMSPP 9  
| | | |  
Db 1 PPPGMRPP 8

## RESULT 50

US-09-718-693A-3  
; Sequence 3, Application US/09718693A  
; Patent No. 6642008  
; GENERAL INFORMATION:  
; APPLICANT: Oklahoma Medical Research Foundation  
; APPLICANT: Harley, John B.  
; APPLICANT: James, Judith A.  
; APPLICANT: Kautman, Kenneth M.  
; TITLE OF INVENTION: Assays and Therapies For Latent Viral Infection  
; FILE REFERENCE: OMRP 177  
; CURRENT APPLICATION NUMBER: US/09/718,693A  
; PRIOR FILING DATE: 2000-11-22  
; PRIOR FILING DATE: 1999-11-24  
; NUMBER OF SEQ ID NOS: 3  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO 3  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Human herpesvirus 4  
US-09-718-693A-3

Query Match 27.6%; Score 29; DB 2; Length 8;  
Best Local Similarity 62.5%; Pred. No. 4.6e+05;  
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 PAKGMSPP 9  
| | | |  
Db 1 PPPGMRPP 8

## RESULT 51

US-07-867-819D-147  
; Sequence 147, Application US/07867819D  
; Patent No. 6897287  
; GENERAL INFORMATION:  
; APPLICANT: Harley, John  
; TITLE OF INVENTION: Methods and Reagents for Diagnosis of Autoantibodies  
; FILE REFERENCE: OMRP 114 CIP (2)  
; CURRENT APPLICATION NUMBER: US/07/867,819D  
; CURRENT FILING DATE: 1992-04-13  
; PRIOR APPLICATION NUMBER: 07/472,947  
; PRIOR FILING DATE: 1990-01-31  
; PRIOR APPLICATION NUMBER: 07/648,205  
; PRIOR FILING DATE: 1991-01-31  
; NUMBER OF SEQ ID NOS: 161  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO 147  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-07-867-819D-147

Query Match 27.6%; Score 29; DB 2; Length 8;  
Best Local Similarity 62.5%; Pred. No. 4.6e+05;  
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 PAKGMSPP 9  
| | | |  
Db 1 PPPGMRPP 8

## RESULT 52

US-07-867-819D-149

; Sequence 149, Application US/07867819D  
; Patent No. 6897287  
; GENERAL INFORMATION:  
; APPLICANT: Harley, John  
; TITLE OF INVENTION: Methods and Reagents for Diagnosis of Autoantibodies  
; FILE REFERENCE: OMRP 114 CIP (2)  
; CURRENT APPLICATION NUMBER: US/07/867,819D  
; CURRENT FILING DATE: 1992-04-13  
; PRIOR APPLICATION NUMBER: 07/472,947  
; PRIOR FILING DATE: 1990-01-31  
; PRIOR APPLICATION NUMBER: 07/648,205  
; PRIOR FILING DATE: 1991-01-31  
; NUMBER OF SEQ ID NOS: 161  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO 149  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-07-867-819D-149

Query Match 27.6%; Score 29; DB 2; Length 8;  
Best Local Similarity 62.5%; Pred. No. 4.6e+05;  
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 PAKGMSPP 9  
| | | |  
Db 1 PPPGMRPP 8

## RESULT 53

US-07-867-819D-157  
; Sequence 157, Application US/07867819D  
; Patent No. 6897287  
; GENERAL INFORMATION:  
; APPLICANT: Harley, John  
; TITLE OF INVENTION: Methods and Reagents for Diagnosis of Autoantibodies  
; FILE REFERENCE: OMRP 114 CIP (2)  
; CURRENT APPLICATION NUMBER: US/07/867,819D  
; CURRENT FILING DATE: 1992-04-13  
; PRIOR APPLICATION NUMBER: 07/472,947  
; PRIOR FILING DATE: 1990-01-31  
; PRIOR APPLICATION NUMBER: 07/648,205  
; PRIOR FILING DATE: 1991-01-31  
; NUMBER OF SEQ ID NOS: 161  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO 157  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-07-867-819D-157

Query Match 27.6%; Score 29; DB 2; Length 8;  
Best Local Similarity 62.5%; Pred. No. 4.6e+05;  
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 PAKGMSPP 9  
| | | |  
Db 1 PPPGMRPP 8

## RESULT 54

US-08-475-955-10  
; Sequence 10, Application US/08475955  
; Patent No. 6641813  
; GENERAL INFORMATION:  
; APPLICANT: Harley, John  
; TITLE OF INVENTION: METHODS AND REAGENTS FOR DIAGNOSIS OF  
; TITLE OF INVENTION: AUTOANTIBODIES  
; NUMBER OF SEQUENCES: 218  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Patrea L. Pabst  
; STREET: 2800 One Atlantic Center, 1250 West Peachtree Street  
; CITY: Atlanta

STATE: GA  
COUNTRY: USA  
ZIP: 30309-3450  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/475,955  
FILING DATE: June 7, 1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/867,819  
FILING DATE: April 13, 1992  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/648,205  
FILING DATE: January 31, 1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/472,947  
FILING DATE: January 31, 1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Pabst, Patrea L.  
REGISTRATION NUMBER: 31,284  
REFERENCE/DOCKET NUMBER: OMRP114CIP(2) DIV  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (404)-873-8794  
TELEFAX: (404)-873-8795  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Binding-site  
LOCATION: 3..10  
US-08-475-955-10

Query Match 27.6%; Score 29; DB 2; Length 11;  
Best local Similarity 62.5%; Pred. No. 2.2e+02;  
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 PAKGMRP 9  
DB 3 PPGMRP 10

RESULT 55  
US-07-867-819D-10  
Sequence 10, Application US/07867819D  
Patent No. 6897287  
GENERAL INFORMATION:  
APPLICANT: Harley, John  
TITLE OF INVENTION: Methods and Reagents for Diagnosis of Autoantibodies  
FILE REFERENCE: OMRP 114 CIP (2)  
CURRENT APPLICATION NUMBER: US/07/867,819D  
CURRENT FILING DATE: 1992-04-13  
PRIOR APPLICATION NUMBER: 07/472,947  
PRIOR FILING DATE: 1990-01-31  
PRIOR APPLICATION NUMBER: 07/648,205  
PRIOR FILING DATE: 1991-01-31  
NUMBER OF SEQ ID NOS: 161  
SOFTWARE: Patentin version 3.1  
SEQ ID NO 10  
LENGTH: 11  
TYPE: PRT  
ORGANISM: homo sapien  
FEATURE:  
NAME/KEY: MISC FEATURE  
LOCATION: (3)..(10)

OTHER INFORMATION: Binding site  
US-07-867-819D-10

Query Match 27.6%; Score 29; DB 2; Length 11;  
Best local Similarity 62.5%; Pred. No. 2.2e+02;  
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 PAKGMRP 9  
DB 3 PPGMRP 10

RESULT 56  
US-08-475-955-14  
Sequence 14, Application US/08475955  
Patent No. 6641813  
GENERAL INFORMATION:  
APPLICANT: Harley, John  
TITLE OF INVENTION: METHODS AND REAGENTS FOR DIAGNOSIS OF  
NUMBER OF SEQUENCES: 218  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Patrea L. Pabst  
STREET: 2800 One Atlantic Center, 1250 West Peachtree Street  
CITY: Atlanta  
STATE: GA  
COUNTRY: USA  
ZIP: 30309-3450  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/475,955  
FILING DATE: June 7, 1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/867,819  
FILING DATE: April 13, 1992  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/648,205  
FILING DATE: January 31, 1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/472,947  
FILING DATE: January 31, 1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Pabst, Patrea L.  
REGISTRATION NUMBER: 31,284  
REFERENCE/DOCKET NUMBER: OMRP114CIP(2) DIV  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (404)-873-8794  
TELEFAX: (404)-873-8795  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Binding-site  
LOCATION: 3..10  
NAME/KEY: Modified-site  
LOCATION: 6  
OTHER INFORMATION: /note= "The arginine at position 8 can be  
OTHER INFORMATION: substituted with F, G, H, I, K, S, T, V,  
OTHER INFORMATION: and Y."  
US-08-475-955-14

Query Match 27.6%; Score 29; DB 2; Length 12;

Best Local Similarity 62.5%; Pred. No. 2.5e+02;  
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 PAKGMRP 9  
DB 4 PPGMRP 11

## RESULT 57

US-07-994-469A-21  
Sequence 21, Application US/07994469A  
Patent No. 5519119  
GENERAL INFORMATION:  
APPLICANT: Yamada, No. 5519119utosh  
APPLICANT: Kato, Masanari  
APPLICANT: Miyata, Keizo  
APPLICANT: Aoyama, Yoshiyuki  
APPLICANT: Shikama, Hiroshi  
TITLE OF INVENTION: Polypeptide  
NUMBER OF SEQUENCES: 101  
CORRESPONDENCE ADDRESSES:  
ADDRESSES: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,  
ADDRESSER: P.C. Jefferson Davis Highway, Fourth Floor  
CITY: Arlington  
STATE: Virginia  
ZIP: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/994,469A  
FILING DATE: 21-DEC-1992  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Oblon, No. 5519119man F.  
REGISTRATION NUMBER: 24,618  
REFERENCE/DOCKET NUMBER: 72-085-0 FWC  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703)413-3000  
TELEFAX: (703)413-2220  
TELEX: 248855 OPAT UR  
INFORMATION FOR SEQ ID NO: 21:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-07-994-469A-21

Query Match 27.6%; Score 29; DB 1; Length 16;  
Best Local Similarity 62.5%; Pred. No. 3.4e+02;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DPAKMRP 8  
DB 1 DPGMRP 8

## RESULT 58

US-08-482-142-186  
Sequence 186, Application US/08482142  
Patent No. 5820862  
GENERAL INFORMATION:  
APPLICANT: Garman, Richard  
APPLICANT: Greenstein, Julia  
APPLICANT: Kuo, Mei-chang  
APPLICANT: Rogers, Bruce  
APPLICANT: Franzen, Henry  
APPLICANT: Chen, Xian  
APPLICANT: Evans, Sean

APPLICANT: Shaked, Ze'ev  
TITLE OF INVENTION: T CELL EPITOPES OF THE MAJOR ALLERGENS  
FROM DERMATOPHAGOIDES (HOUSE DUST MITE)  
NUMBER OF SEQUENCES: 207  
CORRESPONDENCE ADDRESS:  
ADDRESSES: IMMULOGIC PHARMACEUTICAL CORPORATION  
STREET: 610 LINCOLN STREET  
CITY: WALTHAM  
STATE: MA  
COUNTRY: USA  
ZIP: 02154

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII TEXT  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/482,142  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/445,307  
FILING DATE: 07 June 1995  
ATTORNEY/AGENT INFORMATION:  
NAME: CRAIG, ANNE I.  
REGISTRATION NUMBER: 32,976  
REFERENCE/DOCKET NUMBER: 017.6US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 466-6000  
TELEFAX: (617) 466-6040  
INFORMATION FOR SEQ ID NO: 186:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: internal  
US-08-482-142-186

Query Match 27.6%; Score 29; DB 1; Length 16;  
Best Local Similarity 55.6%; Pred. No. 3.4e+02;  
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 12 IYEGGVLS 20  
DB 6 LVGDNGVLA 14

## RESULT 59

US-08-478-572-186  
Sequence 186, Application US/08478572  
Patent No. 5968526  
GENERAL INFORMATION:  
APPLICANT: Garman, Richard  
APPLICANT: Greenstein, Julia  
APPLICANT: Kuo, Mei-chang  
APPLICANT: Rogers, Bruce  
APPLICANT: Franzen, Henry  
APPLICANT: Chen, Xian  
APPLICANT: Evans, Sean  
APPLICANT: Shaked, Ze'ev  
TITLE OF INVENTION: T CELL EPITOPES OF THE MAJOR ALLERGENS  
FROM DERMATOPHAGOIDES (HOUSE DUST MITE)  
NUMBER OF SEQUENCES: 207  
CORRESPONDENCE ADDRESS:  
ADDRESSES: IMMULOGIC PHARMACEUTICAL CORPORATION  
STREET: 610 LINCOLN STREET  
CITY: WALTHAM  
STATE: MA  
COUNTRY: USA  
ZIP: 02154  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII TEXT  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/478,572  
FILING DATE: 07-June-1995  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/445,307  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: CRAIG, ANNE I.  
REGISTRATION NUMBER: 32,976  
REFERENCE/DOCKET NUMBER: 017.6US  
TELEPHONE: (617) 466-6000  
TELEFAX: (617) 466-6040  
INFORMATION FOR SEQ ID NO: 186:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: internal  
US-08-478-572-186

Query Match 27.6%; Score 29; DB 1; Length 16;  
Best Local Similarity 55.6%; Pred. No. 3.4e+02;  
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 12 IYVGEVGLS 20  
DB 6 LVGDNGVLA 14

RESULT 60  
US-08-484-296-186  
Sequence 186, Application US/08484296  
Patent No. 6268491  
GENERAL INFORMATION:  
APPLICANT: Garman, Richard  
APPLICANT: Greenstein, Julia  
APPLICANT: Kuo, Mei-chang  
APPLICANT: Rogers, Bruce  
APPLICANT: Franzén, Henry  
APPLICANT: Chen, Xian  
APPLICANT: Evans, Sean  
APPLICANT: Shaked, Ze'ev  
TITLE OF INVENTION: T CELL EPITOPES OF THE MAJOR ALLEGENS  
TITLE OF INVENTION: FROM DERMATOPHAGOIDES (HOUSE DUST MITE)  
NUMBER OF SEQUENCES: 207  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: IMMUNOLOGIC PHARMACEUTICAL CORPORATION  
STREET: 610 LINCOLN STREET  
CITY: WALTHAM  
STATE: MA  
COUNTRY: USA  
ZIP: 02154  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII TEXT  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/484,296  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/445,307  
FILING DATE: 07 June 1995  
ATTORNEY/AGENT INFORMATION:  
NAME: CRAIG, ANNE I.  
REGISTRATION NUMBER: 32,976

REFERENCE/DOCKET NUMBER: 017.6US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 466-6000  
TELEFAX: (617) 466-6040  
INFORMATION FOR SEQ ID NO: 186:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: internal  
US-08-484-296-186

Query Match 27.6%; Score 29; DB 2; Length 16;  
Best Local Similarity 55.6%; Pred. No. 3.4e+02;  
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 12 IYVGEVGLS 20  
DB 6 LVGDNGVLA 14

RESULT 61  
US-08-990-888-24  
Sequence 24, Application US/08990888B  
Patent No. 6387879  
GENERAL INFORMATION:  
APPLICANT: Blume, Arthur J.  
APPLICANT: Brissette, Renee  
APPLICANT: Carcamo, Juan  
APPLICANT: Mandeckl, Wlodeck S.  
APPLICANT: Tang, Pauline M.  
TITLE OF INVENTION: Assays For Compounds Which Bind Growth Hormone Receptor  
FILE REFERENCE: 2598-4002  
CURRENT APPLICATION NUMBER: US/08/990,888B  
CURRENT FILING DATE: 1997-12-15  
NUMBER OF SEQ ID NOS: 81  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 24  
LENGTH: 18  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURES:  
OTHER INFORMATION: H5 peptide secondary library sequence  
US-08-990-888-24

Query Match 27.6%; Score 29; DB 2; Length 18;  
Best Local Similarity 41.7%; Pred. No. 3.9e+02;  
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 3 AKGMSPPGPIV 14  
DB 4 ALGVTVPGWLAG 15

RESULT 62  
US-08-990-888-46  
Sequence 46, Application US/08990888B  
Patent No. 6387879  
GENERAL INFORMATION:  
APPLICANT: Blume, Arthur J.  
APPLICANT: Brissette, Renee  
APPLICANT: Carcamo, Juan  
APPLICANT: Mandeckl, Wlodeck S.  
APPLICANT: Tang, Pauline M.  
TITLE OF INVENTION: Assays For Compounds Which Bind Growth Hormone Receptor  
FILE REFERENCE: 2598-4002  
CURRENT APPLICATION NUMBER: US/08/990,888B  
CURRENT FILING DATE: 1997-12-15  
NUMBER OF SEQ ID NOS: 81  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 46  
LENGTH: 18

```
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: H5 peptide secondary library sequence
US-08-990-888-46

Query Match
Best Local Similarity 27.6%; Score 29; DB 2; Length 18;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 5 GMSPPGFIVG 14
DB 6 GVSFPGWLAG 15

RESULT 63
US-08-990-888-62
/ Sequence 62, Application US/08990888B
/ Patent No. 6387879
/ GENERAL INFORMATION:
/ APPLICANT: Blume, Arthur J.
/ APPLICANT: Brisse, Renee
/ APPLICANT: Carcano, Juan
/ APPLICANT: Mandeckl, Wlodek S.
/ APPLICANT: Tang, Pauline M.
/ TITLE OF INVENTION: Assays for Compounds which Bind Growth Hormone Receptor
/ FILE REFERENCE: 2598-4002
/ CURRENT APPLICATION NUMBER: US/08/990,888B
/ NUMBER OF SEQ ID NOS: 81
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 62
/ LENGTH: 18
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: H5 peptide secondary library sequence
US-08-990-888-62

Query Match
Best Local Similarity 27.6%; Score 29; DB 2; Length 18;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 5 GMSPPGFIVG 14
DB 6 GVSFPGWLAG 15

RESULT 64
US-09-010-999-8
/ Sequence 8, Application US/09010999
/ Patent No. 6132976
/ GENERAL INFORMATION:
/ APPLICANT: Poole, Anthony R.
/ APPLICANT: Hollander, Anthony P.
/ APPLICANT: Billingham, R. C.
/ TITLE OF INVENTION: IMMUNOASSAYS FOR THE MEASUREMENT OF
/ TITLE OF INVENTION: COLLAGEN DENATURATION AND CLEAVAGE IN CARTILAGE
/ NUMBER OF SEQUENCES: 16
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Foley & Lardner
/ STREET: 3000 K Street, N.W., Suite 500
/ CITY: Washington
/ STATE: D.C.
/ COUNTRY: USA
/ ZIP: 20007-5109
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: IBM PC compatible
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/010,999
```

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/ FILING DATE: 22-JAN-1998
/ CLASSIFICATION: 4335
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/448,501
/ FILING DATE: 17-JUL-1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/984,123
/ FILING DATE: 04-DEC-1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Bent, Stephen A.
/ REGISTRATION NUMBER: 29,768
/ REFERENCE/DOCKET NUMBER: 032931/0212
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (202)672-5300
/ TELEFAX: (202)672-5399
/ TELEX: 904136
/ INFORMATION FOR SEQ ID NO: 8:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 19 amino acids
/ TYPE: amino acid
/ STRANDEDNESS:
/ TOPOLOGY: linear
/ MOLECULAR TYPE: peptide
/ FEATURE:
/ NAME/KEY: Modified-site
/ LOCATION: 6
/ OTHER INFORMATION: /product="Pro(OH)"
US-09-010-999-8

Query Match
Best Local Similarity 27.6%; Score 29; DB 2; Length 19;
Matches 5; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 3 AKGSPPGIVEEGVL 19
DB 2 AEGPYPGQLAGQGRGIV 18

RESULT 65
US-09-980-177A-77
/ Sequence 77, Application US/09980177A
/ Patent No. 6838084
/ GENERAL INFORMATION:
/ APPLICANT: Jochims, Ingrid
/ APPLICANT: Nieland, John
/ TITLE OF INVENTION: Cytotoxic T-Cell Epitopes of the
/ TITLE OF INVENTION: Papilloma Virus L1-Protein and Use Thereof in Diagnosis and
/ FILE REFERENCE: 50125/036001
/ CURRENT APPLICATION NUMBER: US/09/980,177A
/ PRIOR FILING DATE: 2001-11-29
/ PRIOR APPLICATION NUMBER: PCT/EP00/05006
/ PRIOR FILING DATE: 2000-05-31
/ PRIOR APPLICATION NUMBER: DE 19925199.1
/ NUMBER OF SEQ ID NOS: 77
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 77
/ LENGTH: 20
/ TYPE: PRT
/ ORGANISM: Influenza virus type A
US-09-980-177A-77

Query Match
Best Local Similarity 27.6%; Score 29; DB 2; Length 20;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 14 GREGVL 19
DB 7 GREGVL 12

RESULT 66
```

US-10-007-700-413  
; Sequence 413, Application US/10007700  
; Patent No. 6960570  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Tonglong  
; APPLICANT: Wang, Aljun  
; APPLICANT: Skeiky, Yasir A.W.  
; APPLICANT: Li, Samuel X.  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: Henderson, Robert A.  
; APPLICANT: McNeill, Patricia D.  
; APPLICANT: Fanger, Neil  
; APPLICANT: Recter, Marc W.  
; APPLICANT: Durham, Margareta  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Vedvick, Thomas S.  
; APPLICANT: Carter, Darrick  
; APPLICANT: Matanabe, Yoshihiro  
; APPLICANT: Peckman, David W.  
; APPLICANT: Cai, Peng  
; APPLICANT: Roy, Teresa M.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER  
; FILE REFERENCE: 210121.455C17  
; CURRENT APPLICATION NUMBER: US/10/007,700  
; CURRENT FILING DATE: 2001-11-30  
; NUMBER OF SEQ ID NOS: 469  
; SOFTWARE: PatcSeq for Windows Version 4.0  
; SEQ ID NO 413  
; LENGTH: 20  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-007-700-413

Query Match 27.6%; Score 29; DB 2; Length 20;  
Best Local Similarity 62.5%; Pred. No. 4.4e+02;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 10 GPTVREG 17  
DB 9 GALTREG 16

RESULT 67  
US-10-394-980-140  
; Sequence 140, Application US/10394980  
; Patent No. 6908740  
; GENERAL INFORMATION:  
; APPLICANT: Vandekerckhove, Joel  
; APPLICANT: Gevaert, Kris  
; TITLE OF INVENTION: METHODS AND APPARATUS FOR GEL-FREE QUALITATIVE AND  
; TITLE OF INVENTION: QUANTITATIVE PROTEOME ANALYSIS, AND USES THEREFOR  
; FILE REFERENCE: VBV-001  
; CURRENT APPLICATION NUMBER: US/10/394,980  
; CURRENT FILING DATE: 2003-03-21  
; PRIOR APPLICATION NUMBER: PCT/EP02/03368  
; PRIOR FILING DATE: 2002-03-22  
; PRIOR APPLICATION NUMBER: US60/278,171  
; PRIOR FILING DATE: 2001-03-22  
; PRIOR APPLICATION NUMBER: US60/318,749  
; PRIOR FILING DATE: 2001-09-12  
; PRIOR APPLICATION NUMBER: US60/323,999  
; PRIOR FILING DATE: 2001-09-20  
; NUMBER OF SEQ ID NOS: 473  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 140  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURES:  
; NAME/KEY: MISC FEATURE  
; OTHER INFORMATION: part of KPC1\_HUMAN (P05771, protein kinase C, beta-I type)  
US-10-394-980-140

Query Match 27.1%; Score 28.5; DB 2; Length 18;  
Best Local Similarity 47.4%; Pred. No. 4.7e+02;  
Matches 9; Conservative 1; Mismatches 6; Indels 3; Gaps 2;

QY 1 DPAKMSPPGIVREGVL 19  
DB 2 DPAAG-PPPS-EGESTV 17

RESULT 68  
US-08-488-470A-7  
; Sequence 7, Application US/08488470A  
; Patent No. 5708153  
; GENERAL INFORMATION:  
; APPLICANT: Dower, William J.  
; APPLICANT: Barrett, Ronald W.  
; APPLICANT: Gallop, Mark A.  
; TITLE OF INVENTION: Method of Synthesizing Diverse  
; TITLE OF INVENTION: Collections of Oligomers  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESSER: Affymax Technologies, N.V.  
; STREET: 4001 Miranda Ave.  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/488,470A  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/762,522  
; FILING DATE: 18-SEP-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Stevens, Lauren L.  
; REGISTRATION NUMBER: 36,691  
; REFERENCE/DOCKET NUMBER: 1007E  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-812-8803  
; TELEFAX: 415-424-0832  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULAR TYPE: peptide  
US-08-488-470A-7

Query Match 26.7%; Score 28; DB 1; Length 5;  
Best Local Similarity 80.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 PPGFI 12  
DB 1 PPGFI 5

RESULT 69  
US-07-946-239-15  
; Sequence 15, Application US/07946239  
; Patent No. 5770358  
; GENERAL INFORMATION:  
; APPLICANT: DOWER, WILLIAM J  
; APPLICANT: BARRETT, RONALD W  
; APPLICANT: GALLOP, MARK A

APPLICANT: NEEDLES, MICHAEL C  
TITLE OF INVENTION: METHOD OF SYNTHESIZING DIVERSE  
COLLECTIONS OF OLIGOMERS  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESS: TOWNSEND AND TOWNSEND  
STREET: 1 MARKET PLAZA, STEWART TOWER, SUITE 2000  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/946,239  
FILING DATE: 19920916  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M.  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 11509-36-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-543-9600  
TELEFAX: 415-543-5043  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: linear  
MOLECULE TYPE: peptide

US-07-946-239-15

Query Match 26.7%; Score 28; DB 1; Length 5;  
Best Local Similarity 80.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 8 PGF1 12  
Db 1 PGF1 5

RESULT 70

US-08-484-505A-7  
Sequence 7, Application US/08484505A  
Patent No. 5789162  
GENERAL INFORMATION:  
APPLICANT: Dower, William J.  
APPLICANT: Barrett, Ronald W.  
APPLICANT: Gallop, Mark A.  
TITLE OF INVENTION: Method of Synthesizing Diverse  
COLLECTIONS OF OLIGOMERS  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESS: Affymax Technologies, N.V.  
STREET: 4001 Miranda Ave.  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/484,505A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/484,085

FILING DATE: 07-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/762,522  
FILING DATE: 18-SEP-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Stevens, Lauren L.  
REGISTRATION NUMBER: 36,691  
REFERENCE/DOCKET NUMBER: 1007B  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-496-2300  
TELEFAX: 415-424-0832  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide

US-08-484-505A-7

Query Match 26.7%; Score 28; DB 1; Length 5;  
Best Local Similarity 80.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 8 PGF1 12  
Db 1 PGF1 5

RESULT 71

US-08-383-766-3  
Sequence 3, Application US/08383766  
Patent No. 6087186  
GENERAL INFORMATION:  
APPLICANT: Cargill, John  
APPLICANT: Armstrong, Robert W.  
TITLE OF INVENTION: METHODS AND APPARATUS FOR SYNTHESIZING  
LABELED COMBINATORIAL CHEMISTRY LIBRARIES  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESS: Pennie and Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/383,766  
FILING DATE: 01-FEB-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Halluin, Albert P.  
REGISTRATION NUMBER: 25,227  
REFERENCE/DOCKET NUMBER: 8140-009  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-854-3660  
TELEFAX: 415-854-3694  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide

US-08-383-766-3

Query Match 26.7%; Score 28; DB 2; Length 5;



Best Local Similarity 80.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 PGF1 12  
1 PGF1 5

RESULT 72  
US-09-151-467-15  
Sequence 15, Application US/09151467  
Patent No. 6140493  
GENERAL INFORMATION:  
APPLICANT: DOWER, WILLIAM J  
APPLICANT: BARRETT, RONALD W  
APPLICANT: GALLOP, MARK A  
APPLICANT: NEEDLE, MICHAEL C  
TITLE OF INVENTION: METHOD OF SYNTHESIZING DIVERSE  
NUMBER OF SEQUENCES: 16  
COLLECTIONS OF OLIGOMERS  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: TOWNSEND AND TOWNSEND  
STREET: 1 MARKET PLAZA, STEWART TOWER, SUITE 2000  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/151,467  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/946,239  
FILING DATE: 1992-09-16  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M.  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 11509-36-1  
TELEPHONE: 415-543-9600  
TELEFAX: 415-543-5043  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-151-467-15

Query Match 26.7%; Score 28; DB 2; Length 5;  
Best Local Similarity 80.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 PGF1 12  
1 PGF1 5

Db 1 PGF1 5

RESULT 73  
US-09-078-403A-7  
Sequence 7, Application US/09078403A  
Patent No. 6165717  
GENERAL INFORMATION:  
APPLICANT: DOWER, WILLIAM  
APPLICANT: BARRETT, RONALD  
APPLICANT: GALLOP, MARK  
TITLE OF INVENTION: Method of synthesizing diverse  
collections of compounds

NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:

ADDRESSEE: Atiyah Research Institute  
STREET: 4001 Miranda Avenue  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA

ZIP: 94034

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/078,403A

FILING DATE: 13-MAY-1998

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/484,505

FILING DATE: 07-JUN-1995

APPLICATION NUMBER: 07/762,522

FILING DATE: 18-SEP-1991

ATTORNEY/AGENT INFORMATION:

NAME: Stevens, Lauren L.

REGISTRATION NUMBER: 36,691

REFERENCE/DOCKET NUMBER: 1007F

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650 812 8803

TELEFAX: 650 424 0832

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 5 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-09-078-403A-7

Query Match 26.7%; Score 28; DB 2; Length 5;  
Best Local Similarity 80.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 PGF1 12  
1 PGF1 5

Db 1 PGF1 5

RESULT 74  
US-09-256-838-15  
Sequence 15, Application US/09256838  
Patent No. 6416949  
GENERAL INFORMATION:  
APPLICANT: DOWER, WILLIAM J  
APPLICANT: BARRETT, RONALD W  
APPLICANT: GALLOP, MARK A  
APPLICANT: NEEDLE, MICHAEL C  
TITLE OF INVENTION: METHOD OF SYNTHESIZING DIVERSE  
COLLECTIONS OF OLIGOMERS  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: TOWNSEND AND TOWNSEND  
STREET: 1 MARKET PLAZA, STEWART TOWER, SUITE 2000  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:

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/ APPLICATION NUMBER: US/09/256,838
/ FILING DATE: 24-Feb-1999
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/07/946,239
/ FILING DATE: <Unknown>
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Smith, William M.
/ REGISTRATION NUMBER: 30,223
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 415-543-9600
/ TELEFAX: 415-543-5043
/ INFORMATION FOR SEQ ID NO: 15:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 5 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-256-838-15

Query Match      26.7%; Score 28; DB 2; Length 5;
Best Local Similarity 80.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      8 PGF1 12
       ||||:
Db      1 PGF1 5

RESULT 75
US-09-261-718-3
/ Sequence 3, Application US/09261718
/ Patent No. 6417010
/ GENERAL INFORMATION:
/ APPLICANT: Cargill, John
/ APPLICANT: Armstrong, Robert W
/ TITLE OF INVENTION: Methods and Apparatus for Synthesizing Labeled
/ TITLE OF INVENTION: Combinatorial Chemistry Libraries
/ FILE REFERENCE: 7638-PA02C
/ CURRENT APPLICATION NUMBER: US/09/261,718
/ CURRENT FILING DATE: 1999-03-03
/ NUMBER OF SEQ ID NOS: 6
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 3
/ LENGTH: 5
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Peptide
US-09-261-718-3

Query Match      26.7%; Score 28; DB 2; Length 5;
Best Local Similarity 80.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      8 PGF1 12
       ||||:
Db      1 PGF1 5

RESULT 76
PCT-US92-07815-15
/ Sequence 15, Application PC/TUS9207815
/ GENERAL INFORMATION:
/ APPLICANT: DOWER, WILLIAM J
/ APPLICANT: BARRETT, RONALD W
/ APPLICANT: GALLOP, MARK A
/ APPLICANT: NEEDLES, MICHAEL C
/ TITLE OF INVENTION: METHOD OF SYNTHESIZING DIVERSE
/ TITLE OF INVENTION: COLLECTIONS OF OLIGOMERS
/ NUMBER OF SEQUENCES: 16
```

```
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: TOWNSEND AND TOWNSEND
/ STREET: 1 MARKET PLAZA, STEUART TOWER, SUITE 2000
/ CITY: SAN FRANCISCO
/ STATE: CALIFORNIA
/ COUNTRY: USA
/ ZIP: 94105
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: PCT/US92/07815
/ FILING DATE: 19920916
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Smith, William M.
/ REGISTRATION NUMBER: 30,223
/ REFERENCE/DOCKET NUMBER: 11509-36-1
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 415-543-9600
/ TELEFAX: 415-543-5043
/ INFORMATION FOR SEQ ID NO: 15:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 5 amino acids
/ TYPE: AMINO ACID
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
PCT-US92-07815-15

Query Match      26.7%; Score 28; DB 4; Length 5;
Best Local Similarity 80.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      8 PGF1 12
       ||||:
Db      1 PGF1 5

RESULT 77
US-08-475-955-117
/ Sequence 117, Application US/08475955
/ Patent No. 6641813
/ GENERAL INFORMATION:
/ APPLICANT: Harley, John
/ TITLE OF INVENTION: METHODS AND REAGENTS FOR DIAGNOSIS OF
/ TITLE OF INVENTION: AUTOANTIBODIES
/ NUMBER OF SEQUENCES: 218
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Patrea L. Pabst
/ STREET: 2800 One Atlantic Center, 1250 West Peachtree Street
/ CITY: Atlanta
/ STATE: GA
/ COUNTRY: USA
/ ZIP: 30309-3450
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/475,955
/ FILING DATE: June 7, 1995
/ CLASSIFICATION: 424
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 07/667,819
/ FILING DATE: April 13, 1992
/ CLASSIFICATION: 424
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 07/648,205
/ FILING DATE: January 31, 1991
/ PRIOR APPLICATION DATA:
```

APPLICATION NUMBER: 07/472,947  
FILING DATE: January 31, 1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Pabst, Patrea L.  
REGISTRATION NUMBER: 31,284  
REFERENCE/DOCKET NUMBER: OMRP114CIP(2)DIV  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (404)-873-8794  
TELEFAX: (404)-873-8795  
INFORMATION FOR SEQ ID NO: 117:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-475-955-117

Query Match 26.7%; Score 28; DB 2; Length 8;  
Best Local Similarity 62.5%; Pred. No. 4.6e+05;  
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 PAKGMSPP 9  
DB 1 PPGMWIP 8

RESULT 78  
US-07-867-819D-117  
Sequence 117, Application US/07867819D  
Patent No. 6897287  
GENERAL INFORMATION:  
APPLICANT: Harley, John  
TITLE OF INVENTION: Method and Reagents for Diagnosis of Autoantibodies  
FILE REFERENCE: OMRP 114 CIP (2)  
CURRENT APPLICATION NUMBER: US/07/867,819D  
CURRENT FILING DATE: 1992-04-13  
PRIOR APPLICATION NUMBER: 07/472,947  
PRIOR FILING DATE: 1990-01-31  
PRIOR APPLICATION NUMBER: 07/648,205  
PRIOR FILING DATE: 1991-01-31  
NUMBER OF SEQ ID NOS: 161  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 117  
LENGTH: 8  
TYPE: PRT  
ORGANISM: homo sapien  
US-07-867-819D-117

Query Match 26.7%; Score 28; DB 2; Length 8;  
Best Local Similarity 62.5%; Pred. No. 4.6e+05;  
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 PAKGMSPP 9  
DB 1 PPGMWIP 8

RESULT 79  
US-09-769-180-31  
Sequence 31, Application US/09769180  
Patent No. 6680173  
GENERAL INFORMATION:  
APPLICANT: VanMechelen, Eugene  
APPLICANT: Vanderstichelen, Hugo  
TITLE OF INVENTION: Diagnosis of Tauopathies  
FILE REFERENCE: US 112,1181  
CURRENT APPLICATION NUMBER: US/09/769,180  
CURRENT FILING DATE: 2001-01-24  
PRIOR APPLICATION NUMBER: EP 00870008.8  
PRIOR FILING DATE: 2000-01-24  
PRIOR APPLICATION NUMBER: EP 00870280.5  
PRIOR FILING DATE: 2000-11-22

PRIOR APPLICATION NUMBER: US 60/178,391  
PRIOR FILING DATE: 2000-01-27  
NUMBER OF SEQ ID NOS: 54  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 31  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-769-180-31

Query Match 26.7%; Score 28; DB 2; Length 9;  
Best Local Similarity 57.1%; Pred. No. 4.6e+05;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 KGMSPPG 10  
DB 1 RGAAPPG 7

RESULT 80  
US-08-476-509B-30  
Sequence 30, Application US/08476509B  
Patent No. 6034212  
GENERAL INFORMATION:  
APPLICANT: SUDOL, MARIUS  
APPLICANT: PEER, BORK  
APPLICANT: HENRY, CHEN  
TITLE OF INVENTION: A SH2 DOMAIN ASSOCIATED PROTEIN, A  
TITLE OF INVENTION: SIGNALING DOMAIN THEREIN, NUCLEIC ACIDS ENCODING THE  
TITLE OF INVENTION: PROTEIN AND THE DOMAIN, AND DIAGNOSTIC AND THERAPEUTICS  
NUMBER OF SEQUENCES: 50  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Klauber & Jackson  
STREET: 411 Hackensack Avenue  
CITY: Hackensack  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07601  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/476,509B  
FILING DATE: 01-DEC-1994  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Jackson Esq., David A.  
REGISTRATION NUMBER: 26,742  
REFERENCE/DOCKET NUMBER: 600-1-101 CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201 487-5800  
TELEFAX: 201 343-1684  
TELEX: 133521  
INFORMATION FOR SEQ ID NO: 30:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULAR TYPE: peptide  
HYPOTHETICAL: NO  
US-08-476-509B-30

Query Match 26.7%; Score 28; DB 2; Length 10;  
Best Local Similarity 50.0%; Pred. No. 2.9e+02;  
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 5 GMSPPGIVG 14  
DB 1 GTPPPYTVG 10

RESULT 81  
US-08-915-498B-22  
Sequence 22, Application US/08915498B  
Patent No. 6132954  
GENERAL INFORMATION:  
APPLICANT: James R. Lupeki, Robert A. Britton, Donald L.  
APPLICANT: Court and Bradford S. Powell  
TITLE OF INVENTION: Methods of Screening for Agents that  
TITLE OF INVENTION: Delay a Cell Cycle and Compositions Comprising ERA and an Anal  
TITLE OF INVENTION: of Wild-Type ERA  
NUMBER OF SEQUENCES: 37  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Woodburn Kurtz Mackiewicz  
ADDRESS: 6 No. 6132954's LLP  
STREET: One Liberty Place - 46th Floor  
CITY: Philadelphia  
STATE: PA  
COUNTRY: USA  
ZIP: 19103  
COMPUTER READABLE FORM:  
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: PC-DOS  
SOFTWARE: WORDPERFECT for WINDOWS 6.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/915,498B  
FILING DATE: August 20, 1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/023,353  
FILING DATE: August 20, 1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Lori Y. Beardsell  
REGISTRATION NUMBER: 34,293  
REFERENCE/DOCKET NUMBER: BYLR-0037  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 568-3100  
TELEFAX: (215) 568-3439  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-915-498B-22

Query Match 26.7%; Score 28; DB 2; Length 11;  
Best Local Similarity 36.4%; Pred. No. 3.3e+02;  
Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 7 SPGPVIBEG 17  
| : : : :  
| : : : :  
Db 1 SOKGIVIGKG 11

RESULT 82  
US-10-394-980-15  
Sequence 15, Application US/10394980  
Patent No. 6908740  
GENERAL INFORMATION:  
APPLICANT: Vandekerckhove, Joel  
APPLICANT: Gevaert, Kris  
TITLE OF INVENTION: METHODS AND APPARATUS FOR GEL-FREE QUALITATIVE AND  
TITLE OF INVENTION: QUANTITATIVE PROTEOME ANALYSIS, AND USES THEREFOR  
FILE REFERENCE: VBV-001  
CURRENT APPLICATION NUMBER: US/10/394,980  
CURRENT FILING DATE: 2003-03-21  
PRIOR APPLICATION NUMBER: PCT/EP02/03368  
PRIOR FILING DATE: 2002-03-22  
PRIOR APPLICATION NUMBER: US60/278,171  
PRIOR FILING DATE: 2001-03-22

PRIOR APPLICATION NUMBER: US60/318,749  
PRIOR FILING DATE: 2001-09-12  
PRIOR APPLICATION NUMBER: US60/323,999  
PRIOR FILING DATE: 2001-09-20  
NUMBER OF SEQ ID NOS: 473  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 15  
LENGTH: 12  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: MISC FEATURE  
OTHER INFORMATION: part of GSH\_P\_HUMAN ((P22352) plasma glutathione peroxidase precur  
US-10-394-980-15

Query Match 26.7%; Score 28; DB 2; Length 12;  
Best Local Similarity 50.0%; Pred. No. 3.6e+02;  
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 11 PIVGEGV 18  
| : : : :  
| : : : :  
Db 1 PIVGPDGI 8

RESULT 83  
US-08-630-916A-6  
Sequence 6, Application US/08630916A  
Patent No. 6011137  
GENERAL INFORMATION:  
APPLICANT: Pirozzi, Gregorio  
APPLICANT: Kay, Brian K.  
APPLICANT: Fowlkes, Dana M.  
TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL  
TITLE OF INVENTION: POLYPEPTIDES HAVING WW DOMAINS AND METHODS OF USING SAME  
NUMBER OF SEQUENCES: 124  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: United States  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/630,916A  
FILING DATE: 03-APR-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: MISROCK, S. LESLIE  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 1101-203  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 896-8864/9741  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 13 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-630-916A-6

Query Match 26.7%; Score 28; DB 2; Length 13;  
Best Local Similarity 50.0%; Pred. No. 3.9e+02;  
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 5 GMSPPGIVG 14

Db 3 GTPEPPYTVG 12

RESULT 84  
US-08-630-916A-85  
Sequence 85, Application US/08630916A  
Patent No. 601137  
GENERAL INFORMATION:  
APPLICANT: Pirozzi, Gregorio  
APPLICANT: Kay, Brian K.  
TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL  
POLYPEPTIDES HAVING WW DOMAINS AND METHODS OF USING SAME  
NUMBER OF SEQUENCES: 124  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: United States  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Releasee #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/630,916A  
FILING DATE: 03-APR-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: MISROCK, S. LESLIE  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 1101-203  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 866-8864/9741  
INFORMATION FOR SEQ ID NO: 85:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-630-916A-85

Query Match 26.7%; Score 28; DB 2; Length 14;  
Best Local Similarity 50.0%; Pred. No. 4.3e+02;  
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 5 GMSPPGFIVG 14  
Db 2 GTPEPPYTVG 11

RESULT 85  
US-08-630-915A-141  
Sequence 141, Application US/08630915A  
Patent No. 6309820  
GENERAL INFORMATION:  
APPLICANT: SPARKS, Andrew B.  
APPLICANT: HOFFMAN, No. 6309820h  
APPLICANT: KAY, Brian K.  
APPLICANT: FOWLKES, Dana M.  
TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL  
DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND  
USING SAME  
NUMBER OF SEQUENCES: 227  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas

CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Releasee #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/630,915A  
FILING DATE: 03-APR-1996  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: MISROCK, S. LESLIE  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 1101-174  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 866-8864/9741  
TELEX: 66141 PENNIR  
INFORMATION FOR SEQ ID NO: 141:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-630-915A-141

Query Match 26.7%; Score 28; DB 2; Length 14;  
Best Local Similarity 50.0%; Pred. No. 4.3e+02;  
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 5 GMSPPGFIVG 14  
Db 2 GTPEPPYTVG 11

RESULT 86  
US-09-879-957-141  
Sequence 141, Application US/09879957  
Patent No. 6709821  
GENERAL INFORMATION:  
APPLICANT: SPARKS, Andrew B.  
APPLICANT: HOFFMAN, No. 6709821h  
APPLICANT: KAY, Brian K.  
APPLICANT: FOWLKES, Dana M.  
TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL  
DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND  
USING SAME  
NUMBER OF SEQUENCES: 227  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Releasee #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/879,957  
FILING DATE: 13-Jun-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/630,915  
FILING DATE: 03-APR-1996  
ATTORNEY/AGENT INFORMATION:

NAME: Mastrook, S. Leslie  
REGISTRATION NUMBER: 18, 872  
REFERENCE/DOCKET NUMBER: 1101-174  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-8864/9741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 141:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 amino acids  
TYPE: amino acid  
STRADENESS: <Unknown>  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 141:  
US-09-879-957-141

Query Match	26.7%	Score 28	DB 2	Length 14
Best Local Similarity	50.0%	Pred. No. 4	3e+02	
Matches	5	Conservative	1	Mismatches 4
				Indels 0
				Gaps 0
QY	5	GMSPPGPIVIG	14	
DB	2	GPPPPYTVIG	11	

```

RESULT 87
5187078-4
; Patent No. 5187078
; APPLICANT: HOYA, MASAMI;MIZOGUCHI, JUNZO;ONozAMA, TAKASHI
; TITLE OF INVENTION: PLASMA-TYPE GLUTHIONE PEROXIDASE GENE
; AND APPLICATION OF THE SAME
; NUMBER OF SEQUENCES: 24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/540,115
; FILING DATE: 19-JUN-1990
; SEQ ID NO:4:
; LENGTH: 15
5187078-4

```

Query Match	26.7%	Score 28	DB 6	length 15
Best Local Similarity	50.0%	Pred. No. 4	6e-02	
Matches	4	Conservative	3	Mismatches 1
				Indels 0
				Gaps 0
Qy	11	FIVEGGV	18	
		: : :		
		: : :		
Pb	5	FLVGGDGI	12	

```

1      RESULT 88
2      US-08-630-916A-9
3      ; Sequence 9, Application US/08630916A
4      ; Patent No. 6011137
5      ; GENERAL INFORMATION:
6      ; APPLICANT: Pirozzi, Gregorio
7      ; APPLICANT: Kay, Brian K.
8      ; APPLICANT: Fowlkes, Dana M.
9      ; TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL
10     ; TITLE OF INVENTION: POLYPEPTIDES HAVING MW DOMAINS AND METHODS OF USING SAME
11     ; NUMBER OF SEQUENCES: 124
12     ; CORRESPONDENCE ADDRESS:
13     ; ADDRESSEE: Pennie & Edmonds
14     ; STREET: 1155 Avenue of the Americas
15     ; CITY: New York
16     ; STATE: New York
17     ; COUNTRY: United States
18     ; ZIP: 10036-2711
19     ; COMPUTER READABLE FORM:
20     ; MEDIUM TYPE: Floppy disk
21     ; COMPUTER: IBM PC compatible
22     ; OPERATING SYSTEM: PC-DOS/MS-DOS
23     ; SOFTWARE: PatentIn Release #1.0, Version #1.30
24     ; CURRENT APPLICATION DATA:

```

APPLICATION NUMBER: US/08/630,916A  
FILING DATE: 03-APR-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: MISROCK, S. LESLIE  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 1101-203  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 896-8864/9741  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-630-916A-9

```

Query Match      26.7%:  Score 28; DB 2; Length 18;
Best Local Similarity 50.0%:  Pred. No. 5.7e+02;
Matches      5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
OY      5 GMSPPGPIVG 14
      | | | | |
db      6 GTPPPPPYVG 15

```

```

RESULT 89
US-08-990-888-30
; Sequence 30, Application US/08990888B
; Patent No. 6387879
; GENERAL INFORMATION:
; APPLICANT: Blume, Arthur J.
; APPLICANT: Brissette, Renee
; APPLICANT: Carcamo, Juan
; APPLICANT: Mandeckl, Wlodeck S.
; APPLICANT: Tang, Pauline M.
; TITLE OF INVENTION: Assays For Compounds Which Bind Growth Hormone Receptor
; FILE REFERENCE: 2598-4002
; CURRENT APPLICATION NUMBER: US/08/990,888B
; CURRENT FILING DATE: 1997-12-15
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: H5 peptide secondary library sequence
US-08-990-888-30

```

```

Query Match          26.7%:  Score 28; DB 2; Length 18;
Best Local Similarity 40.0%:  Pred. No. 5.7e+02;
Matches          4;  Conservative          4;  Mismatches          2;  Indels          0;  Gaps          0;

OY          5  GMSPPGPIVG 14
      ||: ||: |
Db          6  GLTYPGWLAG 15

RESULT 90
US-08-990-888-69
; Sequence 69, Application US/0890888B
; Patent No. 6387879
; GENERAL INFORMATION:
; APPLICANT: Blume, Arthur J.
; APPLICANT: Brissette, Renee
; APPLICANT: Carcamo, Juan
; APPLICANT: Mandeckl, Wlodeck S.
; APPLICANT: Tang, Pauline M.
; TITLE OF INVENTION: Assays for Compounds which Bind Growth Hormone Receptor
; FILE REFERENCE: 2598-4002

```

/ CURRENT APPLICATION NUMBER: US/08/990,888B  
/ CURRENT FILING DATE: 1997-12-15  
/ NUMBER OF SEQ ID NOS: 81  
/ SOFTWARE: PatentIn Ver. 2.1  
/ SEQ ID NO 69  
/ LENGTH: 18  
/ TYPE: PR  
/ ORGANISM: Artificial Sequence  
/ FEATURE:  
/ OTHER INFORMATION: H5 peptide secondary library sequence  
US-08-990-888-69

Query Match 26.7%; Score 28; DB 2; Length 18;  
Best Local Similarity 50.0%; Pred. No. 5.7e+02;  
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 5 GMSPPGPIV 14  
DB 6 GVTWPGMIG 15

RESULT 91  
US-09-292-225-12  
/ Sequence 12, Application US/09292225  
/ Patent No. 6455686  
/ GENERAL INFORMATION:  
/ APPLICANT: McCall, Catherine A.  
/ APPLICANT: Hunter, Shirley Wu  
/ APPLICANT: Weber, Eric R.  
/ TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS  
/ FILE REFERENCE: AL-2-C3  
/ CURRENT APPLICATION NUMBER: US/09/292,225  
/ CURRENT FILING DATE: 1999-04-15  
/ EARLIER APPLICATION NUMBER: 60/098,909  
/ EARLIER FILING DATE: 1998-09-02  
/ EARLIER APPLICATION NUMBER: 60/085,295  
/ EARLIER FILING DATE: 1998-05-13  
/ EARLIER APPLICATION NUMBER: 60/099,565  
/ EARLIER FILING DATE: 1998-04-17  
/ EARLIER APPLICATION NUMBER: 09/062,013  
/ EARLIER FILING DATE: 1998-04-17  
/ NUMBER OF SEQ ID NOS: 49  
/ SOFTWARE: PatentIn Ver. 2.0  
/ SEQ ID NO 12  
/ LENGTH: 18  
/ TYPE: PR  
/ ORGANISM: Dermatophagoides farinae  
US-09-292-225-12

Query Match 26.7%; Score 28; DB 2; Length 18;  
Best Local Similarity 85.7%; Pred. No. 5.7e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 IYGEGV 18  
DB 12 IYGEGV 18

RESULT 92  
US-09-570-022-12  
/ Sequence 12, Application US/09570022  
/ Patent No. 6573244  
/ GENERAL INFORMATION:  
/ APPLICANT: MOORAD, RICHARD K.  
/ APPLICANT: MOORAD, DEBORAH R.  
/ APPLICANT: DOCTOR, BHUPENDRA P.  
/ APPLICANT: GARCIA, GREGORY E.  
/ TITLE OF INVENTION: PREVINS AS SPECIFIC INHIBITORS AND THERAPEUTIC AGENTS  
/ TITLE OF INVENTION: FOR BOTULINUM TOXIN B AND TETANUS NEUROTOXINS  
/ FILE REFERENCE: 38644-170531  
/ CURRENT APPLICATION NUMBER: US/09/570,022  
/ CURRENT FILING DATE: 2000-05-12

/ PRIOR APPLICATION NUMBER: 60/134,446  
/ PRIOR FILING DATE: 1999-05-17  
/ NUMBER OF SEQ ID NOS: 26  
/ SOFTWARE: PatentIn Ver. 2.1  
/ SEQ ID NO 12  
/ LENGTH: 18  
/ TYPE: PR  
/ ORGANISM: Artificial Sequence  
/ FEATURE:  
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
/ OTHER INFORMATION: peptide  
US-09-570-022-12

Query Match 26.7%; Score 28; DB 2; Length 18;  
Best Local Similarity 50.0%; Pred. No. 5.7e+02;  
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 AKGMSPPGPI 12  
DB 5 AKGLPPGGL 14

RESULT 93  
US-09-068-624-2  
/ Sequence 2, Application US/09068624  
/ Patent No. 6184346  
/ GENERAL INFORMATION:  
/ APPLICANT: KANG, KE-WON  
/ APPLICANT: KIN, DONG-RYOUNG  
/ TITLE OF INVENTION: NOVEL PROTEASE INHIBITORS  
/ TITLE OF INVENTION: DERIVED FROM GUANERIN  
/ NUMBER OF SEQUENCES: 3  
/ CORRESPONDENCE ADDRESS:  
/ ADDRESSER: Knobbe, Martens, Olson & Bear  
/ STREET: 620 Newport Center Drive 16th Floor  
/ CITY: Newport Beach  
/ STATE: CA  
/ COUNTRY: U.S.A.  
/ ZIP: 92660  
/ COMPUTER READABLE FORM:  
/ MEDIUM TYPE: Diskette  
/ COMPUTER: IBM Compatible  
/ OPERATING SYSTEM: DOS  
/ SOFTWARE: FastSeq Version 1.5  
/ CURRENT APPLICATION DATA:  
/ APPLICATION NUMBER: US/09/068,624  
/ FILING DATE:  
/ CLASSIFICATION: 514  
/ PRIOR APPLICATION DATA:  
/ APPLICATION NUMBER:  
/ FILING DATE:  
/ ATTORNEY/AGENT INFORMATION:  
/ NAME: Altman, Daniel E  
/ REGISTRATION NUMBER: 34,115  
/ REFERENCE/DOCKET NUMBER: HYLEB16.001APC  
/ TELECOMMUNICATION INFORMATION:  
/ TELEPHONE: 714-760-0404  
/ TELEFAX: 714-760-9502  
/ TELEEX:  
/ INFORMATION FOR SEQ ID NO: 2:  
/ SEQUENCE CHARACTERISTICS:  
/ LENGTH: 19 amino acids  
/ TYPE: amino acid  
/ STRANDEDNESS: single  
/ TOPOLOGY: linear  
/ MOLECULE TYPE: peptide  
US-09-068-624-2

Query Match 26.7%; Score 28; DB 2; Length 19;  
Best Local Similarity 60.0%; Pred. No. 6.1e+02;  
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 8 PPGPIVGEVG 17

Db 10 PNGFKVDENG 19

RESULT 94  
US-09-068-624-3  
Sequence 3, Application US/09068624  
Patent No. 6184346  
GENERAL INFORMATION:  
APPLICANT: KANG, KE-MON  
TITLE OF INVENTION: NOVEL PROTEASE INHIBITORS  
TITLE OF INVENTION: DERIVED FROM GUAMERIN  
NUMBER OF SEQUENCES: 3  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Knobbe, Martens, Olson & Bear  
STREET: 620 Newport Center Drive 16th Floor  
CITY: Newport Beach  
STATE: CA  
COUNTRY: U.S.A.  
ZIP: 92660  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/068,624  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
ATTORNEY/AGENT INFORMATION:  
NAME: Altman, Daniel E  
REGISTRATION NUMBER: 34,115  
REFERENCE/DOCKET NUMBER: HYLEE16.001APC  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 714-760-0404  
TELEFAX: 714-760-9502  
TELEX:  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-068-624-3  
Query Match 26.7%; Score 28; DB 2; Length 19;  
Best Local Similarity 60.0%; Pred. No. 6.1e+02;  
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
Qy 8 PPGFVGEEG 17  
Db 10 PNGFKVDENG 19  
RESULT 95  
US-07-956-848A-17  
Sequence 17, Application US/07956848A  
Patent No. 5447914  
GENERAL INFORMATION:  
APPLICANT: Travels, James  
APPLICANT: Shafer, William M.  
APPLICANT: Bangalore, Neellesh  
APPLICANT: Pohl, Jan  
TITLE OF INVENTION: Antimicrobial Peptides  
NUMBER OF SEQUENCES: 59  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Greenlee and Winner, P.C.  
STREET: 5370 Manhattan Circle, Suite 201

CITY: Boulder  
STATE: Colorado  
COUNTRY: USA  
ZIP: 80303  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/956,848A  
FILING DATE: 02-OCT-1992  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Feiber, Donna M.  
REGISTRATION NUMBER: 33,878  
REFERENCE/DOCKET NUMBER: 3-90B  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (303) 499-8080  
TELEFAX: (303) 499-8089  
TELEX: 49617824  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-07-956-848A-17

Query Match 26.7%; Score 28; DB 1; Length 20;  
Best Local Similarity 60.0%; Pred. No. 6.5e+02;  
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 10 GFVGESEVL 19  
Db 11 GFVREDEVL 20

RESULT 96  
US-08-468-514-7  
Sequence 7, Application US/08468514  
Patent No. 5576296  
GENERAL INFORMATION:  
APPLICANT: Bartel, Thomas  
APPLICANT: Hofkelt, Tomas  
APPLICANT: Langell, Ulo  
APPLICANT: Ahren, Bo  
APPLICANT: Lindskog, Stefan  
APPLICANT: Consolo, Silvana  
APPLICANT: Land, Tilt  
APPLICANT: Wiesenfeld-Hallin, Zuzanna  
TITLE OF INVENTION: GALANIN ANTAGONIST  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSER: White & Case  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10036-2787  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/468,514  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/146,139  
FILING DATE: 12-NOV-1993



APPLICATION NUMBER: PCT/SE92/00316  
FILING DATE: 14-MAY-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: SE 9101472-0  
FILING DATE: 15-MAY-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Steiner Ph.D., Richard J.  
REGISTRATION NUMBER: 35,372  
REFERENCE/DOCKET NUMBER: 1103326-074  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-819-8783  
TELEFAX: 212-354-8113  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHEICAL: NO  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 20  
OTHER INFORMATION: /note= "amide or free acid"  
US-08-468-514-7

Query Match 26.7%; Score 28; DB 1; Length 20;  
Best Local Similarity 66.7%; Pred. No. 6.5e+02;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 6 MSPPGF 11  
Db 11 LGPPGF 16

RESULT 97  
US-08-471-956-17  
Sequence 17, Application US/08471956  
Patent No. 5798336  
GENERAL INFORMATION:  
APPLICANT: Travls, James  
APPLICANT: Shafer, William M.  
APPLICANT: Bangalore, Neelash  
APPLICANT: Pohl, Jan  
TITLE OF INVENTION: Antimicrobial Peptides  
NUMBER OF SEQUENCES: 59  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Greenlee and Winner, P.C.  
STREET: 5370 Manhattan Circle, Suite 201  
CITY: Boulder  
STATE: Colorado  
COUNTRY: USA  
ZIP: 80303  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/471,956  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/956,848  
FILING DATE: 02-OCT-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/541,635  
FILING DATE: 21-JUN-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Ferber, Donna M.  
REGISTRATION NUMBER: 33,878  
REFERENCE/DOCKET NUMBER: 3-90D  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (303) 499-8080

TELEFAX: (303) 499-8089  
TELEX: 48617824  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-471-956-17

Query Match 26.7%; Score 28; DB 1; Length 20;  
Best Local Similarity 60.0%; Pred. No. 6.5e+02;  
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 10 GPVIGEGVL 19  
Db 11 GFLVRDPL 20

RESULT 98  
US-08-786-455B-2  
Sequence 2, Application US/08786455B  
Patent No. 6193971  
GENERAL INFORMATION:  
APPLICANT: HORMANN, Joachim  
APPLICANT: SCHMID, Karlheinz  
TITLE OF INVENTION: DICTYOCALUS VIVIPARUS ANTIGEN FOR  
TITLE OF INVENTION: DIAGNOSING LUNGWORM INFESTATION AND FOR VACCINATION  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/786,455B  
FILING DATE: 21-JAN-1997  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE 196 01 754.8  
FILING DATE: 19-JAN-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: GRANDOS, Patricia D.  
REGISTRATION NUMBER: 33,683  
REFERENCE/DOCKET NUMBER: 18748/327  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 672-5300  
TELEFAX: (202) 672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-786-455B-2

Query Match 26.7%; Score 28; DB 2; Length 20;  
Best Local Similarity 55.6%; Pred. No. 6.5e+02;  
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DPAKMSPP 9  
Db 5 DPASGVLDP 13

RESULT 99  
US-09-715-838A-6  
Sequence 6, Application US/09715838A  
Patent No. 6846907  
GENERAL INFORMATION:  
APPLICANT: Shaugnessy, S.  
APPLICANT: Austin, R.  
TITLE OF INVENTION: OSTEOPOROSIS TREATMENT  
FILE REFERENCE: MDSP-P03-180  
CURRENT APPLICATION NUMBER: US/09/715,838A  
CURRENT FILING DATE: 2000-11-17  
PRIOR APPLICATION NUMBER: PCT/CA99/00516  
PRIOR FILING DATE: 1999-05-19  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 6  
LENGTH: 20  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-715-838A-6

Query Match 26.2%; Score 27.5; DB 2; Length 20;  
Best Local Similarity 42.9%; Pred. No. 7.8e+02;  
Matches 6; Conservative 3; Mismatches 2; Indels 3; Gaps 1;

QY 1 DPAKGM---SPPGF 11  
DB 6 DPQGLRVESVPGY 19

RESULT 100  
US-08-475-955-195  
Sequence 195, Application US/084755955  
Patent No. 6641813

GENERAL INFORMATION:  
APPLICANT: Harley, John  
TITLE OF INVENTION: METHODS AND REAGENTS FOR DIAGNOSIS OF  
TITLE OF INVENTION: AUTOANTIBODIES  
NUMBER OF SEQUENCES: 218  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Patrea L. Pabst  
STREET: 2800 One Atlantic Center, 1250 West Peachtree Street  
CITY: Atlanta  
STATE: GA  
COUNTRY: USA  
ZIP: 30309-3450  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/475,955  
FILING DATE: June 7, 1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/867,819  
FILING DATE: April 13, 1992  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/648,205  
FILING DATE: January 31, 1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/472,947  
FILING DATE: January 31, 1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Pabst, Patrea L.  
REGISTRATION NUMBER: 31,284  
REFERENCE/DOCKET NUMBER: OMRF14CIP(2)DIV  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (404)-873-8794  
TELEFAX: (404)-873-8795

INFORMATION FOR SEQ ID NO: 195:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-475-955-195  
Query Match 25.7%; Score 27; DB 2; Length 8;  
Best Local Similarity 50.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 PAKGMSP 9  
DB 1 PERGTTPP 8

Search completed: January 20, 2006, 19:14:13  
Job time : 21.9615 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2006 CompuGen Ltd.

OW protein - protein search, using SW model

Run on: January 20, 2006, 19:11:21 ; Search time 72.1154 Seconds  
(without alignment)  
115.878 Million cell updates/sec

Title: US-09-662-293-4

Perfect score: 105

Sequence: 1 DPAKMSPPGFIVGEEGVLS 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 380452

Minimum DB seq length: 0  
Maximum DB seq length: 20

Post-processing: Minimum Match 0%

Listing first 100 summaries

Database :

Published Applications AA Main:\*

- 1: /cgn2\_6/prodata/1/pubppaa/US07\_PUBCOMB.pep:\*
- 2: /cgn2\_6/prodata/1/pubppaa/US08\_PUBCOMB.pep:\*
- 3: /cgn2\_6/prodata/1/pubppaa/US09\_PUBCOMB.pep:\*
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- 5: /cgn2\_6/prodata/1/pubppaa/US10B\_PUBCOMB.pep:\*
- 6: /cgn2\_6/prodata/1/pubppaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	105	100.0	20	4 US-10-218-743-13	Sequence 13, Appl1
3	35	33.3	20	4 US-10-280-066-302	Sequence 302, Appl
4	34	32.4	8	4 US-10-012-756-6	Sequence 6, Appl1
5	34	32.4	8	4 US-10-376-121A-116	Sequence 116, Appl
6	34	32.4	9	4 US-10-376-121A-100	Sequence 100, Appl
7	33	31.4	15	3 US-09-953-510-67	Sequence 67, Appl1
8	33	31.4	15	3 US-09-953-413-67	Sequence 67, Appl1
9	33	31.4	15	5 US-10-147-255-67	Sequence 67, Appl1
10	33	31.4	15	5 US-10-695-155-67	Sequence 67, Appl1
11	33	31.4	20	3 US-09-884-441-397	Sequence 397, Appl
12	33	31.4	20	3 US-09-907-969-397	Sequence 397, Appl
13	33	31.4	20	3 US-09-827-771-397	Sequence 397, Appl
14	33	31.4	20	4 US-10-198-053-397	Sequence 397, Appl
15	33	31.4	20	4 US-10-198-053-603	Sequence 603, Appl
16	33	31.4	20	5 US-10-660-790-397	Sequence 397, Appl
17	33	31.4	20	5 US-10-660-790-603	Sequence 603, Appl
18	33	31.4	20	5 US-10-661-156-146	Sequence 146, Appl
19	32	30.5	16	3 US-09-838-785-26	Sequence 58, Appl1
20	32	30.5	16	3 US-09-838-785-26	Sequence 58, Appl1
21	32	30.5	16	5 US-10-953-901-593	Sequence 593, Appl
22	32	30.5	20	5 US-10-661-156-170	Sequence 170, Appl
23	31	29.5	14	4 US-10-307-956-25	Sequence 25, Appl1
24	31	29.5	15	4 US-10-211-088-356	Sequence 356, Appl
25	31	29.5	17	5 US-10-950-163-8	Sequence 8, Appl1
26	31	29.5	18	3 US-09-999-781-10	Sequence 10, Appl1
27	31	29.5	18	5 US-10-854-646-13	Sequence 13, Appl1

28	31	29.5	18	6 US-11-059-218-29	Sequence 29, Appl1
29	31	29.5	20	3 US-09-897-778-463	Sequence 463, Appl
30	31	29.5	20	4 US-10-007-700-463	Sequence 463, Appl
31	31	29.5	20	4 US-10-117-982-463	Sequence 463, Appl
32	31	29.5	20	4 US-10-313-986-463	Sequence 463, Appl
33	31	29.5	20	4 US-10-313-986-541	Sequence 541, Appl
34	31	29.5	20	5 US-10-775-972-463	Sequence 463, Appl
35	31	29.5	20	5 US-10-775-972-541	Sequence 541, Appl
36	31	29.5	20	5 US-10-922-124-463	Sequence 463, Appl
37	31	29.5	20	5 US-10-922-124-541	Sequence 541, Appl
38	30	28.6	8	4 US-10-376-121A-12	Sequence 12, Appl1
39	30	28.6	8	4 US-10-376-121A-123	Sequence 123, Appl
40	30	28.6	8	4 US-10-376-121A-205	Sequence 205, Appl
41	30	28.6	10	3 US-10-376-121A-206	Sequence 206, Appl
42	30	28.6	10	3 US-09-572-404B-272	Sequence 272, Appl
43	30	28.6	10	3 US-09-572-404B-274	Sequence 274, Appl
44	30	28.6	12	4 US-10-376-121A-14	Sequence 14, Appl1
45	30	28.6	13	5 US-10-972-236A-27	Sequence 27, Appl1
46	30	28.6	14	4 US-10-185-050-53	Sequence 53, Appl1
47	30	28.6	14	4 US-10-185-050-54	Sequence 54, Appl1
48	30	28.6	15	4 US-10-434-906-3	Sequence 3, Appl1
49	30	28.6	15	5 US-10-972-236A-28	Sequence 28, Appl1
50	30	28.6	16	4 US-10-285-394-376	Sequence 376, Appl
51	30	28.6	18	4 US-10-029-386-32096	Sequence 32096, A
52	30	28.6	18	5 US-10-862-195-907	Sequence 907, Appl
53	30	28.6	19	4 US-10-714-212-27	Sequence 27, Appl1
54	29.5	28.1	14	4 US-10-307-956-24	Sequence 24, Appl1
55	29	27.6	7	3 US-09-990-832C-57	Sequence 57, Appl1
56	29	27.6	8	4 US-10-012-756-4	Sequence 4, Appl1
57	29	27.6	8	5 US-10-646-132-3	Sequence 3, Appl1
58	29	27.6	9	4 US-10-224-999A-2893	Sequence 2893, Appl
59	29	27.6	10	3 US-09-572-404B-1350	Sequence 1350, Appl
60	29	27.6	10	3 US-09-572-404B-1352	Sequence 1352, Appl
61	29	27.6	10	3 US-09-573-822C-684	Sequence 684, Appl
62	29	27.6	10	4 US-10-224-999A-2899	Sequence 2899, Appl
63	29	27.6	11	4 US-10-224-999A-2900	Sequence 2900, Appl
64	29	27.6	11	4 US-10-224-999A-2906	Sequence 2906, Appl
65	29	27.6	11	4 US-10-224-999A-2907	Sequence 2907, Appl
66	29	27.6	11	4 US-10-224-999A-2908	Sequence 2908, Appl
67	29	27.6	11	4 US-10-376-121A-10	Sequence 10, Appl1
68	29	27.6	11	4 US-10-285-394-140	Sequence 140, Appl1
69	29	27.6	12	4 US-10-286-457-50	Sequence 50, Appl1
70	29	27.6	12	4 US-10-224-999A-2914	Sequence 2914, Appl
71	29	27.6	12	4 US-10-224-999A-2915	Sequence 2915, Appl
72	29	27.6	12	4 US-10-224-999A-2916	Sequence 2916, Appl
73	29	27.6	12	4 US-10-224-999A-2917	Sequence 2917, Appl
74	29	27.6	13	4 US-10-224-999A-2923	Sequence 2923, Appl
75	29	27.6	13	4 US-10-224-999A-2924	Sequence 2924, Appl
76	29	27.6	13	4 US-10-224-999A-2925	Sequence 2925, Appl
77	29	27.6	13	4 US-10-224-999A-2926	Sequence 2926, Appl
78	29	27.6	13	4 US-10-224-999A-2927	Sequence 2927, Appl
79	29	27.6	14	5 US-10-948-707-1350	Sequence 1350, Appl
80	29	27.6	14	4 US-10-224-999A-2933	Sequence 2933, Appl
81	29	27.6	14	4 US-10-224-999A-2934	Sequence 2934, Appl
82	29	27.6	14	4 US-10-224-999A-2935	Sequence 2935, Appl
83	29	27.6	14	4 US-10-224-999A-2936	Sequence 2936, Appl
84	29	27.6	14	4 US-10-224-999A-2937	Sequence 2937, Appl
85	29	27.6	14	4 US-10-224-999A-2938	Sequence 2938, Appl
86	29	27.6	14	4 US-10-149-240-12	Sequence 12, Appl1
87	29	27.6	15	4 US-10-224-999A-2944	Sequence 2944, Appl
88	29	27.6	15	4 US-10-224-999A-2945	Sequence 2945, Appl
89	29	27.6	15	4 US-10-224-999A-2946	Sequence 2946, Appl
90	29	27.6	15	4 US-10-224-999A-2947	Sequence 2947, Appl
91	29	27.6	15	4 US-10-224-999A-2948	Sequence 2948, Appl
92	29	27.6	15	4 US-10-224-999A-2949	Sequence 2949, Appl
93	29	27.6	15	4 US-10-224-999A-2950	Sequence 2950, Appl
94	29	27.6	15	4 US-10-128-520-38	Sequence 38, Appl1
95	29	27.6	16	4 US-10-225-567A-1513	Sequence 1513, Appl
96	29	27.6	16	4 US-10-224-999A-2956	Sequence 2956, Appl
97	29	27.6	16	4 US-10-224-999A-2957	Sequence 2957, Appl
98	29	27.6	16	4 US-10-224-999A-2958	Sequence 2958, Appl
99	29	27.6	16	4 US-10-224-999A-2959	Sequence 2959, Appl
100	29	27.6	16	4 US-10-224-999A-2960	Sequence 2960, Appl



APPLICATION NUMBER: US/10/012,756  
FILING DATE: 24-Oct-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/81,296  
FILING DATE: 13-JAN-1997  
APPLICATION NUMBER: 60/019,053  
FILING DATE: 16-MAY-1996  
APPLICATION NUMBER: 08/160,604  
FILING DATE: 30-NOV-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Pabst, Patrea L.  
REGISTRATION NUMBER: 31,284  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (404)873-8794  
TELEFAX: (404)873-8795  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
US-10-012-756-6

Query Match 32.4%; Score 34; DB 4; Length 8;  
Best Local Similarity 75.0%; Pred. No. 1.7e+06;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PAKGMRPP 9  
DB 1 PAKGMRPP 8

RESULT 5  
US-10-376-121A-116  
Sequence 116, Application US/10376121A  
Publication No. US20030216544A1  
GENERAL INFORMATION:  
APPLICANT: Harley, John  
TITLE OF INVENTION: METHODS AND REAGENTS FOR DIAGNOSIS OF  
AUTOANTIBODIES  
NUMBER OF SEQUENCES: 218  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Patrea L. Pabst  
STREET: Suite 2000, 1201 West Peachtree Street, N.E.  
CITY: Atlanta  
STATE: GA  
COUNTRY: USA  
ZIP: 30309-3400  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/376,121A  
FILING DATE: 27-Mar-2003  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/867,819  
FILING DATE: April 13, 1992  
APPLICATION NUMBER: 07/648,205  
FILING DATE: January 31, 1991  
APPLICATION NUMBER: 07/472,947  
FILING DATE: January 31, 1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Pabst, Patrea L.  
REGISTRATION NUMBER: 31,284

REFERENCE/DOCKET NUMBER: OMRF114CIP(2)DIV(2)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (404)-817-8473  
TELEFAX: (404)-817-8588  
INFORMATION FOR SEQ ID NO: 116:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 116:  
US-10-376-121A-116

Query Match 32.4%; Score 34; DB 4; Length 8;  
Best Local Similarity 75.0%; Pred. No. 1.7e+06;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PAKGMRPP 9  
DB 1 PAKGMRPP 8

RESULT 6  
US-10-376-121A-100  
Sequence 100, Application US/10376121A  
Publication No. US20030216544A1  
GENERAL INFORMATION:  
APPLICANT: Harley, John  
TITLE OF INVENTION: METHODS AND REAGENTS FOR DIAGNOSIS OF  
AUTOANTIBODIES  
NUMBER OF SEQUENCES: 218  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Patrea L. Pabst  
STREET: Suite 2000, 1201 West Peachtree Street, N.E.  
CITY: Atlanta  
STATE: GA  
COUNTRY: USA  
ZIP: 30309-3400  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/376,121A  
FILING DATE: 27-Mar-2003  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/867,819  
FILING DATE: April 13, 1992  
APPLICATION NUMBER: 07/648,205  
FILING DATE: January 31, 1991  
APPLICATION NUMBER: 07/472,947  
FILING DATE: January 31, 1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Pabst, Patrea L.  
REGISTRATION NUMBER: 31,284  
REFERENCE/DOCKET NUMBER: OMRF114CIP(2)DIV(2)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (404)-817-8473  
TELEFAX: (404)-817-8588  
INFORMATION FOR SEQ ID NO: 100:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Binding-site  
LOCATION: 1..8  
SEQUENCE DESCRIPTION: SEQ ID NO: 100:

US-10-376-121A-100

Query Match 32.4%; Score 34; DB 4; Length 9;  
Best Local Similarity 75.0%; Pred. No. 1.7e+06;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PAKGMSPP 9  
2 PAKGMRPP 9  
DB 2 PAKGMRPP 9

RESULT 7  
US-09-953-510-67

; Sequence 67, Application US/09953510  
; Patent No. US20020131975A1

; GENERAL INFORMATION:  
; APPLICANT: Horwitz, Marcus A.  
; TITLE OF INVENTION: Abundant Extracellular  
; Products and Methods for Their Production and Use

; NUMBER OF SEQUENCES: 91  
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Kurt A. Maclean  
; STREET: 2029 Century Park East, Suite 3800  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90067

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0,  
; Version #1.30

; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/953,510  
; FILING DATE: 14-Sep-2001  
; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/447,398  
; FILING DATE: 23-MAY-1995  
; APPLICATION NUMBER: US 08/289,667  
; FILING DATE: 12-AUG-1994  
; APPLICATION NUMBER: US 08/156,358  
; FILING DATE: 23-NOV-1993

; ATTORNEY/AGENT INFORMATION:  
; NAME: Maclean, Kurt A.  
; REGISTRATION NUMBER: 31,118  
; REFERENCE/DOCKET NUMBER: 112-272  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (310) 788-5000  
; TELEFAX: (310) 277-1297

; INFORMATION FOR SEQ ID NO: 67:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: <Unknown>  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: Internal  
; ORIGINAL SOURCE:  
; ORGANISM: Mycobacterium tuberculosis  
; STRAIN: Erdman

; SEQUENCE DESCRIPTION: SEQ ID NO: 67:  
US-09-953-510-67

Query Match 31.4%; Score 33; DB 3; Length 15;  
Best Local Similarity 62.5%; Pred. No. 5.4e+02;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
QY 1 DPAKMSPP 8  
1 DPAKMRPP 8  
DB 1 DPAKMRPP 8

DB 4 DPAKMSPP 11

RESULT 8  
US-09-953-413-67  
; Sequence 67, Application US/09953413  
; Publication No. US20040018209A1

; GENERAL INFORMATION:  
; APPLICANT: Horwitz, Marcus A.  
; TITLE OF INVENTION: Abundant Extracellular  
; Products and Methods for Their Production and Use

; NUMBER OF SEQUENCES: 91  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Kurt A. Maclean  
; STREET: 2029 Century Park East, Suite 3800  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90067

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0,  
; Version #1.30

; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/953,413  
; FILING DATE: 14-Sep-2001  
; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/447,398  
; FILING DATE: 23-MAY-1995  
; APPLICATION NUMBER: US 08/289,667  
; FILING DATE: 12-AUG-1994  
; APPLICATION NUMBER: US 08/156,358  
; FILING DATE: 23-NOV-1993

; ATTORNEY/AGENT INFORMATION:  
; NAME: Maclean, Kurt A.  
; REGISTRATION NUMBER: 31,118  
; REFERENCE/DOCKET NUMBER: 112-272  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (310) 788-5000  
; TELEFAX: (310) 277-1297

; INFORMATION FOR SEQ ID NO: 67:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: <Unknown>  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: Internal  
; ORIGINAL SOURCE:  
; ORGANISM: Mycobacterium tuberculosis  
; STRAIN: Erdman

; SEQUENCE DESCRIPTION: SEQ ID NO: 67:  
US-09-953-413-67

Query Match 31.4%; Score 33; DB 3; Length 15;  
Best Local Similarity 62.5%; Pred. No. 5.4e+02;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
QY 1 DPAKMSPP 8  
1 DPAKMRPP 8  
DB 4 DPAKMRPP 11

RESULT 9  
US-10-147-255-67  
; Sequence 67, Application US/10147255  
; Publication No. US20030152584A1  
; GENERAL INFORMATION:

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; APPLICANT: Horwitz, Marcus A.
; TITLE OF INVENTION: Abundant Extracellular
; Products and Methods for Their Production and Use
;
; NUMBER OF SEQUENCES: 91
; CORRESPONDENCE ADDRESSES:
; ADDRESSER: Kurt A. Maclean
; STREET: 2029 Century Park East, Suite 3800
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90067
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0,
; Version #1.30
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/147,255
; FILING DATE: 15-May-2002
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/226,539A
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/447,398
; FILING DATE: 23-MAY-1995
; APPLICATION NUMBER: US 08/289,667
; FILING DATE: 12-AUG-1994
; APPLICATION NUMBER: US 08/156,358
; FILING DATE: 23-NOV-1993
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Maclean, Kurt A.
; REGISTRATION NUMBER: 31,118
; REFERENCE/DOCKET NUMBER: 112-272
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (310) 788-5000
; TELEFAX: (310) 277-1297
;
; INFORMATION FOR SEQ ID NO: 67:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; ORGANISM: Mycobacterium tuberculosis
; STRAIN: Erdman
; SEQUENCE DESCRIPTION: SEQ ID NO: 67:
US-10-147-255-67

Query Match          31.4%; Score 33; DB 4; Length 15;
Best Local Similarity 62.5%; Pred. No. 5.4e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      1 DPAKGMP 8
|:|:|:|
Db      4 DPGQGMGP 11

RESULT 10
US-10-695-155-67
; Sequence 67, Application US/10695155
; Publication No. US2004022873A1
; GENERAL INFORMATION:
; APPLICANT: HORWITZ, MARCUS A.
; APPLICANT: HARTH, GUNTER
; APPLICANT: LEE, BAI-YU
; TITLE OF INVENTION: ABUNDANT EXTRACELLULAR PRODUCTS AND METHODS FOR THEIR PRODUCTION
; TITLE OF INVENTION: AND USE
; FILE REFERENCE: 51326-00004
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; CURRENT APPLICATION NUMBER: US/10/695,155
; CURRENT FILING DATE: 2003-10-27
; PRIOR APPLICATION NUMBER: 08/652,842
; PRIOR FILING DATE: 1996-03-23
; PRIOR APPLICATION NUMBER: 08/568,357
; PRIOR FILING DATE: 1995-12-06
; PRIOR APPLICATION NUMBER: 08/551,149
; PRIOR FILING DATE: 1995-10-31
; PRIOR APPLICATION NUMBER: 08/447,398
; PRIOR FILING DATE: 1995-05-23
; PRIOR APPLICATION NUMBER: 08/289,667
; PRIOR FILING DATE: 1994-08-12
; PRIOR APPLICATION NUMBER: 08/156,358
; PRIOR FILING DATE: 1993-11-23
; PRIOR APPLICATION NUMBER: 08/545,926
; PRIOR FILING DATE: 1995-10-20
; NUMBER OF SEQ ID NOS: 167
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 67
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-10-695-155-67

Query Match          31.4%; Score 33; DB 5; Length 15;
Best Local Similarity 62.5%; Pred. No. 5.4e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      1 DPAKGMP 8
|:|:|:|
Db      4 DPGQGMGP 11

RESULT 11
US-09-884-441-397
; Sequence 397, Application US/09884441
; Patent No. US20020119158A1
; GENERAL INFORMATION:
; APPLICANT: Algate, Paul A.
; APPLICANT: Carter, Darlick
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.462c7
; CURRENT APPLICATION NUMBER: US/09/884,441
; CURRENT FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 489
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 397
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-884-441-397

Query Match          31.4%; Score 33; DB 3; Length 20;
Best Local Similarity 62.5%; Pred. No. 7.4e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy      13 VGESEGVLS 20
|:|:|:|:|
Db      3 IGEDGILS 10

RESULT 12
US-09-907-969-397
; Sequence 397, Application US/09907969
; Publication No. US20030091580A1
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: King, Gordon B.
; APPLICANT: Algate, Paul A.
; APPLICANT: Fling, Steven P.
; APPLICANT: Retter, Marc W.
; APPLICANT: Fanger, Gary Richard
```

```
/ APPLICANT: Reed, Steven G.
/ APPLICANT: Vedvyck, Thomas S.
/ APPLICANT: Carter, Darrick
/ APPLICANT: Hill, Paul
/ APPLICANT: Albone, Earl
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
/ FILE REFERENCE: 210121.462C8
/ CURRENT APPLICATION NUMBER: US/09/907,969
/ CURRENT FILING DATE: 2001-07-17
/ NUMBER OF SEQ ID NOS: 596
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 397
/ LENGTH: 20
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-907-969-397

Query Match      31.4%; Score 33; DB 3; Length 20;
Best Local Similarity 62.5%; Pred. No. 7.4e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      13 VGEBCVLS 20
DB      3 IGEDGILS 10

RESULT 13
US-09-827-271-397
/ Sequence 397, Application US/09827271
/ Publication No. US20030165504A1
/ GENERAL INFORMATION:
/ APPLICANT: Retter, Marc W.
/ APPLICANT: Fanger, Gary R.
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
/ FILE REFERENCE: 210121.462C6
/ CURRENT APPLICATION NUMBER: US/09/827,271
/ CURRENT FILING DATE: 2001-04-04
/ NUMBER OF SEQ ID NOS: 461
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 397
/ LENGTH: 20
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-827-271-397

Query Match      31.4%; Score 33; DB 3; Length 20;
Best Local Similarity 62.5%; Pred. No. 7.4e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      13 VGEBCVLS 20
DB      3 IGEDGILS 10

RESULT 14
US-10-198-053-397
/ Sequence 397, Application US/10198053
/ Publication No. US2003012410A1
/ GENERAL INFORMATION:
/ APPLICANT: Bangur, Chaitanya S.
/ APPLICANT: Retter, Marc W.
/ APPLICANT: Fanger, Gary R.
/ APPLICANT: Hill, Paul
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
/ FILE REFERENCE: 210121.462C9
/ CURRENT APPLICATION NUMBER: US/10/198,053
/ CURRENT FILING DATE: 2002-07-17
/ NUMBER OF SEQ ID NOS: 624
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 397
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/ LENGTH: 20
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-198-053-397

Query Match      31.4%; Score 33; DB 4; Length 20;
Best Local Similarity 62.5%; Pred. No. 7.4e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      13 VGEBCVLS 20
DB      3 IGEDGILS 10

RESULT 15
US-10-198-053-603
/ Sequence 603, Application US/10198053
/ Publication No. US2003012410A1
/ GENERAL INFORMATION:
/ APPLICANT: Bangur, Chaitanya S.
/ APPLICANT: Retter, Marc W.
/ APPLICANT: Fanger, Gary R.
/ APPLICANT: Hill, Paul
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
/ FILE REFERENCE: 210121.462C9
/ CURRENT APPLICATION NUMBER: US/10/198,053
/ CURRENT FILING DATE: 2002-07-17
/ NUMBER OF SEQ ID NOS: 624
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 603
/ LENGTH: 20
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-198-053-603

Query Match      31.4%; Score 33; DB 4; Length 20;
Best Local Similarity 62.5%; Pred. No. 7.4e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      13 VGEBCVLS 20
DB      3 IGEDGILS 10

RESULT 16
US-10-860-790-397
/ Sequence 397, Application US/10860790
/ Publication No. US20050031634A1
/ GENERAL INFORMATION:
/ APPLICANT: Bangur, Chaitanya S.
/ APPLICANT: Retter, Marc W.
/ APPLICANT: Fanger, Gary R.
/ APPLICANT: Hill, Paul
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
/ FILE REFERENCE: 210121.462C11
/ CURRENT APPLICATION NUMBER: US/10/860,790
/ CURRENT FILING DATE: 2004-06-02
/ NUMBER OF SEQ ID NOS: 624
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 397
/ LENGTH: 20
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-860-790-397

Query Match      31.4%; Score 33; DB 5; Length 20;
Best Local Similarity 62.5%; Pred. No. 7.4e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      13 VGEBCVLS 20
DB      3 IGEDGILS 10
```



Db 3 IGEDGILS 10

RESULT 17  
US-10-860-790-603  
Sequence 603, Application US/10860790  
Publication No. US20050031634A1  
GENERAL INFORMATION:  
APPLICANT: Bangur, Chaitanya S.  
APPLICANT: Reiter, Marc W.  
APPLICANT: Fanger, Gary R.  
APPLICANT: Hill, Paul  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
FILE REFERENCE: 210121.462C11  
CURRENT APPLICATION NUMBER: US/10/860.790  
CURRENT FILING DATE: 2004-06-02  
NUMBER OF SEQ ID NOS: 624  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 603  
LENGTH: 20  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-860-790-603

Query Match  
Best Local Similarity 31.4%; Score 33; DB 5; Length 20;  
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 13 VGESEGVLS 20  
:|:|:|  
Db 3 IGEDGILS 10

RESULT 18  
US-10-661-156-146  
Sequence 146, Application US/10661156  
Publication No. US20050100963A1  
GENERAL INFORMATION:  
APPLICANT: Sato, Aaron K.  
APPLICANT: Sexton, Daniel J.  
APPLICANT: Dymafield, Daniel T.  
APPLICANT: Ladner, Robert C.  
APPLICANT: Arbogast, Christophe  
APPLICANT: Buseac, Philippe  
APPLICANT: Fan, Hong  
APPLICANT: Khuzana, Sucha  
APPLICANT: Linder, Karen E.  
APPLICANT: Marinelli, Edmund R.  
APPLICANT: Nanjappan, Palenappa  
APPLICANT: Nunn, Adrian  
APPLICANT: Pillai, Radhakrishna  
APPLICANT: Pochon, Sibyllle  
APPLICANT: Ramalingam, Kondareddiar  
APPLICANT: Shrivastava, Ajay  
APPLICANT: Song, Bo  
APPLICANT: Swenson, Rolf E.  
APPLICANT: Von Wronski, Mathew A.  
TITLE OF INVENTION: KDR and VEGF/KDR Binding Peptides and  
FILE REFERENCE: D0617.70012US00  
CURRENT APPLICATION NUMBER: US/10/661.156  
CURRENT FILING DATE: 2003-09-11  
PRIOR APPLICATION NUMBER: US 10/382.082  
PRIOR FILING DATE: 2003-03-03  
PRIOR APPLICATION NUMBER: PCT/US03/06731  
PRIOR FILING DATE: 2003-03-03  
PRIOR FILING DATE: 2003-01-15  
PRIOR APPLICATION NUMBER: US 60/440.411  
PRIOR FILING DATE: 2002-03-01  
PRIOR APPLICATION NUMBER: US 60/360.851  
NUMBER OF SEQ ID NOS: 617  
SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 146  
LENGTH: 20  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Library Isolate  
US-10-661-156-146

Query Match  
Best Local Similarity 31.4%; Score 33; DB 5; Length 20;  
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 8 PGEFTVGEQVL 19  
|||:|  
Db 2 PGEFTVGEQVL 13

RESULT 19  
US-10-328-916-58  
Sequence 58, Application US/10328916  
Publication No. US20040002114A1  
GENERAL INFORMATION:  
APPLICANT: Gregoire, Francine M.  
APPLICANT: Johnson, Jeffrey D.  
APPLICANT: Blume, John E.  
APPLICANT: Metabolix, Inc.  
TITLE OF INVENTION: Nucleic Acids Encoding a G-Protein Coupled Receptor  
FILE REFERENCE: 016325-007210US  
CURRENT APPLICATION NUMBER: US/10/328.916  
CURRENT FILING DATE: 2003-01-06  
PRIOR APPLICATION NUMBER: US 60/345.697  
PRIOR FILING DATE: 2002-01-04  
NUMBER OF SEQ ID NOS: 59  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 58  
LENGTH: 15  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:C-terminal  
US-10-328-916-58

Query Match  
Best Local Similarity 30.5%; Score 32; DB 4; Length 15;  
Matches 6; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 6 MPPPTVGE 16  
|||:|  
Db 4 MPPPTVGE 14

RESULT 20  
US-09-838-785-26  
Sequence 26, Application US/09838785  
Patent No. US20020009455A1  
GENERAL INFORMATION:  
APPLICANT: Lau, Ted  
APPLICANT: Lin, Rick  
APPLICANT: Parkes, Debbie  
APPLICANT: Parry, Gordon  
APPLICANT: Schneider, Douglas  
APPLICANT: Steindricher, Renate  
APPLICANT: Van Heult, Pam T  
APPLICANT: Wu, John  
TITLE OF INVENTION: DNA Encoding a No. US20020009455A1 PROST 03  
FILE REFERENCE: 51831AUSM1  
CURRENT APPLICATION NUMBER: US/09/838.785  
CURRENT FILING DATE: 2001-04-20  
PRIOR APPLICATION NUMBER: 60/200.065  
PRIOR FILING DATE: 2000-04-27  
NUMBER OF SEQ ID NOS: 26

/ SOFTWARE: PatentIn Ver. 2.0  
/ SEQ ID NO 26  
/ LENGTH: 16  
/ TYPE: PRT  
/ ORGANISM: Homo sapiens  
US-09-838-785-26

Query Match 30.5%; Score 32; DB 3; Length 16;  
Best Local Similarity 55.6%; Pred. No. 8.2e+02;  
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DPAKMSPP 9  
: |||: |  
Db 3 BPAEGHSAP 11

RESULT 21  
US-10-953-901-593  
/ Sequence 593, Application US/10953901  
/ Publication No. US20050181464A1  
/ GENERAL INFORMATION:  
/ APPLICANT: EDWARDS, ALED  
/ APPLICANT: DHARAMSI, AKIL  
/ APPLICANT: VEDADI, MASOUD  
/ APPLICANT: ALAM, MUHAMMAD ZAHOOR  
/ APPLICANT: ARROWSMITH, CHERYL  
/ APPLICANT: AMREY, DONALD E.  
/ APPLICANT: BEATTIE, BRYAN  
/ APPLICANT: BUZADZIVA, KRISTINA  
/ APPLICANT: CLARKE, TERESA  
/ APPLICANT: DOMAGALA, MEGAN  
/ APPLICANT: HOUSTON, SIMON  
/ APPLICANT: KANAGARAJAH, DHUSHY  
/ APPLICANT: LI, QIN  
/ APPLICANT: MANSOURY, KAMRAN  
/ APPLICANT: McDONALD, MERRY-LYNN  
/ APPLICANT: NETHERY, KATHLEEN  
/ APPLICANT: NG, IVY  
/ APPLICANT: OUYANG, HUI  
/ APPLICANT: RICHARDS, DAMN  
/ APPLICANT: VALLEE, FRANCOIS  
/ APPLICANT: VIRING, CRISTINA  
/ TITLE OF INVENTION: NOVEL PURIFIED POLYPEPTIDES FROM BACTERIA  
/ FILE REFERENCE: IPT-207.01  
/ CURRENT APPLICATION NUMBER: US/10/953,901  
/ PRIOR FILING DATE: 2004-09-29  
/ PRIOR APPLICATION NUMBER: PCT/CA03/00465  
/ PRIOR FILING DATE: 2003-04-04  
/ PRIOR APPLICATION NUMBER: 60/370,060  
/ PRIOR FILING DATE: 2002-04-04  
/ PRIOR APPLICATION NUMBER: 60/369,831  
/ PRIOR FILING DATE: 2002-04-04  
/ PRIOR APPLICATION NUMBER: 60/369,819  
/ PRIOR FILING DATE: 2002-04-04  
/ PRIOR APPLICATION NUMBER: 60/369,826  
/ PRIOR FILING DATE: 2002-04-04  
/ PRIOR APPLICATION NUMBER: 60/370,852  
/ PRIOR FILING DATE: 2002-04-08  
/ PRIOR APPLICATION NUMBER: 60/370,681  
/ PRIOR FILING DATE: 2002-04-08  
/ PRIOR APPLICATION NUMBER: 60/371,014  
/ PRIOR FILING DATE: 2002-04-09  
/ PRIOR APPLICATION NUMBER: 60/371,180  
/ PRIOR FILING DATE: 2002-04-09  
/ PRIOR APPLICATION NUMBER: 60/371,008  
/ PRIOR FILING DATE: 2002-04-09  
/ PRIOR APPLICATION NUMBER: 60/371,008  
/ PRIOR FILING DATE: 2002-04-09  
/ Remaining Prior Application data removed - See file Wrapper or PALM.  
/ NUMBER OF SEQ ID NOS: 901  
/ SOFTWARE: PatentIn Ver. 3.3  
/ SEQ ID NO 593  
/ LENGTH: 16  
/ TYPE: PRT  
/ ORGANISM: Staphylococcus aureus

US-10-953-901-593

Query Match 30.5%; Score 32; DB 5; Length 16;  
Best Local Similarity 70.0%; Pred. No. 8.2e+02;  
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 10 GTIVGESEVTL 19  
: ||| |||:  
Db 5 GDIVGESEVTL 14

RESULT 22  
US-10-661-156-170  
/ Sequence 170, Application US/10661156  
/ Publication No. US20050100963A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Sato, Aaron K.  
/ APPLICANT: Sexton, Daniel J.  
/ APPLICANT: Dransfield, Daniel T.  
/ APPLICANT: Ladner, Robert C.  
/ APPLICANT: Arbogast, Christophe  
/ APPLICANT: Buesat, Philippe  
/ APPLICANT: Fan, Hong  
/ APPLICANT: Khurana, Sudha  
/ APPLICANT: Linder, Karen E.  
/ APPLICANT: Marinelli, Edmund R.  
/ APPLICANT: Nanjappa, Palaniappa  
/ APPLICANT: Nunn, Adrian  
/ APPLICANT: Pillai, Radhakrishna  
/ APPLICANT: Pochon, Sibyllie  
/ APPLICANT: Ramalingam, Kondareddiar  
/ APPLICANT: Shrivastava, Ajay  
/ APPLICANT: Song, Bo  
/ APPLICANT: Swenson, Rolf E.  
/ APPLICANT: Von Wronski, Mathew A.  
/ TITLE OF INVENTION: KDR and VEGF/KDR Binding Peptides and  
/ TITLE OF INVENTION: Their Use in Diagnosis and Therapy  
/ FILE REFERENCE: D0617.70012US00  
/ CURRENT APPLICATION NUMBER: US/10/661,156  
/ CURRENT FILING DATE: 2003-09-11  
/ PRIOR APPLICATION NUMBER: US 10/382,082  
/ PRIOR FILING DATE: 2003-03-03  
/ PRIOR APPLICATION NUMBER: PCT/US03/06731  
/ PRIOR FILING DATE: 2003-03-03  
/ PRIOR APPLICATION NUMBER: US 60/440,411  
/ PRIOR FILING DATE: 2003-01-15  
/ PRIOR APPLICATION NUMBER: US 60/360,851  
/ PRIOR FILING DATE: 2002-03-01  
/ NUMBER OF SEQ ID NOS: 617  
/ SOFTWARE: FastSeq for Windows Version 4.0  
/ SEQ ID NO 170  
/ LENGTH: 20  
/ TYPE: PRT  
/ ORGANISM: Artificial Sequence  
/ FEATURE:  
/ OTHER INFORMATION: Library Isolate  
US-10-661-156-170

Query Match 30.5%; Score 32; DB 5; Length 20;  
Best Local Similarity 50.0%; Pred. No. 1e+03;  
Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 8 PGFVGESEVTL 19  
: ||| |||:  
Db 2 PGFSEYEQALV 13

RESULT 23  
US-10-307-956-25  
/ Sequence 25, Application US/10307956  
/ Publication No. US20030119072A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Hoekstra, Merl F.

APPLICANT: Xie, Weilin  
APPLICANT: Murray, Brian  
APPLICANT: Mercutio, Frank  
TITLE OF INVENTION: METHODS FOR MODULATING SIGNAL  
TITLE OF INVENTION: TRANSDUCTION MEDIATED BY TGF-BETA AND RELATED PROTEINS  
FILE REFERENCE: 860098.433  
CURRENT APPLICATION NUMBER: US/10/307,956  
CURRENT FILING DATE: 2002-12-02  
PRIOR APPLICATION NUMBER: US/09/385,918  
PRIOR FILING DATE: 1999-08-30  
NUMBER OF SEQ ID NOS: 32  
SOFTWARE: PaacSeq for Windows Version 3.0  
SEQ ID NO 25  
LENGTH: 14  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-307-956-25

Query Match 29.5%; Score 31; DB 4; Length 14;  
Best Local Similarity 38.5%; Pred. No. 1e+03;  
Matches 5; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 5 GMSPPGVGSEEG 17  
DB 2 GLTPPGVLSBDG 14

RESULT 24  
US-10-211-088-356  
Sequence 356, Application US/10211088  
Publication No. US20030104479A1  
GENERAL INFORMATION:  
APPLICANT: Bright, Gary R.  
APPLICANT: Premkumar, D. David  
APPLICANT: Chen, Yih-Tai  
TITLE OF INVENTION: NO. US20030104479A1 Fusion Proteins And Assays For Molecular B  
FILE REFERENCE: 01-1022-US  
CURRENT APPLICATION NUMBER: US/10/211,088  
CURRENT FILING DATE: 2002-10-15  
PRIOR APPLICATION NUMBER: 60/309,395  
PRIOR FILING DATE: 2001-08-01  
PRIOR APPLICATION NUMBER: 60/341,589  
PRIOR FILING DATE: 2001-12-13  
NUMBER OF SEQ ID NOS: 366  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 356  
LENGTH: 15  
TYPE: PRT  
ORGANISM: Artificial sequence  
FEATURE:  
OTHER INFORMATION: Post-translational modification site  
US-10-211-088-356

Query Match 29.5%; Score 31; DB 4; Length 15;  
Best Local Similarity 55.6%; Pred. No. 1.1e+03;  
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 PAKGMSPPG 10  
DB 2 PGKGVKSPG 10

RESULT 25  
US-10-950-163-8  
Sequence 8, Application US/10950163  
Publication No. US20050152911A1  
GENERAL INFORMATION:  
APPLICANT: Hardy, Michele  
TITLE OF INVENTION: NOROVIRUS MONOCLONAL ANTIBODIES AND PEPTIDES  
FILE REFERENCE: 33576/US/2  
CURRENT APPLICATION NUMBER: US/10/950,163  
CURRENT FILING DATE: 2004-09-24  
PRIOR APPLICATION NUMBER: US 60/508,262

PRIOR FILING DATE: 2003-09-24  
NUMBER OF SEQ ID NOS: 159  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 8  
LENGTH: 17  
TYPE: PRT  
ORGANISM: Grimsby virus  
US-10-950-163-8

Query Match 29.5%; Score 31; DB 5; Length 17;  
Best Local Similarity 71.4%; Pred. No. 1.2e+03;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 PAKGMSPPG 8  
DB 7 PAKGLSP 13

RESULT 26  
US-09-999-781-10  
Sequence 10, Application US/09999781  
Publication No. US20040082496A1  
GENERAL INFORMATION:  
APPLICANT: ACTON, SUSAN L.  
APPLICANT: OCCAIN, TIMOTHY D.  
APPLICANT: GOULD, ALEXANDRA  
APPLICANT: DALES, NATALIE A.  
APPLICANT: GUAN, BING  
APPLICANT: BROWN, JAMES A.  
APPLICANT: PATANE, MICHAEL  
APPLICANT: KADAMBI, VIVEK J.  
APPLICANT: SOLOMON, MICHAEL  
APPLICANT: STRICKER-KRONGRAD, ALAIN  
TITLE OF INVENTION: ACE-2 MODULATING COMPOUNDS AND METHODS  
FILE REFERENCE: MEI-082CP4  
CURRENT APPLICATION NUMBER: US/09/999,781  
CURRENT FILING DATE: 2001-10-31  
PRIOR APPLICATION NUMBER: 09/870,382  
PRIOR FILING DATE: 2001-05-29  
PRIOR APPLICATION NUMBER: 09/704,216  
PRIOR FILING DATE: 2000-11-01  
PRIOR APPLICATION NUMBER: 60/XXX,XXX  
PRIOR FILING DATE: 2001-10-19  
NUMBER OF SEQ ID NOS: 34  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 10  
LENGTH: 18  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-999-781-10

Query Match 29.5%; Score 31; DB 3; Length 18;  
Best Local Similarity 54.5%; Pred. No. 1.3e+03;  
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 DPAKMSPPGF 11  
DB 1 DISKGENNPGF 11

RESULT 27  
US-10-854-646-13  
Sequence 13, Application US/10854646  
Publication No. US20050113304A1  
GENERAL INFORMATION:  
APPLICANT: GORDON, RICHARD K.  
APPLICANT: MOORAD, DEBORAH R.  
APPLICANT: DOCTOR, BHUPENDRA P.  
APPLICANT: GARCIA, GREGORY B.  
TITLE OF INVENTION: PREVINS AS SPECIFIC INHIBITORS AND THERAPEUTIC AGENTS  
TITLE OF INVENTION: FOR BOTULINUM TOXIN B AND TETANUS NEUROTOXINS  
FILE REFERENCE: 38644-202822

```
/ CURRENT APPLICATION NUMBER: US/10/854,646
/ CURRENT FILING DATE: 2004-05-27
/ PRIOR APPLICATION NUMBER: 60/134,446
/ PRIOR FILING DATE: 1998-05-17
/ NUMBER OF SEQ ID NOS: 25
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 13
/ LENGTH: 18
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-854-646-13

Query Match      29.5%; Score 31; DB 5; Length 18;
Best Local Similarity 54.5%; Pred. No. 1.3e+03;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      3 AKGMSPPGFIV 13
      |||: ||: |
Db      5 AKGLOPGLMV 15

RESULT 28
US-11-059-218-29
/ Sequence 29, Application US/11059218
/ Publication No. US20050147600A1
/ GENERAL INFORMATION:
/ APPLICANT: Acton, Susan L. et al.
/ TITLE OF INVENTION: ANGIOTENSIN CONVERTING ENZYME HOMOLOG AND THERAPEUTIC
/ FILE REFERENCE: NMI-132CP3
/ CURRENT APPLICATION NUMBER: US/11/059,218
/ CURRENT FILING DATE: 2005-02-16
/ PRIOR APPLICATION NUMBER: US/09/635,501
/ PRIOR FILING DATE: 2000-08-09
/ PRIOR APPLICATION NUMBER: 09/407,427
/ PRIOR FILING DATE: 1999-09-29
/ PRIOR APPLICATION NUMBER: 09/163,648
/ PRIOR FILING DATE: 1998-09-30
/ PRIOR APPLICATION NUMBER: 08/989,299
/ PRIOR FILING DATE: 1997-12-11
/ NUMBER OF SEQ ID NOS: 107
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 29
/ LENGTH: 18
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: motifs
US-11-059-218-29

Query Match      29.5%; Score 31; DB 6; Length 18;
Best Local Similarity 54.5%; Pred. No. 1.3e+03;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      1 DPAKMSPPGPF 11
      |:|: |:|
Db      1 DISKGNNGPF 11

RESULT 29
US-09-897-778-463
/ Sequence 463, Application US/09897778
/ Patent No. US20020147143A1
/ GENERAL INFORMATION:
/ APPLICANT: Wang, Tongtong
/ APPLICANT: Marnerakis, Margarita
/ APPLICANT: Ranger, Gary R.
/ APPLICANT: Vedvick, Thomas S.
/ APPLICANT: Carter, Darrick
/ APPLICANT: Watanabe, Yoshihiro
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/ APPLICANT: Henderson, Robert A.
/ APPLICANT: Peckham, David W.
/ APPLICANT: Ranger, Neil
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
/ FILE REFERENCE: 210121.455C16
/ CURRENT APPLICATION NUMBER: US/09/897,778
/ CURRENT FILING DATE: 2001-06-28
/ NUMBER OF SEQ ID NOS: 467
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 463
/ LENGTH: 20
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-897-778-463

Query Match      29.5%; Score 31; DB 3; Length 20;
Best Local Similarity 62.5%; Pred. No. 1.5e+03;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 PAKGMSPP 9
      |||: |||
Db      9 PTSGMPP 16

RESULT 30
US-10-007-700-463
/ Sequence 463, Application US/10007700
/ Publication No. US20030064947A1
/ GENERAL INFORMATION:
/ APPLICANT: Wang, Tongtong
/ APPLICANT: Wang, Aijun
/ APPLICANT: Skelky, Yasir A.W.
/ APPLICANT: Li, Samuel X.
/ APPLICANT: Kalos, Michael D.
/ APPLICANT: Henderson, Robert A.
/ APPLICANT: McNeill, Patricia D.
/ APPLICANT: Ranger, Neil
/ APPLICANT: Retter, Marc W.
/ APPLICANT: Durham, Margarita
/ APPLICANT: Ranger, Gary R.
/ APPLICANT: Vedvick, Thomas S.
/ APPLICANT: Carter, Darrick
/ APPLICANT: Watanabe, Yoshihiro
/ APPLICANT: Peckham, David W.
/ APPLICANT: Cai, Feng
/ APPLICANT: Foy, Teresa M.
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
/ FILE REFERENCE: 210121.455C17
/ CURRENT APPLICATION NUMBER: US/10/007,700
/ CURRENT FILING DATE: 2001-11-30
/ NUMBER OF SEQ ID NOS: 469
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 463
/ LENGTH: 20
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-007-700-463

Query Match      29.5%; Score 31; DB 4; Length 20;
Best Local Similarity 62.5%; Pred. No. 1.5e+03;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 PAKGMSPP 9
      |||: |||
Db      9 PTSGMPP 16

RESULT 31
US-10-117-982-463
/ Sequence 463, Application US/10117982
/ Publication No. US20030138438A1
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; GENERAL INFORMATION:
; APPLICANT: Foy, Teresa M.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darlick
; APPLICANT: Matanabe, Yoshihiro
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kaios, Michael D.
; APPLICANT: Meticle, Barbara
; APPLICANT: Spies, Gregory A.
; APPLICANT: Fan, Liqun
; APPLICANT: Wang, Tongtong
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C18
; CURRENT APPLICATION NUMBER: US/10/117,982
; CURRENT FILING DATE: 2002-04-05
; NUMBER OF SEQ ID NOS: 484
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 463
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-982-463

Query Match      29.5%; Score 31; DB 4; Length 20;
Best Local Similarity 62.5%; Pred. No. 1.5e+03;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 PAKGMSPP 9
Db      9 PTSGMPP 16

RESULT 32
US-10-313-986-463
; Sequence 463, Application US/10313986
; Publication No. US20030236209A1
; GENERAL INFORMATION:
; APPLICANT: Foy, Teresa M.
; APPLICANT: McNabb, Andria
; APPLICANT: Matanabe, Yoshihiro
; APPLICANT: Reed, Steven G.
; APPLICANT: Wang, Tongtong
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C19
; CURRENT APPLICATION NUMBER: US/10/313,986
; CURRENT FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 560
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 463
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-313-986-463

Query Match      29.5%; Score 31; DB 4; Length 20;
Best Local Similarity 62.5%; Pred. No. 1.5e+03;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 PAKGMSPP 9
Db      9 PTSGMPP 16

RESULT 33
US-10-313-986-541
; Sequence 541, Application US/10313986
; Publication No. US20030236209A1
; GENERAL INFORMATION:
; APPLICANT: Foy, Teresa M.
; APPLICANT: McNabb, Andria

```

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; APPLICANT: Matanabe, Yoshihiro
; APPLICANT: Reed, Steven G.
; APPLICANT: Wang, Tongtong
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C19
; CURRENT APPLICATION NUMBER: US/10/313,986
; CURRENT FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 560
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 541
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-313-986-541

Query Match      29.5%; Score 31; DB 4; Length 20;
Best Local Similarity 62.5%; Pred. No. 1.5e+03;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 PAKGMSPP 9
Db      9 PTSGMPP 16

RESULT 34
US-10-775-972-463
; Sequence 463, Application US/10775972
; Publication No. US20040235072A1
; GENERAL INFORMATION:
; APPLICANT: Henderson, Robert A.
; APPLICANT: Bangur, Chaltanya S.
; APPLICANT: Wang, Tongtong
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C21
; CURRENT APPLICATION NUMBER: US/10/775,972
; CURRENT FILING DATE: 2004-02-10
; NUMBER OF SEQ ID NOS: 563
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 463
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-775-972-463

Query Match      29.5%; Score 31; DB 5; Length 20;
Best Local Similarity 62.5%; Pred. No. 1.5e+03;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 PAKGMSPP 9
Db      9 PTSGMPP 16

RESULT 35
US-10-775-972-541
; Sequence 541, Application US/10775972
; Publication No. US20040235072A1
; GENERAL INFORMATION:
; APPLICANT: Henderson, Robert A.
; APPLICANT: Bangur, Chaltanya S.
; APPLICANT: Wang, Tongtong
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C21
; CURRENT APPLICATION NUMBER: US/10/775,972
; CURRENT FILING DATE: 2004-02-10
; NUMBER OF SEQ ID NOS: 563
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 541
; LENGTH: 20
; TYPE: PRT

```

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; ORGANISM: Homo sapiens
US-10-775-972-541

Query Match      29.5%; Score 31; DB 5; Length 20;
Best Local Similarity 62.5%; Pred. No. 1.5e+03;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 PAKGMSPP 9
      | | | | |
Db      9 PTSGMPP 16

RESULT 36
US-10-922-124-463
; Sequence 463, Application US/10922124
; Publication No. US20050142620A1
; GENERAL INFORMATION:
; APPLICANT: Bangur, Chaltanya S.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C22
; CURRENT APPLICATION NUMBER: US/10/922,124
; PRIOR FILING DATE: 2004-08-18
; PRIOR APPLICATION NUMBER: 10/775,972
; PRIOR FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: 10/623,155
; PRIOR FILING DATE: 2003-07-17
; PRIOR APPLICATION NUMBER: 10/313,986
; PRIOR FILING DATE: 2002-12-04
; PRIOR APPLICATION NUMBER: 10/117,982
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 10/007,700
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: 09/897,778
; PRIOR FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: 09/850,716
; PRIOR FILING DATE: 2001-05-07
; PRIOR APPLICATION NUMBER: 09/735,705
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 09/685,696
; PRIOR FILING DATE: 2000-10-09
; PRIOR APPLICATION NUMBER: 09/662,786
; PRIOR FILING DATE: 2000-09-15
; Remaining Prior Application data removed - See file Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 563
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 463
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-922-124-463

Query Match      29.5%; Score 31; DB 5; Length 20;
Best Local Similarity 62.5%; Pred. No. 1.5e+03;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 PAKGMSPP 9
      | | | | |
Db      9 PTSGMPP 16

RESULT 37
US-10-922-124-541
; Sequence 541, Application US/10922124
; Publication No. US20050142620A1
; GENERAL INFORMATION:
; APPLICANT: Bangur, Chaltanya S.
; APPLICANT: Zehentner-Wilkinson, Barbara K.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C22
; CURRENT APPLICATION NUMBER: US/10/922,124

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; CURRENT FILING DATE: 2004-08-18
; PRIOR APPLICATION NUMBER: 10/775,972
; PRIOR FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: 10/623,155
; PRIOR FILING DATE: 2003-07-17
; PRIOR APPLICATION NUMBER: 10/313,986
; PRIOR FILING DATE: 2002-12-04
; PRIOR APPLICATION NUMBER: 10/117,982
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 10/007,700
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: 09/897,778
; PRIOR FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: 09/850,716
; PRIOR FILING DATE: 2001-05-07
; PRIOR APPLICATION NUMBER: 09/735,705
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 09/685,696
; PRIOR FILING DATE: 2000-10-09
; PRIOR APPLICATION NUMBER: 09/662,786
; PRIOR FILING DATE: 2000-09-15
; Remaining Prior Application data removed - See file Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 563
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 541
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-922-124-541

Query Match      29.5%; Score 31; DB 5; Length 20;
Best Local Similarity 62.5%; Pred. No. 1.5e+03;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 PAKGMSPP 9
      | | | | |
Db      9 PTSGMPP 16

RESULT 38
US-10-376-121A-12
; Sequence 12, Application US/10376121A
; Publication No. US2003021654A1
; GENERAL INFORMATION:
; APPLICANT: Harley, John
; TITLE OF INVENTION: METHODS AND REAGENTS FOR DIAGNOSIS OF
; AUTOANTIBODIES
; NUMBER OF SEQUENCES: 218
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Patrea L. Pabst
; STREET: Suite 2000, 1201 West Peachtree Street, N.E.
; CITY: Atlanta
; STATE: GA
; COUNTRY: USA
; ZIP: 30309-3400
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/376,121A
; FILING DATE: 27-Mar-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/867,819
; FILING DATE: April 13, 1992
; APPLICATION NUMBER: 07/648,205
; FILING DATE: January 31, 1991
; APPLICATION NUMBER: 07/472,947
; FILING DATE: January 31, 1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.

```

REGISTRATION NUMBER: 31,284  
REFERENCE/DOCKET NUMBER: OMRP114CIP(2)DIV(2)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (404)-817-8473  
TELEFAX: (404)-817-8588  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Binding-site  
LOCATION: 1..8  
SEQUENCE DESCRIPTION: SEQ ID NO: 12:  
US-10-376-121A-12

Query Match 28.6%; Score 30; DB 4; Length 8;  
Best Local Similarity 83.3%; Pred. No. 1.7e+06;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GMSPPG 10  
DB 3 GMPPPG 8

RESULT 39  
US-10-376-121A-123  
Sequence 123, Application US/10376121A  
Publication No. US20030216544A1  
GENERAL INFORMATION:  
APPLICANT: Harley, John  
TITLE OF INVENTION: METHODS AND REAGENTS FOR DIAGNOSIS OF  
AUTOANTIBODIES  
NUMBER OF SEQUENCES: 218  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Patrea L. Pabst  
STREET: Suite 2000, 1201 West Peachtree Street, N.E.  
CITY: Atlanta  
STATE: GA  
COUNTRY: USA  
ZIP: 30309-3400  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/376,121A  
FILING DATE: 27-Mar-2003  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/867,819  
FILING DATE: April 13, 1992  
APPLICATION NUMBER: 07/648,205  
FILING DATE: January 31, 1991  
APPLICATION NUMBER: 07/472,947  
FILING DATE: January 31, 1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Pabst, Patrea L.  
REGISTRATION NUMBER: 31,284  
REFERENCE/DOCKET NUMBER: OMRP114CIP(2)DIV(2)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (404)-817-8473  
TELEFAX: (404)-817-8588  
INFORMATION FOR SEQ ID NO: 123:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide

FEATURE:  
NAME/KEY: Misc Feature  
LOCATION: 6  
OTHER INFORMATION: /note= "The Xaa at position 6 can be  
R, F, G, H, I, K, S, T, V,  
and Y."  
SEQUENCE DESCRIPTION: SEQ ID NO: 123:  
US-10-376-121A-123

Query Match 28.6%; Score 30; DB 4; Length 8;  
Best Local Similarity 62.5%; Pred. No. 1.7e+06;  
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 PAKGSP 9  
DB 1 PPPGKPP 8

RESULT 40  
US-10-376-121A-205  
Sequence 205, Application US/10376121A  
Publication No. US20030216544A1  
GENERAL INFORMATION:  
APPLICANT: Harley, John  
TITLE OF INVENTION: METHODS AND REAGENTS FOR DIAGNOSIS OF  
AUTOANTIBODIES  
NUMBER OF SEQUENCES: 218  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Patrea L. Pabst  
STREET: Suite 2000, 1201 West Peachtree Street, N.E.  
CITY: Atlanta  
STATE: GA  
COUNTRY: USA  
ZIP: 30309-3400  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/376,121A  
FILING DATE: 27-Mar-2003  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/867,819  
FILING DATE: April 13, 1992  
APPLICATION NUMBER: 07/648,205  
FILING DATE: January 31, 1991  
APPLICATION NUMBER: 07/472,947  
FILING DATE: January 31, 1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Pabst, Patrea L.  
REGISTRATION NUMBER: 31,284  
REFERENCE/DOCKET NUMBER: OMRP114CIP(2)DIV(2)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (404)-817-8473  
TELEFAX: (404)-817-8588  
INFORMATION FOR SEQ ID NO: 205:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 205:  
US-10-376-121A-205

Query Match 28.6%; Score 30; DB 4; Length 8;  
Best Local Similarity 83.3%; Pred. No. 1.7e+06;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GMSPPG 10  
DB 3 GMPPPG 8

Db 2 GMPpg 7

## RESULT 41

US-10-376-121A-206

Sequence 206, Application US/10376121A  
Publication No. US2003021654A1

GENERAL INFORMATION:

APPLICANT: Harley, John

TITLE OF INVENTION: METHODS AND REAGENTS FOR DIAGNOSIS OF  
AUTANTIBODIES

NUMBER OF SEQUENCES: 218

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Patrea L. Pabst

STREET: Suite 2000, 1201 West Peachtree Street, N.E.

CITY: Atlanta

STATE: GA

COUNTRY: USA

ZIP: 30309-3400

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION NUMBER: US/10/376,121A

APPLICATION NUMBER: 27-Mar-2003

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/867,819

FILING DATE: April 13, 1992

APPLICATION NUMBER: 07/648,205

FILING DATE: January 31, 1991

APPLICATION NUMBER: 07/472,947

FILING DATE: January 31, 1990

ATTORNEY/AGENT INFORMATION:

NAME: Pabst, Patrea L.

REGISTRATION NUMBER: 31,284

REFERENCE/DOCKET NUMBER: OMR114CIP(2)DIV(2)

TELEPHONE: (404)-817-8473

TELEFAX: (404)-817-8588

INFORMATION FOR SEQ ID NO: 206:

SEQUENCE CHARACTERISTICS:

LENGTH: 8 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 206:

US-10-376-121A-206

Query Match 28.6%; Score 30; DB 4; Length 8;  
Best Local Similarity 83.3%; Pred. No. 1.7e+06;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 GMSPPG 10

Db 1 GMPpg 6

## RESULT 42

US-09-572-404B-272

Sequence 272, Application US/09572404B

Publication No. US2003007837A1

GENERAL INFORMATION:

APPLICANT: Proteom Ltd

TITLE OF INVENTION: Complementary peptide ligands from the human genome

FILE REFERENCE: Human patent

CURRENT APPLICATION NUMBER: US/09/572,404B

CURRENT FILING DATE: 2000-05-17

NUMBER OF SEQ ID NOS: 4203

SOFTWARE: ProtPatent version 1.0

SEQ ID NO 272

LENGTH: 10

TYPE: PRT

ORGANISM: Homo Sapiens

FEATURE:

OTHER INFORMATION: sequence located in RGS12 at 1275-1284 and may interact with Sequ

US-09-572-404B-272

Query Match 28.6%; Score 30; DB 3; Length 10;

Best Local Similarity 55.6%; Pred. No. 9.8e+02;

Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 PAKGSPG 10

Db 1 PGSASPPG 9

## RESULT 43

US-09-572-404B-274

Sequence 274, Application US/09572404B

Publication No. US2003007837A1

GENERAL INFORMATION:

APPLICANT: Proteom Ltd

TITLE OF INVENTION: Complementary peptide ligands from the human genome

FILE REFERENCE: Human patent

CURRENT APPLICATION NUMBER: US/09/572,404B

CURRENT FILING DATE: 2000-05-17

NUMBER OF SEQ ID NOS: 4203

SOFTWARE: ProtPatent version 1.0

SEQ ID NO 274

LENGTH: 10

TYPE: PRT

ORGANISM: Homo Sapiens

FEATURE:

OTHER INFORMATION: sequence located in RGS12 at 1274-1283 and may interact with Sequ

US-09-572-404B-274

Query Match 28.6%; Score 30; DB 3; Length 10;

Best Local Similarity 55.6%; Pred. No. 9.8e+02;

Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 PAKGSPG 10

Db 2 PGSASPPG 10

## RESULT 44

US-10-376-121A-14

Sequence 14, Application US/10376121A

Publication No. US2003021654A1

GENERAL INFORMATION:

APPLICANT: Harley, John

TITLE OF INVENTION: METHODS AND REAGENTS FOR DIAGNOSIS OF  
AUTANTIBODIES

NUMBER OF SEQUENCES: 218

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Patrea L. Pabst

STREET: Suite 2000, 1201 West Peachtree Street, N.E.

CITY: Atlanta

STATE: GA

COUNTRY: USA

ZIP: 30309-3400

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/376,121A

FILING DATE: 27-Mar-2003

CLASSIFICATION: <Unknown>



PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/867,819  
FILING DATE: April 13, 1992  
APPLICATION NUMBER: 07/648,205  
FILING DATE: January 31, 1991  
APPLICATION NUMBER: 07/472,947  
FILING DATE: January 31, 1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Pabst, Patricia L.  
REGISTRATION NUMBER: 31,284  
REFERENCE/DOCKET NUMBER: OMRF114CIP(2)DIV(2)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (404)-817-8473  
TELEFAX: (404)-817-8588  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Binding-site  
LOCATION: 3..10  
LOCATION: 9  
OTHER INFORMATION: /note= "The Xaa at position 9 can be  
R, P, G, H, I, K, S, T, V,  
and Y."

US-10-376-121A-14

SEQUENCE DESCRIPTION: SEQ ID NO: 14:  
US-10-376-121A-14

Query Match 28.6%; Score 30; DB 4; Length 12;  
Best Local Similarity 62.5%; Pred. No. 1.2e+03;  
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 PAKMSP 9  
DB 4 PPKMKP 11

RESULT 45  
US-10-972-236A-27  
Sequence 27, Application US/10972236A  
Publication No. US20050215470A1  
GENERAL INFORMATION:  
APPLICANT: Ng, Gordon  
APPLICANT: Li, Yue-sheng  
APPLICANT: Gegg, Colin  
APPLICANT: Askew, Jr., Benny  
APPLICANT: Storz, Thomas  
APPLICANT: Lu, Yuelie  
APPLICANT: D'Amico, Derin  
TITLE OF INVENTION: ANTAGONISTS OF THE BRADYKININ B1 RECEPTOR  
FILE REFERENCE: A-836B  
CURRENT APPLICATION NUMBER: US/10/972,236A  
CURRENT FILING DATE: 2004-10-21  
PRIOR APPLICATION NUMBER: 60/538,929  
PRIOR FILING DATE: 2004-01-24  
PRIOR APPLICATION NUMBER: 60/513,913  
PRIOR FILING DATE: 2003-10-22  
NUMBER OF SEQ ID NOS: 60  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 27  
LENGTH: 13  
TYPE: PRT  
ORGANISM: ARTIFICIAL  
FEATURE:  
OTHER INFORMATION: SYNTHETICALLY PRODUCED  
US-10-972-236A-27

Query Match 28.6%; Score 30; DB 5; Length 13;

Best Local Similarity 71.4%; Pred. No. 1.3e+03;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 GMSPPG 11  
DB 4 GKRPGP 10

RESULT 46  
US-10-185-050-53  
Sequence 53, Application US/10185050  
Publication No. US20030077577A1  
GENERAL INFORMATION:  
APPLICANT: Pirozzi, Gregorio  
Kay, Brian K.  
Fowlkes, Dana M.  
TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL  
POLYPEPTIDES HAVING WW DOMAINS AND METHODS OF USING SAME  
NUMBER OF SEQUENCES: 233  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PENNIE & EDMONDS LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/185,050  
FILING DATE: 28-Jun-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/826,516  
FILING DATE: 03-Apr-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: MISROCK, S. LESLIE  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 1101-208-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 896-8864/9741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 53:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 53:  
US-10-185-050-53

Query Match 28.6%; Score 30; DB 4; Length 14;  
Best Local Similarity 50.0%; Pred. No. 1.4e+03;  
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 5 GMSPPG 14  
DB 2 GTAPPYTVG 11

RESULT 47  
US-10-185-050-54  
Sequence 54, Application US/10185050  
Publication No. US20030077577A1  
GENERAL INFORMATION:  
APPLICANT: Pirozzi, Gregorio  
Kay, Brian K.  
Fowlkes, Dana M.

TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL  
POLYPEPTIDES HAVING WW DOMAINS AND METHODS OF USING SAME  
NUMBER OF SEQUENCES: 233  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PENNIE & EDMONDS LLP  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/185,050  
FILING DATE: 28-Jun-2002  
CLASSIFICATION: <Unknown>  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US/08/826,516  
FILING DATE: 03-Apr-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: MISROCK, S. LESLIE  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 1101-208-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9990  
TELEFAX: (212) 896-8864/9741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 54:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 54:  
US-10-185-050-54  
Query Match 28.6%; Score 30; DB 4; Length 14;  
Best Local Similarity 50.0%; Pred. No. 1.4e+03;  
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
QY 5 GMSPPGTVG 14  
DB 2 GTPPPATVWG 11  
RESULT 48  
US-10-434-906-3  
Sequence 3, Application US/10434906  
Publication No. US20030212000A1  
GENERAL INFORMATION:  
APPLICANT: William P. Van Antwerp  
TITLE OF INVENTION: IMMUNOPROTECTIVE METHODS FOR BETA CELL  
FILE REFERENCE: 130.59-US-U1  
CURRENT APPLICATION NUMBER: US/10/434,906  
CURRENT FILING DATE: 2003-05-09  
PRIOR APPLICATION NUMBER: 60/379,202  
PRIOR FILING DATE: 2002-05-09  
NUMBER OF SEQ ID NOS: 4  
SOFTWARE: PatsSeq for Windows Version 4.0  
SEQ ID NO 3  
LENGTH: 15  
TYPE: PRT  
ORGANISM: Homo Sapiens  
US-10-434-906-3  
Query Match 28.6%; Score 30; DB 4; Length 15;  
Best Local Similarity 50.0%; Pred. No. 1.5e+03;  
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 DPAGMSPPG 10  
DB 5 DPTOSTERNG 14  
RESULT 49  
US-10-972-236A-28  
Sequence 28, Application US/10972236A  
Publication No. US20050215470A1  
GENERAL INFORMATION:  
APPLICANT: Ng, Gordon  
APPLICANT: Li, Yue-Sheng  
APPLICANT: Gegg, Colin  
APPLICANT: Askew, Jr., Benny  
APPLICANT: Storz, Thomas  
APPLICANT: Lu, Yuelie  
APPLICANT: D'Amico, Derin  
TITLE OF INVENTION: ANTAGONISTS OF THE BRADYKININ B1 RECEPTOR  
FILE REFERENCE: A-836B  
CURRENT APPLICATION NUMBER: US/10/972,236A  
CURRENT FILING DATE: 2004-10-21  
PRIOR APPLICATION NUMBER: 60/538,929  
PRIOR FILING DATE: 2004-01-24  
PRIOR APPLICATION NUMBER: 60/513,913  
PRIOR FILING DATE: 2003-10-22  
NUMBER OF SEQ ID NOS: 60  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 28  
LENGTH: 15  
TYPE: PRT  
ORGANISM: ARTIFICIAL  
FEATURE:  
OTHER INFORMATION: SYNTHETICALLY PRODUCED  
US-10-972-236A-28  
Query Match 28.6%; Score 30; DB 5; Length 15;  
Best Local Similarity 71.4%; Pred. No. 1.5e+03;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 5 GMSPPGF 11  
DB 6 GRRPPGF 12  
RESULT 50  
US-10-285-394-376  
Sequence 376, Application US/10285394  
Publication No. US20030228583A1  
GENERAL INFORMATION:  
APPLICANT: AMACHER, DAVID E.  
APPLICANT: PASULO, LISA M.  
APPLICANT: HERATH, HERATH MODIYANSELAGE ATHULA CHANDRASIRI  
APPLICANT: HOLT, GORDON DUANE  
APPLICANT: STIGER, THOMAS R.  
TITLE OF INVENTION: BIOMARKERS OF LIVER RESPONSE  
FILE REFERENCE: POA-003.01  
CURRENT APPLICATION NUMBER: US/10/285,394  
CURRENT FILING DATE: 2003-02-07  
PRIOR APPLICATION NUMBER: 60/335,964  
PRIOR FILING DATE: 2001-10-31  
NUMBER OF SEQ ID NOS: 412  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 376  
LENGTH: 16  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-285-394-376  
Query Match 28.6%; Score 30; DB 4; Length 16;  
Best Local Similarity 60.0%; Pred. No. 1.6e+03;  
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 9 PGFVGBGV 18  
 |||||  
 Db 6 PGASGTGGL 15

RESULT 51  
 US-10-029-386-32096  
 ; Sequence 32096, Application US/10029386  
 ; Publication No. US20030194704A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Penn, Sharon G.  
 ; APPLICANT: Rank, David R.  
 ; APPLICANT: Hanzel, David R.  
 ; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR C  
 ; TITLE OF INVENTION: EXPRESSION ANALYSIS TWO  
 ; FILE REFERENCE: AEWICA-X-2  
 ; CURRENT APPLICATION NUMBER: US/10/029,386  
 ; CURRENT FILING DATE: 2001-12-20  
 ; NUMBER OF SEQ ID NOS: 34288  
 ; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1  
 ; SEQ ID NO 32096  
 ; LENGTH: 18  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; FEATURES:  
 ; OTHER INFORMATION: MAP TO AH005332.1  
 ; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.2  
 ; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2  
 ; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.4  
 US-10-029-386-32096

Query Match 28.6%; Score 30; DB 4; Length 18;  
 Best Local Similarity 55.6%; Pred. No. 1.9e+03;  
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 AKGMSPPGF 11  
 :|||  
 Db 2 SSGTLPPGF 10

RESULT 52  
 US-10-862-195-907  
 ; Sequence 907, Application US/10862195  
 ; Publication No. US20050164324A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: GIGI, STEVEN P.  
 ; TITLE OF INVENTION: SYSTEMS, METHODS AND KITS FOR CHARACTERIZING PHOSPHOPROTEOMES  
 ; FILE REFERENCE: 58890(70207)  
 ; CURRENT APPLICATION NUMBER: US/10/862,195  
 ; CURRENT FILING DATE: 2004-06-04  
 ; PRIOR APPLICATION NUMBER: 60/476,010  
 ; PRIOR FILING DATE: 2003-06-04  
 ; NUMBER OF SEQ ID NOS: 2245  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 907  
 ; LENGTH: 18  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; FEATURES:  
 ; OTHER INFORMATION: See specification as filed for preferred embodiments  
 ; OTHER INFORMATION: and description of phosphorylation sites  
 US-10-862-195-907

Query Match 28.6%; Score 30; DB 5; Length 18;  
 Best Local Similarity 62.5%; Pred. No. 1.9e+03;  
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 PAKGSP 9  
 |||||  
 Db 10 PAASLSP 17

RESULT 53

US-10-714-212-27  
 ; Sequence 27, Application US/10714212  
 ; Publication No. US20040077038A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Genencor International, Inc.  
 ; TITLE OF INVENTION: Methods for Production of Proteins in  
 ; TITLE OF INVENTION: Host Cells  
 ; FILE REFERENCE: GC559-PCT  
 ; CURRENT APPLICATION NUMBER: US/10/714,212  
 ; CURRENT FILING DATE: 2003-11-13  
 ; PRIOR APPLICATION NUMBER: US 09/470,830  
 ; PRIOR FILING DATE: 1999-12-23  
 ; NUMBER OF SEQ ID NOS: 44  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 27  
 ; LENGTH: 19  
 ; TYPE: PRT  
 ; ORGANISM: Mycobacterium leprae  
 US-10-714-212-27

Query Match 28.6%; Score 30; DB 4; Length 19;  
 Best Local Similarity 38.5%; Pred. No. 2e+03;  
 Matches 5; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 3 AKGMSPPGVGR 15  
 :|||:|  
 Db 2 AETTPSGLVTP 14

RESULT 54  
 US-10-307-956-24  
 ; Sequence 24, Application US/10307956  
 ; Publication No. US20030119072A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hoeckstra, Merl F.  
 ; APPLICANT: Xie, Weilin  
 ; APPLICANT: Murray, Brian  
 ; APPLICANT: Mercurio, Frank  
 ; TITLE OF INVENTION: METHODS FOR MODULATING SIGNAL  
 ; TITLE OF INVENTION: TRANSDUCTION MEDIATED BY TGF-BETA AND RELATED PROTEINS  
 ; FILE REFERENCE: 860098.433  
 ; CURRENT APPLICATION NUMBER: US/10/307,956  
 ; CURRENT FILING DATE: 2002-12-02  
 ; PRIOR APPLICATION NUMBER: US/09/385,918  
 ; PRIOR FILING DATE: 1999-08-30  
 ; NUMBER OF SEQ ID NOS: 32  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 24  
 ; LENGTH: 14  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-307-956-24

Query Match 28.1%; Score 29.5; DB 4; Length 14;  
 Best Local Similarity 60.0%; Pred. No. 1.7e+03;  
 Matches 6; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

QY 8 PGFVGBGV 17  
 |||||  
 Db 6 PGGYI-SEBG 14

RESULT 55  
 US-09-990-832C-57  
 ; Sequence 57, Application US/09990832C  
 ; Publication No. US20030149235A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: University Court of the University of Glasgow  
 ; TITLE OF INVENTION: Targeting peptides  
 ; FILE REFERENCE: PC/MC/JM/p11910US  
 ; CURRENT APPLICATION NUMBER: US/09/990,832C  
 ; CURRENT FILING DATE: 2003-01-27  
 ; NUMBER OF SEQ ID NOS: 127

/ SOFTWARE: PatentIn version 3.1  
/ SEQ ID NO 57  
/ LENGTH: 7  
/ TYPE: PRT  
/ ORGANISM: Artificial Sequence  
/ FEATURE:  
/ OTHER INFORMATION: Targeting peptide sequence  
US-09-990-832C-57

Query Match 27.6%; Score 29; DB 3; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 MSPPG 10  
Db 1 MSPPG 5

RESULT 56  
US-10-012-756-4  
/ Sequence 4; Application US/10012756  
/ Publication No. US20020164355A1  
/ GENERAL INFORMATION:  
/ APPLICANT: John B. Harley and Judith A. James  
/ TITLE OF INVENTION: Diagnostic And Therapy Of Epstein-Barr  
Virus In Autoimmune Disorders  
/ NUMBER OF SEQUENCES: 38  
/ CORRESPONDENCE ADDRESS:  
/ ADDRESSEE: Patricia L. Peabec  
/ STREET: 2800 One Atlantic Center  
1201 West Peachtree Street  
/ CITY: Atlanta  
/ STATE: Georgia  
/ COUNTRY: USA  
/ ZIP: 30306-3450

COMPUTER READABLE FORM:  
/ MEDIUM TYPE: Floppy disk  
/ COMPUTER: IBM PC compatible  
/ OPERATING SYSTEM: PC-DOS/MS-DOS  
/ SOFTWARE: PatentIn Release #1.0, Version #1.25  
/ CURRENT APPLICATION DATA:  
/ APPLICATION NUMBER: US/10/012,756  
/ FILING DATE: 24-Oct-2001  
/ CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
/ APPLICATION NUMBER: 08/781,296  
/ FILING DATE: 13-JAN-1997  
/ APPLICATION NUMBER: 60/019,053  
/ FILING DATE: 16-MAY-1996  
/ APPLICATION NUMBER: 08/160,604  
/ FILING DATE: 30-NOV-1996

ATTORNEY/AGENT INFORMATION:  
/ NAME: Peabec, Patricia L.  
/ REGISTRATION NUMBER: 31,284  
/ REFERENCE/DOCKET NUMBER: OMRF161  
/ TELECOMMUNICATION INFORMATION:  
/ TELEPHONE: (404)873-8794  
/ TELEFAX: (404)873-8795  
/ INFORMATION FOR SEQ ID NO: 4:  
/ SEQUENCE CHARACTERISTICS:  
/ LENGTH: 8 amino acids  
/ TYPE: amino acid  
/ STRANDEDNESS: single  
/ TOPOLOGY: linear  
/ MOLECULE TYPE: protein  
/ HYPOTHETICAL: NO  
/ ANTI-SENSE: NO  
/ SEQUENCE DESCRIPTION: SEQ ID NO: 4

US-10-012-756-4  
Query Match 27.6%; Score 29; DB 4; Length 8;  
Best Local Similarity 62.5%; Pred. No. 1.7e+06;  
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 PAKGMSPP 9  
Db 1 PPPGMRPP 8

RESULT 57  
US-10-646-132-3  
/ Sequence 3; Application US/10646132  
/ Publication No. US20050074751A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Oklahoma Medical Research Foundation  
/ APPLICANT: Harley, John B.  
/ APPLICANT: Kaufman, Kenneth M.  
/ TITLE OF INVENTION: Assays and Therapies For Latent Viral Infection  
/ FILE REFERENCE: OMRF 177  
/ CURRENT APPLICATION NUMBER: US/10/646,132  
/ CURRENT FILING DATE: 2003-08-22  
/ PRIOR APPLICATION NUMBER: US/09/718,693A  
/ PRIOR FILING DATE: 2000-11-22  
/ PRIOR APPLICATION NUMBER: US 60/167,212  
/ PRIOR FILING DATE: 1999-11-24  
/ NUMBER OF SEQ ID NOS: 3  
/ SOFTWARE: PatentIn version 3.1  
/ SEQ ID NO 3  
/ LENGTH: 8  
/ TYPE: PRT  
/ ORGANISM: Human herpesvirus 4  
US-10-646-132-3

Query Match 27.6%; Score 29; DB 5; Length 8;  
Best Local Similarity 62.5%; Pred. No. 1.7e+06;  
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 PAKGMSPP 9  
Db 1 PPPGMRPP 8

RESULT 58  
US-10-224-999A-2893  
/ Sequence 2893; Application US/10224999A  
/ Publication No. US20030171318A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Myriad Genetics, Inc.  
/ APPLICANT: Morham, Scott  
/ APPLICANT: Zavitz, Kenton  
/ APPLICANT: Hobden, Adrian  
/ TITLE OF INVENTION: Composition and Method for Treating Viral Infection  
/ FILE REFERENCE: 5004, 01  
/ CURRENT APPLICATION NUMBER: US/10/224,999A  
/ CURRENT FILING DATE: 2003-03-03  
/ PRIOR APPLICATION NUMBER: US 60/313,695  
/ PRIOR FILING DATE: 2001-08-20  
/ NUMBER OF SEQ ID NOS: 3484  
/ SOFTWARE: PatentIn version 3.1  
/ SEQ ID NO 2893  
/ LENGTH: 9  
/ TYPE: PRT  
/ ORGANISM: Hepatitis G virus  
US-10-224-999A-2893

Query Match 27.6%; Score 29; DB 4; Length 9;  
Best Local Similarity 80.0%; Pred. No. 1.7e+06;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 8 PPPFI 12  
Db 1 PPPFV 5

RESULT 59

```
US-09-572-404B-1350
; Sequence 1350, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProctPatent version 1.0
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: sequence located in INSM1 OR IAI at 211-220 and may interact with
US-09-572-404B-1350

Query Match      27.6%; Score 29; DB 3; Length 10;
Best Local Similarity 55.6%; Pred. No. 1.4e+03;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      2 PAKGMSPPG 10
DB      1 PAKAVKAPG 9

RESULT 60
US-09-572-404B-1352
; Sequence 1352, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProctPatent version 1.0
; SEQ ID NO 1352
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: sequence located in INSM1 OR IAI at 210-219 and may interact with
US-09-572-404B-1352

Query Match      27.6%; Score 29; DB 3; Length 10;
Best Local Similarity 55.6%; Pred. No. 1.4e+03;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      2 PAKGMSPPG 10
DB      2 PAKAVKAPG 10

RESULT 61
US-09-573-822C-684
; Sequence 684, Application US/09573822C
; Publication No. US20030199011A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands generated from microbial genome seq
; FILE REFERENCE: Microbe patent
; CURRENT APPLICATION NUMBER: US/09/573,822C
; CURRENT FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 804
; SOFTWARE: ProctPatent version 1.0
; SEQ ID NO 684
; LENGTH: 10

; TYPE: PRT
; ORGANISM: mycoplasma genitalium
; FEATURE:
; OTHER INFORMATION: Sequence located in MG469 at 136-145 and may interact with Sequ
US-09-573-822C-684

Query Match      27.6%; Score 29; DB 3; Length 10;
Best Local Similarity 60.0%; Pred. No. 1.4e+03;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      9 PGFVGEQV 18
DB      1 PLFVGEQV 10

RESULT 62
US-10-224-999A-2899
; Sequence 2899, Application US/10224999A
; Publication No. US20030171318A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Composition and Method for Treating Viral Infection
; FILE REFERENCE: 5004.01
; CURRENT APPLICATION NUMBER: US/10/224,999A
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/313,695
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 3484
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2899
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Hepatitis G virus
US-10-224-999A-2899

Query Match      27.6%; Score 29; DB 4; Length 10;
Best Local Similarity 80.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      8 PGFPI 12
DB      2 PGFV 6

RESULT 63
US-10-224-999A-2900
; Sequence 2900, Application US/10224999A
; Publication No. US20030171318A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Composition and Method for Treating Viral Infection
; FILE REFERENCE: 5004.01
; CURRENT APPLICATION NUMBER: US/10/224,999A
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/313,695
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 3484
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2900
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Hepatitis G virus
US-10-224-999A-2900

Query Match      27.6%; Score 29; DB 4; Length 10;
Best Local Similarity 80.0%; Pred. No. 1.4e+03;
```

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Qy 8 PGFPI 12  
|||:  
Db 1 PGFV 5

RESULT 64  
US-10-224-999A-2906  
; Sequence 2906, Application US/10224999A  
; Publication No. US20030171318A1  
; GENERAL INFORMATION:  
; APPLICANT: Myriad Genetics, Inc.  
; APPLICANT: Morham, Scott  
; APPLICANT: Zavitz, Kenton  
; APPLICANT: Hobden, Adrian  
; TITLE OF INVENTION: Composition and Method for Treating Viral Infection  
; FILE REFERENCE: 5004.01  
; CURRENT FILING DATE: 2003-03-03  
; PRIOR APPLICATION NUMBER: US 60/313,695  
; PRIOR FILING DATE: 2001-08-20  
; NUMBER OF SEQ ID NOS: 3484  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2906  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Hepatitis G virus  
US-10-224-999A-2906

Query Match 27.6%; Score 29; DB 4; Length 11;  
Best Local Similarity 80.0%; Pred. No. 1.5e+03;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 8 PGFPI 12  
|||:  
Db 3 PGFV 7

RESULT 65  
US-10-224-999A-2907  
; Sequence 2907, Application US/10224999A  
; Publication No. US20030171318A1  
; GENERAL INFORMATION:  
; APPLICANT: Myriad Genetics, Inc.  
; APPLICANT: Morham, Scott  
; APPLICANT: Zavitz, Kenton  
; APPLICANT: Hobden, Adrian  
; TITLE OF INVENTION: Composition and Method for Treating Viral Infection  
; FILE REFERENCE: 5004.01  
; CURRENT APPLICATION NUMBER: US/10/224,999A  
; CURRENT FILING DATE: 2003-03-03  
; PRIOR APPLICATION NUMBER: US 60/313,695  
; PRIOR FILING DATE: 2001-08-20  
; NUMBER OF SEQ ID NOS: 3484  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2907  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Hepatitis G virus  
US-10-224-999A-2907

Query Match 27.6%; Score 29; DB 4; Length 11;  
Best Local Similarity 80.0%; Pred. No. 1.5e+03;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 8 PGFPI 12  
|||:  
Db 2 PGFV 6

RESULT 66  
US-10-224-999A-2908

; Sequence 2908, Application US/10224999A  
; Publication No. US20030171318A1  
; GENERAL INFORMATION:  
; APPLICANT: Myriad Genetics, Inc.  
; APPLICANT: Morham, Scott  
; APPLICANT: Zavitz, Kenton  
; APPLICANT: Hobden, Adrian  
; TITLE OF INVENTION: Composition and Method for Treating Viral Infection  
; FILE REFERENCE: 5004.01  
; CURRENT APPLICATION NUMBER: US/10/224,999A  
; CURRENT FILING DATE: 2003-03-03  
; PRIOR APPLICATION NUMBER: US 60/313,695  
; PRIOR FILING DATE: 2001-08-20  
; NUMBER OF SEQ ID NOS: 3484  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2908  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Hepatitis G virus  
US-10-224-999A-2908

Query Match 27.6%; Score 29; DB 4; Length 11;  
Best Local Similarity 80.0%; Pred. No. 1.5e+03;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 8 PGFPI 12  
|||:  
Db 1 PGFV 5

RESULT 67  
US-10-376-121A-10  
; Sequence 10, Application US/10376121A  
; Publication No. US20030216544A1  
; GENERAL INFORMATION:  
; APPLICANT: Harley, John  
; TITLE OF INVENTION: METHODS AND REAGENTS FOR DIAGNOSIS OF  
; AUTOANTIBODIES  
; NUMBER OF SEQUENCES: 218  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Patricia L. Pabst  
; STREET: Suite 2000, 1201 West Peachtree Street, N.E.  
; CITY: Atlanta  
; STATE: GA  
; COUNTRY: USA  
; ZIP: 30309-3400  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/376,121A  
; FILING DATE: 27-Mar-2003  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/867,819  
; FILING DATE: April 13, 1992  
; APPLICATION NUMBER: 07/648,205  
; FILING DATE: January 31, 1991  
; APPLICATION NUMBER: 07/472,947  
; FILING DATE: January 31, 1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Pabst, Patricia L.  
; REGISTRATION NUMBER: 31,284  
; REFERENCE/DOCKET NUMBER: OMRP114CIP(2)DIV(2)  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (404)-817-8473  
; TELEFAX: (404)-817-8588  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid

STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Binding-site  
LOCATION: 3..10  
SEQUENCE DESCRIPTION: SEQ ID NO: 10;  
US-10-376-121A-10

Query Match 27.6%; Score 29; DB 4; Length 11;  
Best Local Similarity 62.5%; Pred. No. 1.5e+03;  
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 PAKGMSPP 9  
Db 3 PPGMRPP 10

RESULT 68  
US-10-285-394-140  
Sequence 140; Application US/10285394  
Publication No. US20030228583A1  
GENERAL INFORMATION:  
APPLICANT: AMACHER, DAVID E.  
APPLICANT: PASULO, LISA M.  
APPLICANT: HERATH, HERATH MUDIYANSELAGE ATTULA CHANDRASIRI  
APPLICANT: HOLT, GORDON DUANE  
APPLICANT: STIGER, THOMAS R.  
TITLE OF INVENTION: BIOMARKERS OF LIVER RESPONSE  
FILE REFERENCE: POA-003.01  
CURRENT APPLICATION NUMBER: US/10/285,394  
CURRENT FILING DATE: 2003-02-07  
PRIOR APPLICATION NUMBER: 60/335,964  
PRIOR FILING DATE: 2001-10-31  
NUMBER OF SEQ ID NOS: 412  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 140  
LENGTH: 11  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-285-394-140

Query Match 27.6%; Score 29; DB 4; Length 11;  
Best Local Similarity 62.5%; Pred. No. 1.5e+03;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 11 FIVEGCV 18  
Db 1 FIVEGCV 8

RESULT 69  
US-10-286-457-50  
Sequence 50; Application US/10286457  
Publication No. US20030166004A1  
GENERAL INFORMATION:  
APPLICANT: JENO CYRUS et al.  
TITLE OF INVENTION: ENDOTHelial-CELL BINDING PEPTIDES FOR DIAGNOSIS AND THERAPY  
FILE REFERENCE: GPCI-P01-178  
CURRENT APPLICATION NUMBER: US/10/286,457  
CURRENT FILING DATE: 2002-11-01  
PRIOR APPLICATION NUMBER: 60/334822  
PRIOR FILING DATE: 2001-11-01  
NUMBER OF SEQ ID NOS: 684  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 50  
LENGTH: 12  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: artificial sequence isolated from random peptide libraries, based  
US-10-286-457-50

Query Match 27.6%; Score 29; DB 4; Length 12;  
Best Local Similarity 62.5%; Pred. No. 1.7e+03;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 AKGMSPPG 10  
Db 1 ATGTNPPG 8

RESULT 70  
US-10-224-999A-2914  
Sequence 2914; Application US/10224999A  
Publication No. US20030171318A1  
GENERAL INFORMATION:  
APPLICANT: Myriad Genetics, Inc.  
APPLICANT: Morham, Scott  
APPLICANT: Zavitz, Kenton  
APPLICANT: Hobden, Adrian  
TITLE OF INVENTION: Composition and Method for Treating Viral Infection  
FILE REFERENCE: 5004.01  
CURRENT APPLICATION NUMBER: US/10/224,999A  
CURRENT FILING DATE: 2003-03-03  
PRIOR APPLICATION NUMBER: US 60/313,695  
PRIOR FILING DATE: 2001-08-20  
NUMBER OF SEQ ID NOS: 3484  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 2914  
LENGTH: 12  
TYPE: PRT  
ORGANISM: Hepatitis G virus  
US-10-224-999A-2914

Query Match 27.6%; Score 29; DB 4; Length 12;  
Best Local Similarity 80.0%; Pred. No. 1.7e+03;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 8 PPGFI 12  
Db 4 PPGFV 8

RESULT 71  
US-10-224-999A-2915  
Sequence 2915; Application US/10224999A  
Publication No. US20030171318A1  
GENERAL INFORMATION:  
APPLICANT: Myriad Genetics, Inc.  
APPLICANT: Morham, Scott  
APPLICANT: Zavitz, Kenton  
APPLICANT: Hobden, Adrian  
TITLE OF INVENTION: Composition and Method for Treating Viral Infection  
FILE REFERENCE: 5004.01  
CURRENT APPLICATION NUMBER: US/10/224,999A  
CURRENT FILING DATE: 2003-03-03  
PRIOR APPLICATION NUMBER: US 60/313,695  
PRIOR FILING DATE: 2001-08-20  
NUMBER OF SEQ ID NOS: 3484  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 2915  
LENGTH: 12  
TYPE: PRT  
ORGANISM: Hepatitis G virus  
US-10-224-999A-2915

Query Match 27.6%; Score 29; DB 4; Length 12;  
Best Local Similarity 80.0%; Pred. No. 1.7e+03;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 8 PPGFI 12  
Db 3 PPGFV 7

```
RESULT 72
US-10-224-999A-2916
; Sequence 2916, Application US/10224999A
; Publication No. US20030171318A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Composition and Method for Treating Viral Infection
; FILE REFERENCE: 5004.01
; CURRENT APPLICATION NUMBER: US/10/224,999A
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/313,695
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 3484
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2916
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Hepatitis G virus
US-10-224-999A-2916

Query Match      27.6%; Score 29; DB 4; Length 12;
Best Local Similarity 80.0%; Pred. No. 1.7e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      8 PPGFI 12
      ||||:
Db      2 PPGFV 6

RESULT 73
US-10-224-999A-2917
; Sequence 2917, Application US/10224999A
; Publication No. US20030171318A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Composition and Method for Treating Viral Infection
; FILE REFERENCE: 5004.01
; CURRENT APPLICATION NUMBER: US/10/224,999A
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/313,695
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 3484
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2917
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Hepatitis G virus
US-10-224-999A-2917

Query Match      27.6%; Score 29; DB 4; Length 12;
Best Local Similarity 80.0%; Pred. No. 1.7e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      8 PPGFI 12
      ||||:
Db      1 PPGFV 5

RESULT 74
US-10-224-999A-2923
; Sequence 2923, Application US/10224999A
; Publication No. US20030171318A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
```

```
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Composition and Method for Treating Viral Infection
; FILE REFERENCE: 5004.01
; CURRENT APPLICATION NUMBER: US/10/224,999A
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/313,695
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 3484
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2923
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Hepatitis G virus
US-10-224-999A-2923

Query Match      27.6%; Score 29; DB 4; Length 13;
Best Local Similarity 80.0%; Pred. No. 1.8e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      8 PPGFI 12
      ||||:
Db      5 PPGFV 9

RESULT 75
US-10-224-999A-2924
; Sequence 2924, Application US/10224999A
; Publication No. US20030171318A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Composition and Method for Treating Viral Infection
; FILE REFERENCE: 5004.01
; CURRENT APPLICATION NUMBER: US/10/224,999A
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/313,695
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 3484
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2924
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Hepatitis G virus
US-10-224-999A-2924

Query Match      27.6%; Score 29; DB 4; Length 13;
Best Local Similarity 80.0%; Pred. No. 1.8e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      8 PPGFI 12
      ||||:
Db      4 PPGFV 8

RESULT 76
US-10-224-999A-2925
; Sequence 2925, Application US/10224999A
; Publication No. US20030171318A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Composition and Method for Treating Viral Infection
; FILE REFERENCE: 5004.01
; CURRENT APPLICATION NUMBER: US/10/224,999A
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/313,695
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 3484
; SOFTWARE: PatentIn version 3.1
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/ SEQ ID NO 2925  
/ LENGTH: 13  
/ TYPE: PRT  
/ ORGANISM: Hepatitis G virus  
US-10-224-999A-2925

Query Match 27.6%; Score 29; DB 4; Length 13;  
Best Local Similarity 80.0%; Pred. No. 1.8e+03;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 PGPI 12  
DB 3 PGFV 7

RESULT 77  
US-10-224-999A-2926  
/ Sequence 2926, Application US/10224999A  
/ Publication No. US20030171318A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Myriad Genetics, Inc.  
/ APPLICANT: Morham, Scott  
/ APPLICANT: Zavitz, Kenton  
/ APPLICANT: Hobden, Adrian  
/ TITLE OF INVENTION: Composition and Method for Treating Viral Infection  
/ FILE REFERENCE: 5004.01  
/ CURRENT APPLICATION NUMBER: US/10/224,999A  
/ PRIOR FILING DATE: 2003-03-03  
/ PRIOR APPLICATION NUMBER: US 60/313,695  
/ PRIOR FILING DATE: 2001-08-20  
/ NUMBER OF SEQ ID NOS: 3484  
/ SOFTWARE: PatentIn version 3.1  
/ SEQ ID NO 2926  
/ LENGTH: 13  
/ TYPE: PRT  
/ ORGANISM: Hepatitis G virus  
US-10-224-999A-2926

Query Match 27.6%; Score 29; DB 4; Length 13;  
Best Local Similarity 80.0%; Pred. No. 1.8e+03;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 PGPI 12  
DB 2 PGFV 6

RESULT 78  
US-10-224-999A-2927  
/ Sequence 2927, Application US/10224999A  
/ Publication No. US20030171318A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Myriad Genetics, Inc.  
/ APPLICANT: Morham, Scott  
/ APPLICANT: Zavitz, Kenton  
/ APPLICANT: Hobden, Adrian  
/ TITLE OF INVENTION: Composition and Method for Treating Viral Infection  
/ FILE REFERENCE: 5004.01  
/ CURRENT APPLICATION NUMBER: US/10/224,999A  
/ PRIOR FILING DATE: 2003-03-03  
/ PRIOR APPLICATION NUMBER: US 60/313,695  
/ PRIOR FILING DATE: 2001-08-20  
/ NUMBER OF SEQ ID NOS: 3484  
/ SOFTWARE: PatentIn version 3.1  
/ SEQ ID NO 2927  
/ LENGTH: 13  
/ TYPE: PRT  
/ ORGANISM: Hepatitis G virus  
US-10-224-999A-2927

Query Match 27.6%; Score 29; DB 4; Length 13;  
Best Local Similarity 80.0%; Pred. No. 1.8e+03;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 PGPI 12  
DB 1 PGFV 5

RESULT 79  
US-10-948-707-1350  
/ Sequence 1350, Application US/10948707  
/ Publication No. US20050187147A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Ballatore, Carlo  
/ APPLICANT: Castellino, Angelo  
/ APPLICANT: Desharnais, Joel  
/ APPLICANT: Guo, Zijian  
/ APPLICANT: Li, Qing  
/ APPLICANT: Newman, Michael James  
/ APPLICANT: Sun, Chengzao  
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INCREASING  
/ FILE REFERENCE: 17967-003001  
/ CURRENT APPLICATION NUMBER: US/10/948,707  
/ PRIOR FILING DATE: 2004-09-22  
/ PRIOR APPLICATION NUMBER: 60/505,325  
/ PRIOR FILING DATE: 2003-09-22  
/ PRIOR APPLICATION NUMBER: 60/568,340  
/ PRIOR FILING DATE: 2004-05-04  
/ PRIOR APPLICATION NUMBER: 60/581,835  
/ PRIOR FILING DATE: 2004-06-22  
/ NUMBER OF SEQ ID NOS: 1422  
/ SOFTWARE: PatsSeq for Windows Version 4.0  
/ SEQ ID NO 1350  
/ LENGTH: 13  
/ TYPE: PRT  
/ ORGANISM: Homo Sapiens  
US-10-948-707-1350

Query Match 27.6%; Score 29; DB 5; Length 13;  
Best Local Similarity 83.3%; Pred. No. 1.8e+03;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 KGMSP 9  
DB 1 KGMMP 6

RESULT 80  
US-10-224-999A-2933  
/ Sequence 2933, Application US/10224999A  
/ Publication No. US20030171318A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Myriad Genetics, Inc.  
/ APPLICANT: Morham, Scott  
/ APPLICANT: Zavitz, Kenton  
/ APPLICANT: Hobden, Adrian  
/ TITLE OF INVENTION: Composition and Method for Treating Viral Infection  
/ FILE REFERENCE: 5004.01  
/ CURRENT APPLICATION NUMBER: US/10/224,999A  
/ PRIOR FILING DATE: 2003-03-03  
/ PRIOR APPLICATION NUMBER: US 60/313,695  
/ PRIOR FILING DATE: 2001-08-20  
/ NUMBER OF SEQ ID NOS: 3484  
/ SOFTWARE: PatentIn version 3.1  
/ SEQ ID NO 2933  
/ LENGTH: 14  
/ TYPE: PRT  
/ ORGANISM: Hepatitis G virus  
US-10-224-999A-2933

Query Match 27.6%; Score 29; DB 4; Length 14;  
Best Local Similarity 80.0%; Pred. No. 2e+03;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 PPGFI 12  
 ||||:  
 Db 6 PPGFV 10

## RESULT 81

US-10-224-999A-2934  
 ; Sequence 2934, Application US/10224999A  
 ; Publication No. US20030171318A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Myriad Genetics, Inc.  
 ; APPLICANT: Morham, Scott  
 ; APPLICANT: Zavitz, Kenton  
 ; APPLICANT: Hobden, Adrian  
 ; TITLE OF INVENTION: Composition and Method for Treating Viral Infection  
 ; FILE REFERENCE: 5004.01  
 ; CURRENT APPLICATION NUMBER: US/10/224,999A  
 ; CURRENT FILING DATE: 2003-03-03  
 ; PRIOR APPLICATION NUMBER: US 60/313,695  
 ; PRIOR FILING DATE: 2001-08-20  
 ; NUMBER OF SEQ ID NOS: 3484  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 2934  
 ; LENGTH: 14  
 ; TYPE: PRT  
 ; ORGANISM: Hepatitis G virus  
 US-10-224-999A-2934

Query Match 27.6%; Score 29; DB 4; Length 14;  
 Best Local Similarity 80.0%; Pred. No. 2e+03;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 PPGFI 12  
 ||||:  
 Db 5 PPGFV 9

## RESULT 82

US-10-224-999A-2935  
 ; Sequence 2935, Application US/10224999A  
 ; Publication No. US20030171318A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Myriad Genetics, Inc.  
 ; APPLICANT: Morham, Scott  
 ; APPLICANT: Zavitz, Kenton  
 ; APPLICANT: Hobden, Adrian  
 ; TITLE OF INVENTION: Composition and Method for Treating Viral Infection  
 ; FILE REFERENCE: 5004.01  
 ; CURRENT APPLICATION NUMBER: US/10/224,999A  
 ; CURRENT FILING DATE: 2003-03-03  
 ; PRIOR APPLICATION NUMBER: US 60/313,695  
 ; PRIOR FILING DATE: 2001-08-20  
 ; NUMBER OF SEQ ID NOS: 3484  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 2935  
 ; LENGTH: 14  
 ; TYPE: PRT  
 ; ORGANISM: Hepatitis G virus  
 US-10-224-999A-2935

Query Match 27.6%; Score 29; DB 4; Length 14;  
 Best Local Similarity 80.0%; Pred. No. 2e+03;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 PPGFI 12  
 ||||:  
 Db 4 PPGFV 8

## RESULT 83

US-10-224-999A-2936  
 ; Sequence 2936, Application US/10224999A  
 ; Publication No. US20030171318A1

; GENERAL INFORMATION:  
 ; APPLICANT: Myriad Genetics, Inc.  
 ; APPLICANT: Morham, Scott  
 ; APPLICANT: Zavitz, Kenton  
 ; APPLICANT: Hobden, Adrian  
 ; TITLE OF INVENTION: Composition and Method for Treating Viral Infection  
 ; FILE REFERENCE: 5004.01  
 ; CURRENT APPLICATION NUMBER: US/10/224,999A  
 ; CURRENT FILING DATE: 2003-03-03  
 ; PRIOR APPLICATION NUMBER: US 60/313,695  
 ; PRIOR FILING DATE: 2001-08-20  
 ; NUMBER OF SEQ ID NOS: 3484  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 2936  
 ; LENGTH: 14  
 ; TYPE: PRT  
 ; ORGANISM: Hepatitis G virus  
 US-10-224-999A-2936

Query Match 27.6%; Score 29; DB 4; Length 14;  
 Best Local Similarity 80.0%; Pred. No. 2e+03;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 PPGFI 12  
 ||||:  
 Db 3 PPGFV 7

## RESULT 84

US-10-224-999A-2937  
 ; Sequence 2937, Application US/10224999A  
 ; Publication No. US20030171318A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Myriad Genetics, Inc.  
 ; APPLICANT: Morham, Scott  
 ; APPLICANT: Zavitz, Kenton  
 ; APPLICANT: Hobden, Adrian  
 ; TITLE OF INVENTION: Composition and Method for Treating Viral Infection  
 ; FILE REFERENCE: 5004.01  
 ; CURRENT APPLICATION NUMBER: US/10/224,999A  
 ; CURRENT FILING DATE: 2003-03-03  
 ; PRIOR APPLICATION NUMBER: US 60/313,695  
 ; PRIOR FILING DATE: 2001-08-20  
 ; NUMBER OF SEQ ID NOS: 3484  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 2937  
 ; LENGTH: 14  
 ; TYPE: PRT  
 ; ORGANISM: Hepatitis G virus  
 US-10-224-999A-2937

Query Match 27.6%; Score 29; DB 4; Length 14;  
 Best Local Similarity 80.0%; Pred. No. 2e+03;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 PPGFI 12  
 ||||:  
 Db 2 PPGFV 6

## RESULT 85

US-10-224-999A-2938  
 ; Sequence 2938, Application US/10224999A  
 ; Publication No. US20030171318A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Myriad Genetics, Inc.  
 ; APPLICANT: Morham, Scott  
 ; APPLICANT: Zavitz, Kenton  
 ; APPLICANT: Hobden, Adrian  
 ; TITLE OF INVENTION: Composition and Method for Treating Viral Infection  
 ; FILE REFERENCE: 5004.01  
 ; CURRENT APPLICATION NUMBER: US/10/224,999A  
 ; CURRENT FILING DATE: 2003-03-03

```
/ PRIOR APPLICATION NUMBER: US 60/313,695
/ PRIOR FILING DATE: 2001-08-20
/ NUMBER OF SEQ ID NOS: 3484
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 2938
/ LENGTH: 14
/ TYPE: PRT
/ ORGANISM: Hepatitis G virus
US-10-224-999A-2938

Query Match      27.6%; Score 29; DB 4; Length 14;
Best Local Similarity 80.0%; Pred. No. 2e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      8 PPGFI 12
Db      1 PPGFV 5

RESULT 86
US-10-149-240-12
/ Sequence 12, Application US/10149240
/ Publication No. US20030211589A1
/ GENERAL INFORMATION:
/ APPLICANT: Children's Medical Center
/ APPLICANT: Viasum Research Development
/ APPLICANT: Shmuel A. Ben-Sasson
/ TITLE OF INVENTION: Short Peptides from the B4 and B5 Regions of Protein Kinases Whic
/ FILE REFERENCE: 1242.2001002
/ CURRENT APPLICATION NUMBER: US/10/149,240
/ PRIOR FILING DATE: 2002-06-10
/ PRIOR APPLICATION NUMBER: US 09/458,491
/ PRIOR FILING DATE: 1999-12-09
/ NUMBER OF SEQ ID NOS: 37
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 12
/ LENGTH: 14
/ TYPE: PRT
/ ORGANISM: unknown
/ FEATURE:
/ OTHER INFORMATION: BMPR-II
US-10-149-240-12

Query Match      27.6%; Score 29; DB 4; Length 14;
Best Local Similarity 75.0%; Pred. No. 2e+03;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      11 FIVGEGV 18
Db      1 FIVGDERV 8

RESULT 87
US-10-224-999A-2944
/ Sequence 2944, Application US/10224999A
/ Publication No. US20030171318A1
/ GENERAL INFORMATION:
/ APPLICANT: Myriad Genetics, Inc.
/ APPLICANT: Morham, Scott
/ APPLICANT: Zavitz, Kenton
/ APPLICANT: Hobden, Adrian
/ TITLE OF INVENTION: Composition and Method for Treating Viral Infection
/ FILE REFERENCE: 5004.01
/ CURRENT APPLICATION NUMBER: US/10/224,999A
/ PRIOR FILING DATE: 2003-03-03
/ PRIOR APPLICATION NUMBER: US 60/313,695
/ PRIOR FILING DATE: 2001-08-20
/ NUMBER OF SEQ ID NOS: 3484
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 2944
/ LENGTH: 15
/ TYPE: PRT

/ ORGANISM: Hepatitis G virus
US-10-224-999A-2946

Query Match      27.6%; Score 29; DB 4; Length 15;
Best Local Similarity 80.0%; Pred. No. 2.2e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      8 PPGFI 12
Db      6 PPGFV 10

RESULT 89
US-10-224-999A-2946
/ Sequence 2946, Application US/10224999A
/ Publication No. US20030171318A1
/ GENERAL INFORMATION:
/ APPLICANT: Myriad Genetics, Inc.
/ APPLICANT: Morham, Scott
/ APPLICANT: Zavitz, Kenton
/ APPLICANT: Hobden, Adrian
/ TITLE OF INVENTION: Composition and Method for Treating Viral Infection
/ FILE REFERENCE: 5004.01
/ CURRENT APPLICATION NUMBER: US/10/224,999A
/ PRIOR FILING DATE: 2003-03-03
/ PRIOR APPLICATION NUMBER: US 60/313,695
/ PRIOR FILING DATE: 2001-08-20
/ NUMBER OF SEQ ID NOS: 3484
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 2946
/ LENGTH: 15
/ TYPE: PRT
/ ORGANISM: Hepatitis G virus
US-10-224-999A-2946

Query Match      27.6%; Score 29; DB 4; Length 15;
Best Local Similarity 80.0%; Pred. No. 2.2e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      8 PPGFI 12
Db      6 PPGFV 10

RESULT 88
US-10-224-999A-2945
/ Sequence 2945, Application US/10224999A
/ Publication No. US20030171318A1
/ GENERAL INFORMATION:
/ APPLICANT: Myriad Genetics, Inc.
/ APPLICANT: Morham, Scott
/ APPLICANT: Zavitz, Kenton
/ APPLICANT: Hobden, Adrian
/ TITLE OF INVENTION: Composition and Method for Treating Viral Infection
/ FILE REFERENCE: 5004.01
/ CURRENT APPLICATION NUMBER: US/10/224,999A
/ PRIOR FILING DATE: 2003-03-03
/ PRIOR APPLICATION NUMBER: US 60/313,695
/ PRIOR FILING DATE: 2001-08-20
/ NUMBER OF SEQ ID NOS: 3484
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 2945
/ LENGTH: 15
/ TYPE: PRT
/ ORGANISM: Hepatitis G virus
US-10-224-999A-2945

Query Match      27.6%; Score 29; DB 4; Length 15;
Best Local Similarity 80.0%; Pred. No. 2.2e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      8 PPGFI 12
Db      6 PPGFV 10

RESULT 89
US-10-224-999A-2946
/ Sequence 2946, Application US/10224999A
/ Publication No. US20030171318A1
/ GENERAL INFORMATION:
/ APPLICANT: Myriad Genetics, Inc.
/ APPLICANT: Morham, Scott
/ APPLICANT: Zavitz, Kenton
/ APPLICANT: Hobden, Adrian
/ TITLE OF INVENTION: Composition and Method for Treating Viral Infection
/ FILE REFERENCE: 5004.01
/ CURRENT APPLICATION NUMBER: US/10/224,999A
/ PRIOR FILING DATE: 2003-03-03
/ PRIOR APPLICATION NUMBER: US 60/313,695
/ PRIOR FILING DATE: 2001-08-20
/ NUMBER OF SEQ ID NOS: 3484
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 2946
/ LENGTH: 15
/ TYPE: PRT
/ ORGANISM: Hepatitis G virus
US-10-224-999A-2946

Query Match      27.6%; Score 29; DB 4; Length 15;
Best Local Similarity 80.0%; Pred. No. 2.2e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      8 PPGFI 12
Db      6 PPGFV 10
```

Db 5 PGFV 9

RESULT 90

```
US-10-224-999A-2947
; Sequence 2947, Application US/10224999A
; Publication No. US20030171318A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Composition and Method for Treating Viral Infection
; FILE REFERENCE: 5004.01
; CURRENT APPLICATION NUMBER: US/10/224,999A
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/313,695
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 3484
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 2947
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Hepatitis G virus
US-10-224-999A-2947
```

Query Match 27.6%; Score 29; DB 4; Length 15;  
Best Local Similarity 80.0%; Pred. No. 2.2e+03;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 8 PGFV 12

Db 4 PGFV 8

RESULT 91

```
US-10-224-999A-2948
; Sequence 2948, Application US/10224999A
; Publication No. US20030171318A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Composition and Method for Treating Viral Infection
; FILE REFERENCE: 5004.01
; CURRENT APPLICATION NUMBER: US/10/224,999A
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/313,695
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 3484
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 2948
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Hepatitis G virus
US-10-224-999A-2948
```

Query Match 27.6%; Score 29; DB 4; Length 15;  
Best Local Similarity 80.0%; Pred. No. 2.2e+03;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 8 PGFV 12

Db 3 PGFV 7

RESULT 92

```
US-10-224-999A-2949
; Sequence 2949, Application US/10224999A
; Publication No. US20030171318A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
```

```
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Composition and Method for Treating Viral Infection
; FILE REFERENCE: 5004.01
; CURRENT APPLICATION NUMBER: US/10/224,999A
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/313,695
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 3484
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 2949
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Hepatitis G virus
US-10-224-999A-2949
```

Query Match 27.6%; Score 29; DB 4; Length 15;  
Best Local Similarity 80.0%; Pred. No. 2.2e+03;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 8 PGFV 12

Db 2 PGFV 6

RESULT 93

```
US-10-224-999A-2950
; Sequence 2950, Application US/10224999A
; Publication No. US20030171318A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Composition and Method for Treating Viral Infection
; FILE REFERENCE: 5004.01
; CURRENT APPLICATION NUMBER: US/10/224,999A
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/313,695
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 3484
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 2950
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Hepatitis G virus
US-10-224-999A-2950
```

Query Match 27.6%; Score 29; DB 4; Length 15;  
Best Local Similarity 80.0%; Pred. No. 2.2e+03;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 8 PGFV 12

Db 1 PGFV 5

RESULT 94

```
US-10-128-520-38
; Sequence 38, Application US/10128520
; Publication No. US20040105862A1
; GENERAL INFORMATION:
; APPLICANT: PAN et al.
; TITLE OF INVENTION: Human TIMP-1 Antibodies
; FILE REFERENCE: 02973.00073
; CURRENT APPLICATION NUMBER: US/10/128,520
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 60/285,683
; PRIOR FILING DATE: 2001-04-24
; NUMBER OF SEQ ID NOS: 381
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
```

/ LENGTH: 15  
/ TYPE: PRT  
/ ORGANISM: Homo sapiens  
US-10-128-520-38

Query Match 27.6%; Score 29; DB 4; Length 15;  
Best Local Similarity 55.6%; Pred. No. 2.2e+03;  
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 6 MSPGPIV 14  
Db 2 MTPGHYV 10

RESULT 95  
US-10-225-567A-1513

/ Sequence 1513, Application US/10225567A  
/ Publication No. US20030113798A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Lifespan Biosciences  
/ APPLICANT: Brown, Joseph P.  
/ APPLICANT: Burner, Glenn C.  
/ APPLICANT: Roush, Christine L.  
/ TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS  
/ FILE REFERENCE: 1920-4-4  
/ CURRENT APPLICATION NUMBER: US/10/225,567A  
/ CURRENT FILING DATE: 2001-12-19  
/ PRIOR APPLICATION NUMBER: 60/257,144  
/ PRIOR FILING DATE: 2000-12-19  
/ NUMBER OF SEQ ID NOS: 2292  
/ SOFTWARE: PatentIn version 3.1  
/ SEQ ID NO 1513  
/ LENGTH: 16  
/ TYPE: PRT  
/ ORGANISM: Homo sapiens  
US-10-225-567A-1513

Query Match 27.6%; Score 29; DB 4; Length 16;  
Best Local Similarity 33.3%; Pred. No. 2.3e+03;

Matches 4; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DPAKMSPPGPI 12  
Db 4 NPTKDLTPGMV 15

RESULT 96  
US-10-224-999A-2956

/ Sequence 2956, Application US/10224999A  
/ Publication No. US20030171318A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Myriad Genetics, Inc.  
/ APPLICANT: Morham, Scott  
/ APPLICANT: Zavitz, Kenton  
/ APPLICANT: Hobden, Adrian  
/ TITLE OF INVENTION: Composition and Method for Treating Viral Infection  
/ FILE REFERENCE: 5004.01  
/ CURRENT APPLICATION NUMBER: US/10/224,999A  
/ CURRENT FILING DATE: 2003-03-03  
/ PRIOR APPLICATION NUMBER: US 60/313,695  
/ PRIOR FILING DATE: 2001-08-20  
/ NUMBER OF SEQ ID NOS: 3484  
/ SOFTWARE: PatentIn version 3.1  
/ SEQ ID NO 2956  
/ LENGTH: 16  
/ TYPE: PRT  
/ ORGANISM: Hepatitis G virus  
US-10-224-999A-2956

Query Match 27.6%; Score 29; DB 4; Length 16;  
Best Local Similarity 80.0%; Pred. No. 2.3e+03;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 8 PGPI 12  
Db 8 PGPIV 12

RESULT 97  
US-10-224-999A-2957

/ Sequence 2957, Application US/10224999A  
/ Publication No. US20030171318A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Myriad Genetics, Inc.  
/ APPLICANT: Morham, Scott  
/ APPLICANT: Zavitz, Kenton  
/ APPLICANT: Hobden, Adrian  
/ TITLE OF INVENTION: Composition and Method for Treating Viral Infection  
/ FILE REFERENCE: 5004.01  
/ CURRENT APPLICATION NUMBER: US/10/224,999A  
/ CURRENT FILING DATE: 2003-03-03  
/ PRIOR APPLICATION NUMBER: US 60/313,695  
/ PRIOR FILING DATE: 2001-08-20  
/ NUMBER OF SEQ ID NOS: 3484  
/ SOFTWARE: PatentIn version 3.1  
/ SEQ ID NO 2957  
/ LENGTH: 16  
/ TYPE: PRT  
/ ORGANISM: Hepatitis G virus  
US-10-224-999A-2957

Query Match 27.6%; Score 29; DB 4; Length 16;  
Best Local Similarity 80.0%; Pred. No. 2.3e+03;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 8 PGPI 12  
Db 7 PGPIV 11

RESULT 98

US-10-224-999A-2958

/ Sequence 2958, Application US/10224999A  
/ Publication No. US20030171318A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Myriad Genetics, Inc.  
/ APPLICANT: Morham, Scott  
/ APPLICANT: Zavitz, Kenton  
/ APPLICANT: Hobden, Adrian  
/ TITLE OF INVENTION: Composition and Method for Treating Viral Infection  
/ FILE REFERENCE: 5004.01  
/ CURRENT APPLICATION NUMBER: US/10/224,999A  
/ CURRENT FILING DATE: 2003-03-03  
/ PRIOR APPLICATION NUMBER: US 60/313,695  
/ PRIOR FILING DATE: 2001-08-20  
/ NUMBER OF SEQ ID NOS: 3484  
/ SOFTWARE: PatentIn version 3.1  
/ SEQ ID NO 2958  
/ LENGTH: 16  
/ TYPE: PRT  
/ ORGANISM: Hepatitis G virus  
US-10-224-999A-2958

Query Match 27.6%; Score 29; DB 4; Length 16;  
Best Local Similarity 80.0%; Pred. No. 2.3e+03;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 8 PGPI 12  
Db 6 PGPIV 10

RESULT 99  
US-10-224-999A-2959

/ Sequence 2959, Application US/10224999A  
/ Publication No. US20030171318A1

```

/ GENERAL INFORMATION:
/ APPLICANT: Myriad Genetics, Inc.
/ APPLICANT: Morham, Scott
/ APPLICANT: Zavitz, Kenton
/ APPLICANT: Hobden, Adrian
/ TITLE OF INVENTION: Composition and Method for Treating Viral Infection
/ FILE REFERENCE: 5004.01
/ CURRENT APPLICATION NUMBER: US/10/224,999A
/ CURRENT FILING DATE: 2003-03-03
/ PRIOR APPLICATION NUMBER: US 60/313,695
/ PRIOR FILING DATE: 2001-08-20
/ NUMBER OF SEQ ID NOS: 3484
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO: 2959
/ LENGTH: 16
/ TYPE: PRT
/ ORGANISM: Hepatitis G virus
US-10-224-999A-2959

```

```

Query Match      27.6%; Score 29; DB 4; Length 16;
Best Local Similarity 80.0%; Pred. No. 2.3e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      8 PGFV 12
      ||||:
Db      5 PGFV 9

```

```

RESULT 100
US-10-224-999A-2960
/ Sequence 2960, Application US/10224999A
/ Publication No. US20030171318A1
/ GENERAL INFORMATION:
/ APPLICANT: Myriad Genetics, Inc.
/ APPLICANT: Morham, Scott
/ APPLICANT: Zavitz, Kenton
/ APPLICANT: Hobden, Adrian
/ TITLE OF INVENTION: Composition and Method for Treating Viral Infection
/ FILE REFERENCE: 5004.01
/ CURRENT APPLICATION NUMBER: US/10/224,999A
/ CURRENT FILING DATE: 2003-03-03
/ PRIOR APPLICATION NUMBER: US 60/313,695
/ PRIOR FILING DATE: 2001-08-20
/ NUMBER OF SEQ ID NOS: 3484
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO: 2960
/ LENGTH: 16
/ TYPE: PRT
/ ORGANISM: Hepatitis G virus
US-10-224-999A-2960

```

```

Query Match      27.6%; Score 29; DB 4; Length 16;
Best Local Similarity 80.0%; Pred. No. 2.3e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      8 PGFV 12
      ||||:
Db      4 PGFV 8

```

Search completed: January 20, 2006, 19:45:40  
 Job time : 74.1154 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 20, 2006, 19:12:21 : Search time 8.07692 Seconds  
(without alignments)  
25.093 Million cell updates/sec

Title: US-09-662-293-4

Perfect score: 105  
Sequence: 1 DPAKMSPPGPIVGEKVLIS 20

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 70606 seqs, 10133881 residues

Total number of hits satisfying chosen parameters: 34662

Minimum DB seq length: 0  
Maximum DB seq length: 20

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database :

Published Applications AA New:\*  
1: /cgn2\_6/prodata/1/pubppa/US08\_NEW\_PUB.pep:\*  
2: /cgn2\_6/prodata/1/pubppa/US06\_NEW\_PUB.pep:\*  
3: /cgn2\_6/prodata/1/pubppa/US07\_NEW\_PUB.pep:\*  
4: /cgn2\_6/prodata/1/pubppa/FCI\_NEW\_PUB.pep:\*  
5: /cgn2\_6/prodata/1/pubppa/US09\_NEW\_PUB.pep:\*  
6: /cgn2\_6/prodata/1/pubppa/US10\_NEW\_PUB.pep:\*  
7: /cgn2\_6/prodata/1/pubppa/US11\_NEW\_PUB.pep:\*  
8: /cgn2\_6/prodata/1/pubppa/US60\_NEW\_PUB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	33	31.4	20	6	US-10-939-890-146 Sequence 146, App
2	32	30.5	20	6	US-10-939-890-170 Sequence 170, App
3	31	29.5	20	6	US-10-623-155-463 Sequence 463, App
4	31	29.5	20	6	US-10-623-155-541 Sequence 541, App
5	29	27.6	20	6	US-10-623-155-413 Sequence 413, App
6	29	27.6	20	6	US-10-623-155-524 Sequence 524, App
7	29	27.6	20	7	US-11-094-142-16 Sequence 16, App
8	28	26.7	15	6	US-10-889-197-25 Sequence 25, App
9	28	26.7	15	6	US-10-839-890-203 Sequence 203, App
10	28	26.7	16	7	US-11-054-515-3003 Sequence 3003, App
11	28	26.7	20	6	US-10-893-584-212 Sequence 212, App
12	27	25.7	15	6	US-10-516-676-1 Sequence 1, App
13	27	25.7	16	7	US-10-532-426-2 Sequence 2, App
14	27	25.7	16	7	US-11-054-515-2153 Sequence 2153, App
15	27	25.7	16	7	US-11-054-515-2780 Sequence 2780, App
16	27	25.7	16	7	US-11-054-515-2783 Sequence 2783, App
17	27	25.7	20	7	US-11-053-100-18 Sequence 18, App
18	26.5	25.2	20	6	US-10-485-788A-598 Sequence 598, App
19	26	24.8	9	7	US-11-178-269-27 Sequence 27, App
20	26	24.8	15	6	US-10-839-890-193 Sequence 193, App
21	26	24.8	17	6	US-10-893-584-102 Sequence 102, App
22	26	24.8	18	6	US-10-842-206-26 Sequence 26, App
23	26	24.8	18	6	US-10-980-459-12 Sequence 12, App
24	26	24.8	19	6	US-10-503-575-131 Sequence 131, App
25	26	24.8	20	6	US-10-997-201A-31 Sequence 31, App

26	26	24.8	20	6	US-10-623-155-532 Sequence 532, App
27	26	24.8	20	6	US-10-623-155-542 Sequence 542, App
28	26	24.8	20	6	US-10-623-155-543 Sequence 543, App
29	26	24.8	8	6	US-10-989-226-81 Sequence 81, App
30	25	23.8	9	7	US-11-053-100-9 Sequence 9, App
31	25	23.8	11	7	US-11-045-024-1467 Sequence 1467, App
32	25	23.8	11	7	US-11-045-024-6285 Sequence 6285, App
33	25	23.8	14	7	US-11-116-144-285 Sequence 285, App
34	25	23.8	16	7	US-11-060-646-5 Sequence 5, App
35	25	23.8	17	7	US-11-193-512-47 Sequence 47, App
36	25	23.8	19	6	US-10-893-584-233 Sequence 233, App
37	25	23.8	20	6	US-10-623-155-414 Sequence 414, App
38	25	23.8	20	6	US-10-623-155-525 Sequence 525, App
39	24.5	23.3	11	7	US-11-105-708-11 Sequence 11, App
40	24	22.9	7	6	US-10-986-501-338 Sequence 338, App
41	24	22.9	9	7	US-11-045-024-1247 Sequence 1247, App
42	24	22.9	9	7	US-11-045-024-8847 Sequence 8847, App
43	24	22.9	10	6	US-10-919-492-35 Sequence 35, App
44	24	22.9	10	7	US-11-045-024-55231 Sequence 55231, App
45	24	22.9	10	7	US-11-129-104-61 Sequence 61, App
46	24	22.9	10	7	US-11-129-104-62 Sequence 62, App
47	24	22.9	14	7	US-11-129-104-7 Sequence 7, App
48	24	22.9	15	6	US-10-866-120-4 Sequence 4, App
49	24	22.9	15	6	US-10-919-492-6 Sequence 6, App
50	24	22.9	15	6	US-10-919-492-13 Sequence 13, App
51	24	22.9	19	6	US-10-503-575-119 Sequence 119, App
52	24	22.9	20	7	US-11-022-562-145 Sequence 145, App
53	24	22.9	20	7	US-11-022-562-146 Sequence 146, App
54	23	21.9	7	6	US-10-485-788A-79 Sequence 79, App
55	23	21.9	8	6	US-10-485-788A-80 Sequence 80, App
56	23	21.9	9	6	US-10-850-635-26 Sequence 26, App
57	23	21.9	9	7	US-11-010-748A-617 Sequence 617, App
58	23	21.9	9	7	US-11-010-748A-618 Sequence 618, App
59	23	21.9	9	7	US-11-010-748A-620 Sequence 620, App
60	23	21.9	9	7	US-11-010-748A-621 Sequence 621, App
61	23	21.9	9	7	US-11-010-748A-625 Sequence 625, App
62	23	21.9	9	7	US-11-010-748A-635 Sequence 635, App
63	23	21.9	9	7	US-11-055-557-28 Sequence 28, App
64	23	21.9	11	7	US-11-033-365-22 Sequence 22, App
65	23	21.9	12	6	US-10-893-584-102 Sequence 102, App
66	23	21.9	13	6	US-10-893-584-198 Sequence 198, App
67	23	21.9	14	6	US-10-746-950C-5 Sequence 5, App
68	23	21.9	15	6	US-10-939-890-200 Sequence 200, App
69	23	21.9	15	6	US-10-939-890-202 Sequence 202, App
70	23	21.9	15	6	US-10-893-584-247 Sequence 247, App
71	23	21.9	15	7	US-11-187-558-3 Sequence 4, App
72	23	21.9	16	6	US-10-919-492-3 Sequence 3, App
73	23	21.9	16	6	US-10-919-492-10 Sequence 10, App
74	23	21.9	16	7	US-11-108-188-42 Sequence 42, App
75	23	21.9	17	6	US-10-880-238-107 Sequence 107, App
76	23	21.9	17	6	US-10-880-238-109 Sequence 109, App
77	23	21.9	17	7	US-11-010-748A-405 Sequence 405, App
78	23	21.9	18	7	US-11-033-033-1324 Sequence 1324, App
79	23	21.9	19	6	US-10-503-575-3224 Sequence 224, App
80	23	21.9	19	6	US-10-503-575-302 Sequence 302, App
81	23	21.9	19	6	US-10-503-575-303 Sequence 303, App
82	23	21.9	20	6	US-10-623-155-533 Sequence 533, App
83	23	21.9	20	7	US-11-106-415-182 Sequence 182, App
84	23	21.9	20	7	US-11-104-189-118 Sequence 118, App
85	22.5	21.4	17	7	US-11-107-029-11 Sequence 11, App
86	22	21.0	8	6	US-10-485-788A-120 Sequence 120, App
87	22	21.0	8	7	US-11-045-024-5161 Sequence 5161, App
88	22	21.0	8	7	US-11-045-024-7282 Sequence 7282, App
89	22	21.0	9	7	US-11-045-024-13708 Sequence 13708, App
90	22	21.0	9	7	US-11-033-033-24 Sequence 24, App
91	22	21.0	9	7	US-11-033-033-292 Sequence 292, App
92	22	21.0	10	7	US-11-045-024-1311 Sequence 1311, App
93	22	21.0	10	7	US-11-045-024-6377 Sequence 6377, App
94	22	21.0	10	7	US-11-045-024-9066 Sequence 9066, App
95	22	21.0	10	7	US-11-045-024-11266 Sequence 11266, App
96	22	21.0	10	7	US-11-208-541-11 Sequence 11, App
97	22	21.0	11	7	US-11-033-365-5 Sequence 5, App
98	22	21.0	11	7	US-11-045-024-3056 Sequence 3056, App

99 22 21.0 11 7 US-11-045-024-5702  
100 22 21.0 11 7 US-11-045-024-9026

Sequence 5702, Ap  
Sequence 9026, Ap

## ALIGNMENTS

## RESULT 1

US-10-939-890-146

Sequence 146, Application US/10939890

Publication No. US20050250700A1

GENERAL INFORMATION:

APPLICANT: Sato, Aaron K.

APPLICANT: Sexton, Daniel J.

APPLICANT: Dransfield, Daniel T.

APPLICANT: Ladner, Robert C.

APPLICANT: Arbogast, Christophe

APPLICANT: Bussat, Philippe

APPLICANT: Fan, Hong

APPLICANT: Khurana, Sudha

APPLICANT: Linder, Karen E.

APPLICANT: Marinelli, Edmund R.

APPLICANT: Nanjappan, Palaniappa

APPLICANT: Nunn, Adrian D.

APPLICANT: Pillai, Radhakrishna

APPLICANT: Pochon, Sibylle

APPLICANT: Ramalingam, Kondareddiar

APPLICANT: Shrivastava, Ajay

APPLICANT: Song, Bo

APPLICANT: Swenson, Rolf E.

APPLICANT: Von Wronski, Mathew A.

TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES

FILE REFERENCE: D0617.70014US00

CURRENT APPLICATION NUMBER: US/10/939,890

CURRENT FILING DATE: 2004-09-13

PRIOR APPLICATION NUMBER: US 10/661,156

PRIOR FILING DATE: 2003-09-11

PRIOR APPLICATION NUMBER: US 10/382,082

PRIOR FILING DATE: 2003-03-03

PRIOR APPLICATION NUMBER: PCT/US03/06731

PRIOR FILING DATE: 2003-03-03

PRIOR APPLICATION NUMBER: US 60/440,411

PRIOR FILING DATE: 2003-01-15

PRIOR APPLICATION NUMBER: US 60/360,851

PRIOR FILING DATE: 2002-03-01

NUMBER OF SEQ ID NOS: 883

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 146

LENGTH: 20

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Library Isolate

US-10-939-890-146

Query Match 31.4% Score 33; DB 6; Length 20;  
Best Local Similarity 58.3%; Pred. No. 18;  
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 8 PPGFVGEQVVL 19

Db 2 PPGFVGEQVVL 13

## RESULT 2

US-10-939-890-170

Sequence 170, Application US/10939890

Publication No. US20050250700A1

GENERAL INFORMATION:

APPLICANT: Sato, Aaron K.

APPLICANT: Sexton, Daniel J.

APPLICANT: Dransfield, Daniel T.

APPLICANT: Ladner, Robert C.

APPLICANT: Arbogast, Christophe  
APPLICANT: Bussat, Philippe  
APPLICANT: Fan, Hong  
APPLICANT: Khurana, Sudha  
APPLICANT: Linder, Karen E.  
APPLICANT: Marinelli, Edmund R.  
APPLICANT: Nanjappan, Palaniappa  
APPLICANT: Nunn, Adrian D.  
APPLICANT: Pillai, Radhakrishna  
APPLICANT: Pochon, Sibylle  
APPLICANT: Ramalingam, Kondareddiar  
APPLICANT: Shrivastava, Ajay  
APPLICANT: Song, Bo  
APPLICANT: Swenson, Rolf E.  
APPLICANT: Von Wronski, Mathew A.  
TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES  
FILE REFERENCE: D0617.70014US00  
CURRENT APPLICATION NUMBER: US/10/939,890  
CURRENT FILING DATE: 2004-09-13  
PRIOR APPLICATION NUMBER: US 10/661,156  
PRIOR FILING DATE: 2003-09-11  
PRIOR APPLICATION NUMBER: US 10/382,082  
PRIOR FILING DATE: 2003-03-03  
PRIOR APPLICATION NUMBER: PCT/US03/06731  
PRIOR FILING DATE: 2003-03-03  
PRIOR APPLICATION NUMBER: US 60/440,411  
PRIOR FILING DATE: 2003-01-15  
PRIOR APPLICATION NUMBER: US 60/360,851  
PRIOR FILING DATE: 2002-03-01  
NUMBER OF SEQ ID NOS: 883  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 170  
LENGTH: 20  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Library Isolate  
US-10-939-890-170

Query Match 30.5% Score 32; DB 6; Length 20;  
Best Local Similarity 50.0%; Pred. No. 25;  
Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 8 PPGFVGEQVVL 19

Db 2 PPGFVGEQVVL 13

RESULT 3

US-10-623-155-463

Sequence 463, Application US/10623155

Publication No. US20050261166A1

GENERAL INFORMATION:

APPLICANT: Wang, Tonglong

APPLICANT: Peckham, David W.

APPLICANT: Retter, Marc W.

APPLICANT: Fanger, Gary R.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

FILE REFERENCE: 210121.455C20

CURRENT APPLICATION NUMBER: US/10/623,155

CURRENT FILING DATE: 2003-07-17

NUMBER OF SEQ ID NOS: 560

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 463

LENGTH: 20

TYPE: PRT

ORGANISM: Homo sapiens

US-10-623-155-463

Query Match 29.5% Score 31; DB 6; Length 20;  
Best Local Similarity 62.5%; Pred. No. 36;  
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;



QY 2 PAKGMRP 9  
| : : :  
Db 9 PTSGMRP 16

## RESULT 4

US-10-623-155-541  
; Sequence 541, Application US/10623155  
; Publication No. US20050261166A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Tongtong  
; APPLICANT: Peckham, David W.  
; APPLICANT: Retter, Marc W.  
; APPLICANT: Fanger, Gary R.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; FILE REFERENCE: 210121.455C20  
; CURRENT APPLICATION NUMBER: US/10/623,155  
; CURRENT FILING DATE: 2003-07-17  
; NUMBER OF SEQ ID NOS: 560  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 541  
; LENGTH: 20  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-623-155-541

Query Match 29.5%; Score 31; DB 6; Length 20;  
Best Local Similarity 62.5%; Pred. No. 36;  
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 PAKGMRP 9  
| : : :  
Db 9 PTSGMRP 16

## RESULT 5

US-10-623-155-413  
; Sequence 413, Application US/10623155  
; Publication No. US20050261166A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Tongtong  
; APPLICANT: Peckham, David W.  
; APPLICANT: Retter, Marc W.  
; APPLICANT: Fanger, Gary R.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; FILE REFERENCE: 210121.455C20  
; CURRENT APPLICATION NUMBER: US/10/623,155  
; CURRENT FILING DATE: 2003-07-17  
; NUMBER OF SEQ ID NOS: 560  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 413  
; LENGTH: 20  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-623-155-413

Query Match 27.6%; Score 29; DB 6; Length 20;  
Best Local Similarity 62.5%; Pred. No. 74;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 10 GFIYGEV 17  
| : : :  
Db 9 GAIIGKEG 16

RESULT 6  
US-10-623-155-524  
; Sequence 524, Application US/10623155  
; Publication No. US20050261166A1  
; GENERAL INFORMATION:

; APPLICANT: Wang, Tongtong  
; APPLICANT: Peckham, David W.  
; APPLICANT: Retter, Marc W.  
; APPLICANT: Fanger, Gary R.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; FILE REFERENCE: 210121.455C20  
; CURRENT APPLICATION NUMBER: US/10/623,155  
; CURRENT FILING DATE: 2003-07-17  
; NUMBER OF SEQ ID NOS: 560  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 524  
; LENGTH: 20  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-623-155-524

Query Match 27.6%; Score 29; DB 6; Length 20;  
Best Local Similarity 62.5%; Pred. No. 74;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 10 GFIYGEV 17  
| : : :  
Db 9 GAIIGKEG 16

## RESULT 7

US-11-094-142-16  
; Sequence 16, Application US/11094142  
; Publication No. US2005026070A1  
; GENERAL INFORMATION:  
; APPLICANT: Cohen, Irun R.  
; APPLICANT: Quintana, Francisco Javier  
; APPLICANT: Domany, Eytan  
; APPLICANT: Blizgur, Gad  
; APPLICANT: Hagedorn, Peter H.  
; TITLE OF INVENTION: ANTIGEN ARRAY AND DIAGNOSTIC USES THEREOF  
; FILE REFERENCE: 29462  
; CURRENT APPLICATION NUMBER: US/11/094,142  
; CURRENT FILING DATE: 2005-03-31  
; NUMBER OF SEQ ID NOS: 47  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 16  
; LENGTH: 20  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic peptide  
US-11-094-142-16

Query Match 27.6%; Score 29; DB 7; Length 20;  
Best Local Similarity 55.6%; Pred. No. 74;  
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 10 GFIYGEV 18  
| : : :  
Db 7 GAVFGEGL 15

RESULT 8  
US-10-889-197-25  
; Sequence 25, Application US/10889197  
; Publication No. US20050271689A1  
; GENERAL INFORMATION:  
; APPLICANT: HUANG, CHUN-MING  
; APPLICANT: ZHANG, JIANFENG  
; APPLICANT: TANG, DE-CHU

; TITLE OF INVENTION: NOVEL TARGETS AND COMPOSITIONS FOR USE IN  
; TITLE OF INVENTION: DECONTAMINATION, IMMUNOPROPHYLAXIS, AND POST-EXPOSURE  
; FILE REFERENCE: 858610-2006.1  
; CURRENT APPLICATION NUMBER: US/10/889,197  
; CURRENT FILING DATE: 2004-07-12

/ PRIOR APPLICATION NUMBER: 60/486,369  
/ PRIOR FILING DATE: 2003-07-11  
/ NUMBER OF SEQ ID NOS: 44  
/ SOFTWARE: PatentIn Ver. 3.2  
/ SEQ ID NO 25  
/ LENGTH: 12  
/ TYPE: PRF  
/ ORGANISM: Bacillus anthracis  
US-10-889-197-25

Query Match 26.7%; Score 28; DB 6; Length 12;  
Best Local Similarity 55.6%; Pred. No. 59;  
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 8 PRGPRVGR 16  
DB 4 PAGFTFGK 12

## RESULT 9

US-10-939-890-203  
/ Sequence 203, Application US/10939890  
/ Publication No. US20050250700A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Sato, Aaron K.  
/ APPLICANT: Sexton, Daniel J.  
/ APPLICANT: Dransfield, Daniel T.  
/ APPLICANT: Ladner, Robert C.  
/ APPLICANT: Arbogast, Christophe  
/ APPLICANT: Bussat, Philippe  
/ APPLICANT: Fan, Hong  
/ APPLICANT: Khurana, Sudha  
/ APPLICANT: Linder, Karen E.  
/ APPLICANT: Marinelli, Edmund R.  
/ APPLICANT: Nanjappa, Palanippa  
/ APPLICANT: Nunn, Adrian D.  
/ APPLICANT: Pillai, Radhakrishna  
/ APPLICANT: Pochon, Sibylle  
/ APPLICANT: Ramalingam, Kondareddi  
/ APPLICANT: Shrivastava, Ajay  
/ APPLICANT: Song, Bo  
/ APPLICANT: Swenson, Rolf E.  
/ APPLICANT: Von Wronski, Mathew A.  
/ TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES  
/ FILE REFERENCE: D0617, 70014US00  
/ CURRENT APPLICATION NUMBER: US/10/939,890  
/ CURRENT FILING DATE: 2004-09-13  
/ PRIOR APPLICATION NUMBER: US 10/661,156  
/ PRIOR FILING DATE: 2003-09-11  
/ PRIOR APPLICATION NUMBER: US 10/382,082  
/ PRIOR FILING DATE: 2003-03-03  
/ PRIOR APPLICATION NUMBER: PCT/US03/06731  
/ PRIOR FILING DATE: 2003-03-03  
/ PRIOR APPLICATION NUMBER: US 60/440,411  
/ PRIOR FILING DATE: 2003-01-15  
/ PRIOR APPLICATION NUMBER: US 60/360,851  
/ PRIOR FILING DATE: 2002-03-01  
/ NUMBER OF SEQ ID NOS: 883  
/ SOFTWARE: FastSeq for Windows Version 4.0  
/ SEQ ID NO 203  
/ LENGTH: 15  
/ TYPE: PRF  
/ ORGANISM: Artificial Sequence  
/ FEATURE:  
/ OTHER INFORMATION: Library Isolate  
US-10-939-890-203

Query Match 26.7%; Score 28; DB 6; Length 15;  
Best Local Similarity 71.4%; Pred. No. 76;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PAKGMP 8  
DB 1 PAKGMP 8

DB 3 PCKGMLP 9

RESULT 10  
US-11-054-515-3003  
/ Sequence 3003, Application US/11054515  
/ Publication No. US20050255532A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Ruben et al.  
/ TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys  
/ FILE REFERENCE: PR523P3  
/ CURRENT APPLICATION NUMBER: US/11/054,515  
/ CURRENT FILING DATE: 2005-02-10  
/ PRIOR APPLICATION NUMBER: 60/543,296  
/ PRIOR FILING DATE: 2004-02-11  
/ PRIOR APPLICATION NUMBER: 60/580,347  
/ PRIOR FILING DATE: 2004-06-18  
/ PRIOR APPLICATION NUMBER: 10/293,418  
/ PRIOR FILING DATE: 2002-11-14  
/ PRIOR APPLICATION NUMBER: 60/331,469  
/ PRIOR FILING DATE: 2001-11-16  
/ PRIOR APPLICATION NUMBER: 60/340,817  
/ PRIOR FILING DATE: 2001-12-19  
/ PRIOR APPLICATION NUMBER: 09/880,748  
/ PRIOR FILING DATE: 2001-06-15  
/ PRIOR APPLICATION NUMBER: 60/293,499  
/ PRIOR FILING DATE: 2001-05-25  
/ PRIOR APPLICATION NUMBER: 60/277,379  
/ PRIOR FILING DATE: 2001-03-21  
/ PRIOR APPLICATION NUMBER: 60/276,248  
/ PRIOR FILING DATE: 2001-03-16  
/ PRIOR APPLICATION NUMBER: 60/240,816  
/ PRIOR FILING DATE: 2000-10-17  
/ Remaining Prior Application data removed - See File Wrapper or PALM.  
/ NUMBER OF SEQ ID NOS: 3247  
/ SEQ ID NO 3003  
/ LENGTH: 16  
/ TYPE: PRF  
/ ORGANISM: Homo sapiens  
US-11-054-515-3003

Query Match 26.7%; Score 28; DB 7; Length 16;  
Best Local Similarity 54.5%; Pred. No. 82;  
Matches 6; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 DPAKMSPPGF 11  
DB 4 DPLTGYSLDGF 14

RESULT 11  
US-10-893-584-212  
/ Sequence 212, Application US/10893584  
/ Publication No. US20050272048A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Borgford, Thor  
/ APPLICANT: Braun, Curtis  
/ APPLICANT: Purac, Adam  
/ APPLICANT: Stoll, Dominik  
/ TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,  
/ FILE REFERENCE: 10447-025  
/ CURRENT APPLICATION NUMBER: US/10/893,584  
/ CURRENT FILING DATE: 2004-07-19  
/ PRIOR APPLICATION NUMBER: US 09/551,151  
/ PRIOR FILING DATE: 2000-04-14  
/ PRIOR APPLICATION NUMBER: US 09/403,752  
/ PRIOR FILING DATE: 1999-10-29  
/ PRIOR APPLICATION NUMBER: US 10/089,058  
/ PRIOR FILING DATE: 2000-10-04  
/ NUMBER OF SEQ ID NOS: 274  
/ SOFTWARE: PatentIn Ver. 2.0  
/ SEQ ID NO 212

/ LENGTH: 20  
/ TYPE: PRT  
/ ORGANISM: E. coli  
US-10-893-584-212

Query Match 26.7%; Score 28; DB 6; Length 20;  
Best Local Similarity 38.5%; Pred. No. 1.1e+02;  
Matches 5; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 2 PAKGMSPPGTVG 14  
DB 2 GPRVGGPGRVVG 14

## RESULT 12

US-10-516-676-1  
/ Sequence 1, Application US/10516676  
/ Publication No. US20050244393A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Philippart, Pierre  
/ APPLICANT: Brassens, Michele  
/ TITLE OF INVENTION: SEALANT OR TISSUE GENERATING PRODUCT  
/ FILE REFERENCE: 232037  
/ CURRENT APPLICATION NUMBER: US/10/516,676  
/ PRIOR FILING DATE: 2004-12-03  
/ PRIOR APPLICATION NUMBER: 10/176,401  
/ PRIOR FILING DATE: 2002-06-21  
/ NUMBER OF SEQ ID NOS: 1  
/ SOFTWARE: PatentIn version 3.2  
/ SEQ ID NO 1  
/ LENGTH: 15  
/ TYPE: PRT  
/ ORGANISM: Artificial Sequence  
/ FEATURE:  
/ OTHER INFORMATION: Synthesized  
/ FEATURE:  
/ OTHER INFORMATION: PEPGEN P15 (TM) SYNTHETIC PEPTIDE  
US-10-516-676-1

Query Match 25.7%; Score 27; DB 6; Length 15;  
Best Local Similarity 40.0%; Pred. No. 1.1e+02;  
Matches 6; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 5 GMSPPGTVGSEGV 19  
DB 1 GTPGPGIAGQGRGV 15

## RESULT 13

US-10-532-426-2  
/ Sequence 2, Application US/10532426  
/ Publication No. US2006009516A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Rosenberg, Lawrence  
/ TITLE OF INVENTION: USE OF INGP FOR REVERSING DIABETES  
/ FILE REFERENCE: 1912-0308PUS1  
/ CURRENT APPLICATION NUMBER: US/10/532,426  
/ PRIOR FILING DATE: 2005-04-22  
/ PRIOR APPLICATION NUMBER: US 60/420,677  
/ PRIOR FILING DATE: 2002-10-24  
/ NUMBER OF SEQ ID NOS: 2  
/ SOFTWARE: FastSeq for Windows Version 4.0  
/ SEQ ID NO 2  
/ LENGTH: 15  
/ TYPE: PRT  
/ ORGANISM: Artificial Sequence  
/ FEATURE:  
/ OTHER INFORMATION: INGP peptide  
US-10-532-426-2

Query Match 25.7%; Score 27; DB 6; Length 15;  
Best Local Similarity 50.0%; Pred. No. 1.1e+02;  
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 DPAKMSPPG 10  
DB 4 DPLTGYSPDGF 13

## RESULT 14

US-11-054-515-2153  
/ Sequence 2153, Application US/11054515  
/ Publication No. US2005025532A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Ruben et al.  
/ TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys  
/ FILE REFERENCE: PR523P3  
/ CURRENT APPLICATION NUMBER: US/11/054,515  
/ PRIOR FILING DATE: 2005-02-10  
/ PRIOR APPLICATION NUMBER: 60/543,296  
/ PRIOR FILING DATE: 2004-02-11  
/ PRIOR APPLICATION NUMBER: 60/580,347  
/ PRIOR FILING DATE: 2004-06-18  
/ PRIOR APPLICATION NUMBER: 10/293,418  
/ PRIOR FILING DATE: 2002-11-14  
/ PRIOR APPLICATION NUMBER: 60/331,469  
/ PRIOR FILING DATE: 2001-11-16  
/ PRIOR APPLICATION NUMBER: 60/340,817  
/ PRIOR FILING DATE: 2001-12-19  
/ PRIOR APPLICATION NUMBER: 09/880,748  
/ PRIOR FILING DATE: 2001-06-15  
/ PRIOR APPLICATION NUMBER: 60/293,499  
/ PRIOR FILING DATE: 2001-05-25  
/ PRIOR APPLICATION NUMBER: 60/277,379  
/ PRIOR FILING DATE: 2001-03-21  
/ PRIOR APPLICATION NUMBER: 60/276,248  
/ PRIOR FILING DATE: 2001-03-16  
/ PRIOR APPLICATION NUMBER: 60/240,816  
/ PRIOR FILING DATE: 2000-10-17  
/ Remaining Prior Application data removed - See File Wrapper or PALM.  
/ NUMBER OF SEQ ID NOS: 3247  
/ SEQ ID NO 2153  
/ LENGTH: 16  
/ TYPE: PRT  
/ ORGANISM: Homo sapiens  
US-11-054-515-2153

Query Match 25.7%; Score 27; DB 7; Length 16;  
Best Local Similarity 54.5%; Pred. No. 1.2e+02;  
Matches 6; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 DPAKMSPPGF 11  
DB 4 DPLTGYSPDGF 14

## RESULT 15

US-11-054-515-2780  
/ Sequence 2780, Application US/11054515  
/ Publication No. US2005025532A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Ruben et al.  
/ TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys  
/ FILE REFERENCE: PR523P3  
/ CURRENT APPLICATION NUMBER: US/11/054,515  
/ PRIOR FILING DATE: 2005-02-10  
/ PRIOR APPLICATION NUMBER: 60/543,296  
/ PRIOR FILING DATE: 2004-02-11  
/ PRIOR APPLICATION NUMBER: 60/580,347  
/ PRIOR FILING DATE: 2004-06-18  
/ PRIOR APPLICATION NUMBER: 10/293,418  
/ PRIOR FILING DATE: 2002-11-14  
/ PRIOR APPLICATION NUMBER: 60/331,469  
/ PRIOR FILING DATE: 2001-11-16  
/ PRIOR APPLICATION NUMBER: 60/340,817  
/ PRIOR FILING DATE: 2001-12-19

```
/ PRIOR APPLICATION NUMBER: 09/880,748
/ PRIOR FILING DATE: 2001-06-15
/ PRIOR APPLICATION NUMBER: 60/293,499
/ PRIOR FILING DATE: 2001-05-25
/ PRIOR APPLICATION NUMBER: 60/277,379
/ PRIOR FILING DATE: 2001-03-21
/ PRIOR APPLICATION NUMBER: 60/276,248
/ PRIOR FILING DATE: 2001-03-16
/ PRIOR APPLICATION NUMBER: 60/240,816
/ PRIOR FILING DATE: 2000-10-17
/ Remaining Prior Application data removed - See file Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 3247
/ SEQ ID NO 2780
/ LENGTH: 16
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-054-515-2780
```

```
Query Match      25.7% Score 27, DB 7, Length 16;
Best Local Similarity 54.5% Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
```

```
QY 1 DPAKMSPPGF 11
DB 4 DPLTGVSPDGF 14
```

```
RESULT 16
US-11-054-515-2783
```

```
/ Sequence 2783, Application US/11054515
/ Publication No. US20050255532A1
/ GENERAL INFORMATION:
/ APPLICANT: Ruben et al.
/ TITLE OF INVENTION: Antibodies that Immunospecifically Bind BlyS
/ FILE REFERENCE: PF523P3
/ CURRENT APPLICATION NUMBER: US/11/054,515
/ PRIOR FILING DATE: 2005-02-10
/ PRIOR APPLICATION NUMBER: 60/543,296
/ PRIOR FILING DATE: 2004-02-11
/ PRIOR APPLICATION NUMBER: 60/580,347
/ PRIOR FILING DATE: 2004-06-18
/ PRIOR APPLICATION NUMBER: 10/293,418
/ PRIOR FILING DATE: 2002-11-14
/ PRIOR APPLICATION NUMBER: 60/331,469
/ PRIOR FILING DATE: 2001-11-16
/ PRIOR APPLICATION NUMBER: 60/340,817
/ PRIOR FILING DATE: 2001-12-19
/ PRIOR APPLICATION NUMBER: 09/880,748
/ PRIOR FILING DATE: 2001-06-15
/ PRIOR APPLICATION NUMBER: 60/293,499
/ PRIOR FILING DATE: 2001-05-25
/ PRIOR APPLICATION NUMBER: 60/277,379
/ PRIOR FILING DATE: 2001-03-21
/ PRIOR APPLICATION NUMBER: 60/276,248
/ PRIOR FILING DATE: 2001-03-16
/ PRIOR APPLICATION NUMBER: 60/240,816
/ Remaining Prior Application data removed - See file Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 3247
/ SEQ ID NO 2783
/ LENGTH: 16
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-054-515-2783
```

```
Query Match      25.7% Score 27, DB 7, Length 16;
Best Local Similarity 54.5% Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
```

```
QY 1 DPAKMSPPGF 11
DB 4 DPLTGVSPDGF 14
```

```
RESULT 17
US-11-053-100-18
/ Sequence 18, Application US/11053100
/ Publication No. US20050255554A1
/ GENERAL INFORMATION:
/ APPLICANT: CHILKOTI, Ashutosh
/ TITLE OF INVENTION: FUSION PEPTIDES ISOLATABLE BY PHASE TRANSITION
/ FILE REFERENCE: 4176-101 CIP
/ CURRENT APPLICATION NUMBER: US/11/053,100
/ PRIOR FILING DATE: 2005-02-08
/ PRIOR APPLICATION NUMBER: US 09/812,382
/ PRIOR FILING DATE: 2001-03-20
/ PRIOR APPLICATION NUMBER: US 60/190,659
/ PRIOR FILING DATE: 2000-03-20
/ NUMBER OF SEQ ID NOS: 58
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 18
/ LENGTH: 20
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ NAME/KEY: REPEAT
/ LOCATION: (1)..(20)
/ OTHER INFORMATION: BLP1 [K1V2P1-4]
US-11-053-100-18
```

```
Query Match      25.7% Score 27, DB 7, Length 20;
Best Local Similarity 52.9% Pred. No. 1.5e+02;
Matches 9; Conservative 1; Mismatches 3; Indels 4; Gaps 2;
```

```
QY 2 PAKGSPGFVGEKV 18
DB 2 PGKV--PG--VGVPDV 14
```

```
RESULT 18
US-10-485-788A-598
/ Sequence 598, Application US/10485788A
/ Publication No. US20050282743A1
/ GENERAL INFORMATION:
/ APPLICANT: Lu, Peter S.
/ APPLICANT: Rabinowitz, Joshua D.
/ APPLICANT: Carrick, Deanna Marie
/ APPLICANT: Artbor Vita Corporation
/ TITLE OF INVENTION: Molecular Interactions in Cells
/ FILE REFERENCE: 20054-003320US
/ CURRENT APPLICATION NUMBER: US/10/485,788A
/ PRIOR FILING DATE: 2004-02-03
/ PRIOR APPLICATION NUMBER: US 60/309,841
/ PRIOR FILING DATE: 2001-08-03
/ PRIOR APPLICATION NUMBER: US 60/360,061
/ PRIOR FILING DATE: 2002-02-25
/ PRIOR APPLICATION NUMBER: WO PCT/US02/24655
/ PRIOR FILING DATE: 2002-08-02
/ NUMBER OF SEQ ID NOS: 841
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 598
/ LENGTH: 20
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-485-788A-598
```

```
Query Match      25.2% Score 26.5, DB 6, Length 20;
Best Local Similarity 66.7% Pred. No. 1.8e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 1; Gaps 1;
```

```
QY 1 DPAKMSPP 9
DB 10 DPGS-MSP 17
```

```

RESULT 19
US-11-178-269-27
; Sequence 27, Application US/11178269
; Publication No. US20050272661A1
; GENERAL INFORMATION:
; APPLICANT: Richeleau, Elliott
; APPLICANT: Cusack, Bernadette Marie
; APPLICANT: Pang, Yuan-Ping
; APPLICANT: McCormick, Daniel J.
; APPLICANT: Faug, Abdul
; APPLICANT: Tyler, Beth Marie
; APPLICANT: Boules, Mona
; TITLE OF INVENTION: NEO-TRYPTOPHAN
; FILE REFERENCE: 07039/141001
; CURRENT APPLICATION NUMBER: US/11/178,269
; CURRENT FILING DATE: 2005-07-08
; PRIOR APPLICATION NUMBER: US/10/858,226
; PRIOR FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: US/10/265,099
; PRIOR FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: US/09/755,638
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: 09/289,693
; PRIOR FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/098,119
; PRIOR FILING DATE: 1998-08-27
; PRIOR APPLICATION NUMBER: US 60/092,195
; PRIOR FILING DATE: 1998-07-09
; PRIOR APPLICATION NUMBER: US 60/081,356
; PRIOR FILING DATE: 1998-04-10
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-11-178-269-27

Query Match          24.8%; Score 26; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 5.5e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 PPGF 11
Db      2 PPGF 5

RESULT 20
US-10-939-890-193
; Sequence 193, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussert, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen B.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappan, Palaniasappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondaredadar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo

```

```

; APPLICANT: Swenson, Rolf B.
; APPLICANT: Von Wronski, Mathew A.
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
; FILE REFERENCE: D0617.70014US00
; CURRENT APPLICATION NUMBER: US/10/939,890
; CURRENT FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: US 10/661,156
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 10/382,082
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 893
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 193
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Library Isolate
US-10-939-890-193

Query Match          24.8%; Score 26; DB 6; Length 15;
Best Local Similarity 62.5%; Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 DPAKMS 8
Db      2 DPAKMS 9

RESULT 21
US-10-893-584-240
; Sequence 240, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
; APPLICANT: Borgford, Thor
; APPLICANT: Braun, Curtis
; APPLICANT: Purac, Admir
; APPLICANT: Stoll, Dominik
; TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
; FILE REFERENCE: 10447-025
; CURRENT APPLICATION NUMBER: US/10/893,584
; CURRENT FILING DATE: 2004-07-19
; PRIOR APPLICATION NUMBER: US 09/551,151
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US 09/403,752
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 10/089,058
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 240
; LENGTH: 17
; TYPE: PRT
; ORGANISM: E. coli
US-10-893-584-240

Query Match          24.8%; Score 26; DB 6; Length 17;
Best Local Similarity 45.5%; Pred. No. 1.8e+02;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY      9 PGFVGBSGVL 19
Db      4 PGFVGBSGVL 14

RESULT 22

```

US-10-842-206-26  
; Sequence 26, Application US/10842206  
; Publication No. US20050256039A1  
; GENERAL INFORMATION:  
; APPLICANT: Peterson, Jeffrey D  
; APPLICANT: Sciore, Paul J  
; TITLE OF INVENTION: NOVEL FIBROBLAST GROWTH FACTORS AND METHODS OF USE THEREOF  
; FILE REFERENCE: Cura 570A  
; CURRENT APPLICATION NUMBER: US/10/842,206  
; CURRENT FILING DATE: 2004-05-10  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: CuraSeqList version 0.1  
; SEQ ID NO 26  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-842-206-26

Query Match 24.8%; Score 26; DB 6; Length 18;  
Best Local Similarity 55.6%; Pred. No. 1.9e+02;  
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 10 GFVGBEGV 18  
||: ||:  
Db 9 GFLGGLEGL 17

## RESULT 23

US-10-980-459-12  
; Sequence 12, Application US/10980459  
; Publication No. US20050256042A1  
; GENERAL INFORMATION:  
; APPLICANT: Alvarez, Enrique  
; APPLICANT: Chilikuru, Rajeev A.  
; APPLICANT: Jeffers, Michael E.  
; APPLICANT: Larocheille, William J.  
; APPLICANT: Lichenstein, Henri  
; APPLICANT: Namdev, Pradyumna Kumar  
; APPLICANT: Valac, Pascal  
; APPLICANT: Yim, Zachary  
; APPLICANT: Hahne, William  
; TITLE OF INVENTION: Methods of Preventing and Treating Alimentary Mucositis  
; FILE REFERENCE: Cura-57 AM  
; CURRENT APPLICATION NUMBER: US/10/980,459  
; CURRENT FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: 10/435,087  
; PRIOR FILING DATE: 2003-5-9  
; PRIOR APPLICATION NUMBER: 10/842,179  
; PRIOR FILING DATE: 2004-5-10  
; PRIOR APPLICATION NUMBER: 60/541,728  
; PRIOR FILING DATE: 2004-2-4  
; PRIOR APPLICATION NUMBER: 60/545,278  
; PRIOR FILING DATE: 2004-2-18  
; PRIOR APPLICATION NUMBER: 60/\_\_\_\_\_  
; NUMBER OF SEQ ID NOS: 41  
; SOFTWARE: CuraSeqList version 0.1  
; SEQ ID NO 12  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-980-459-12

Query Match 24.8%; Score 26; DB 6; Length 18;  
Best Local Similarity 55.6%; Pred. No. 1.9e+02;  
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 10 GFVGBEGV 18  
||: ||:  
Db 9 GFLGGLEGL 17

## RESULT 24

US-10-503-575-131  
; Sequence 131, Application US/10503575  
; Publication No. US20050244823A1  
; GENERAL INFORMATION:  
; APPLICANT: Drijfhout, Jan Mouter  
; APPLICANT: van Veele, Petrus Antonius  
; APPLICANT: Koning, Frits  
; TITLE OF INVENTION: NOVEL EPITOPES FOR CELIAC DISEASE AND AUTOIMMUNE DISORDERS, METHOD  
; FILE REFERENCE: 2799/72843-PCT-US  
; CURRENT APPLICATION NUMBER: US/10/503,575  
; CURRENT FILING DATE: 2004-08-04  
; PRIOR APPLICATION NUMBER: PCT/NL03/00077  
; PRIOR FILING DATE: 2003-02-04  
; PRIOR APPLICATION NUMBER: EP 02075456.0  
; PRIOR FILING DATE: 2002-02-04  
; NUMBER OF SEQ ID NOS: 340  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 131  
; LENGTH: 19  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-503-575-131

Query Match 24.8%; Score 26; DB 6; Length 19;  
Best Local Similarity 35.7%; Pred. No. 2e+02;  
Matches 5; Conservative 4; Mismatches 3; Indels 2; Gaps 1;

Qy 8 PPG--FVGBEGVL 19  
||| : ||:  
Db 1 PPGFGGLAGRGIV 14

RESULT 25  
US-10-997-201A-31  
; Sequence 31, Application US/10997201A  
; Publication No. US20050249739A1  
; GENERAL INFORMATION:  
; APPLICANT: Marasco, Wayne  
; APPLICANT: Sul, Jianhua  
; TITLE OF INVENTION: Antibodies Against SARS-CoV and Methods of Use Thereof  
; FILE REFERENCE: 20363-026  
; CURRENT APPLICATION NUMBER: US/10/997,201A  
; CURRENT FILING DATE: 2004-11-24  
; PRIOR APPLICATION NUMBER: 60/524,840  
; PRIOR FILING DATE: 2003-11-25  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 31  
; LENGTH: 20  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-997-201A-31

Query Match 24.8%; Score 26; DB 6; Length 20;  
Best Local Similarity 50.0%; Pred. No. 2.1e+02;  
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 6 MSPPGFVIVE 15  
: ||| ||  
Db 9 LGPPGPGPGE 18

RESULT 26  
US-10-623-155-532  
; Sequence 532, Application US/10623155  
; Publication No. US20050261166A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Tongrong  
; APPLICANT: Peckham, David W.  
; APPLICANT: Retter, Marc W.  
; APPLICANT: Fanger, Gary R.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

/ TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER  
/ FILE REFERENCE: 210121.455C20  
/ CURRENT APPLICATION NUMBER: US/10/623,155  
/ CURRENT FILING DATE: 2003-07-17  
/ NUMBER OF SEQ ID NOS: 560  
/ SOFTWARE: PaetSeq for Windows Version 4.0  
/ SEQ ID NO 532  
/ LENGTH: 20  
/ TYPE: PRT  
/ ORGANISM: Homo sapiens  
US-10-623-155-532

Query Match 24.8%; Score 26; DB 6; Length 20;  
Best Local Similarity 50.0%; Pred. No. 2.1e+02;  
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 10 GRIVSEEG 17  
| :|:|  
Db 10 GRIGKEG 17

RESULT 27  
US-10-623-155-542  
/ Sequence 542, Application US/10623155  
/ Publication No. US20050261166A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Wang, Tongtong  
/ APPLICANT: Peckham, David W.  
/ APPLICANT: Retter, Marc W.  
/ APPLICANT: Fanger, Gary R.  
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
/ FILE REFERENCE: 210121.455C20  
/ CURRENT APPLICATION NUMBER: US/10/623,155  
/ CURRENT FILING DATE: 2003-07-17  
/ NUMBER OF SEQ ID NOS: 560  
/ SOFTWARE: PaetSeq for Windows Version 4.0  
/ SEQ ID NO 542  
/ LENGTH: 20  
/ TYPE: PRT  
/ ORGANISM: Homo sapiens  
US-10-623-155-542

Query Match 24.8%; Score 26; DB 6; Length 20;  
Best Local Similarity 50.0%; Pred. No. 2.1e+02;  
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 PAKGMP 9  
| :|:|  
Db 10 PPSAMTPP 17

RESULT 28  
US-10-623-155-545  
/ Sequence 545, Application US/10623155  
/ Publication No. US20050261166A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Wang, Tongtong  
/ APPLICANT: Peckham, David W.  
/ APPLICANT: Retter, Marc W.  
/ APPLICANT: Fanger, Gary R.  
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
/ FILE REFERENCE: 210121.455C20  
/ CURRENT APPLICATION NUMBER: US/10/623,155  
/ CURRENT FILING DATE: 2003-07-17  
/ NUMBER OF SEQ ID NOS: 560  
/ SOFTWARE: PaetSeq for Windows Version 4.0  
/ SEQ ID NO 545  
/ LENGTH: 20  
/ TYPE: PRT  
/ ORGANISM: Homo sapiens  
US-10-623-155-545

Query Match 24.8%; Score 26; DB 6; Length 20;  
Best Local Similarity 50.0%; Pred. No. 2.1e+02;  
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 10 GRIVSEEG 17  
| :|:|  
Db 9 GRIGKEG 16

RESULT 29  
US-10-989-226-81  
/ Sequence 81, Application US/10989226  
/ Publication No. US20050255491A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Lee, Frank D.  
/ APPLICANT: Meng, Xun  
/ APPLICANT: Afeyan, Noubar B.  
/ APPLICANT: Gordon, Neal F.  
/ TITLE OF INVENTION: SMALL MOLECULE AND PEPTIDE ARRAYS AND  
/ FILE REFERENCE: EPTM-P01-005  
/ CURRENT APPLICATION NUMBER: US/10/989,226  
/ CURRENT FILING DATE: 2004-11-15  
/ PRIOR APPLICATION NUMBER: US 60/519,530  
/ PRIOR FILING DATE: 2003-11-13  
/ PRIOR APPLICATION NUMBER: US 60/532,687  
/ PRIOR FILING DATE: 2003-12-24  
/ NUMBER OF SEQ ID NOS: 84  
/ SOFTWARE: PaetSeq for Windows Version 4.0  
/ SEQ ID NO 81  
/ LENGTH: 8  
/ TYPE: PRT  
/ ORGANISM: Homo sapiens  
US-10-989-226-81

Query Match 23.8%; Score 25; DB 6; Length 8;  
Best Local Similarity 80.0%; Pred. No. 5.5e+04;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 MSPPG 10  
| :|:|  
Db 4 VSPPG 8

RESULT 30  
US-11-053-100-9  
/ Sequence 9, Application US/11053100  
/ Publication No. US20050255554A1  
/ GENERAL INFORMATION:  
/ APPLICANT: CHILKOTI, Ashutosh  
/ TITLE OF INVENTION: FUSION PEPTIDES ISOLATABL BY PHASE TRANSITION  
/ FILE REFERENCE: 4176-101 CIP  
/ CURRENT APPLICATION NUMBER: US/11/053,100  
/ CURRENT FILING DATE: 2005-02-08  
/ PRIOR APPLICATION NUMBER: US 09/812,382  
/ PRIOR FILING DATE: 2001-03-20  
/ PRIOR APPLICATION NUMBER: US 60/190,659  
/ PRIOR FILING DATE: 2000-03-20  
/ NUMBER OF SEQ ID NOS: 58  
/ SOFTWARE: PatentIn version 3.3  
/ SEQ ID NO 9  
/ LENGTH: 9  
/ TYPE: PRT  
/ ORGANISM: Artificial  
/ FEATURE:  
/ OTHER INFORMATION: Synthetic Construct  
US-11-053-100-9

Query Match 23.8%; Score 25; DB 7; Length 9;  
Best Local Similarity 83.3%; Pred. No. 5.5e+04;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
QY          9 PGRVIG 14
|||
DB          2 PGRVIG 7

RESULT 31
US-11-045-024-1467
; Sequence 1467, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Celis, Esben
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: BiImmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; PRIOR FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1467
; LENGTH: 11
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-1467

Query Match          23.8%; Score 25; DB 7; Length 11;
Best Local Similarity 45.5%; Pred. No. 1.6e+02;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
```

```
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; PRIOR FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6285
; LENGTH: 11
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-6285

Query Match          23.8%; Score 25; DB 7; Length 11;
Best Local Similarity 45.5%; Pred. No. 1.6e+02;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
```

```
QY          2 PAKGSPPGFI 12
|||
DB          1 PAKPTAPPAPFI 11

RESULT 32
US-11-045-024-6285
; Sequence 6285, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Celis, Esben
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: BiImmune Inc.
US-11-045-024-6285

Query Match          23.8%; Score 25; DB 7; Length 11;
Best Local Similarity 45.5%; Pred. No. 1.6e+02;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
```

```
RESULT 33
US-11-116-144-285
; Sequence 285, Application US/11116144
; Publication No. US20050277181A1
; GENERAL INFORMATION:
; APPLICANT: BERTHET, FRANCOIS XAVIER
; APPLICANT: CASADEVAL, FRANCESC VAYREDA
; APPLICANT: SANZ MARIA, MARIA CRUZ
; APPLICANT: GARCIA, TERESA LLOP
; APPLICANT: OLE, ANGELS MOR
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETECTING PATHOGEN
; TITLE OF INVENTION: INFECTION
; FILE REFERENCE: INT-084
; CURRENT APPLICATION NUMBER: US/11/116,144
; PRIOR FILING DATE: 2005-04-27
; PRIOR APPLICATION NUMBER: PCT/ES04/000581
; PRIOR FILING DATE: 2004-12-23
; PRIOR APPLICATION NUMBER: EP 03380307.3
; PRIOR FILING DATE: 2003-12-23
; NUMBER OF SEQ ID NOS: 301
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 285
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Trypanosoma cruzi
US-11-116-144-285

Query Match          23.8%; Score 25; DB 7; Length 14;
Best Local Similarity 40.0%; Pred. No. 2e+02;
Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
```



RESULT 34  
US-11-060-646-5  
Sequence 5, Application US/11060646  
Publication No. US2005025555A1  
GENERAL INFORMATION:  
APPLICANT: Johns, Terrence Grant  
APPLICANT: Scott, Andrew Mark  
APPLICANT: Burgess, Anthony Wilks  
APPLICANT: Old, Lloyd J.  
APPLICANT: Adams, Timothy E.  
APPLICANT: Wiltup, K. Dane  
APPLICANT: Chao, Ginger  
TITLE OF INVENTION: EGF Receptor Epitope Peptides and Uses  
TITLE OF INVENTION: Theretof  
FILE REFERENCE: 2332-1-011N  
CURRENT APPLICATION NUMBER: US/11/060,646  
CURRENT FILING DATE: 2005-02-17  
PRIOR APPLICATION NUMBER: 60/546,602  
PRIOR FILING DATE: 2004-02-20  
PRIOR APPLICATION NUMBER: 60/584,623  
PRIOR FILING DATE: 2004-07-01  
NUMBER OF SEQ ID NOS: 17  
SOFTWARE: PatsSeq for Windows Version 4.0  
SEQ ID NO 5  
LENGTH: 16  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: epitope peptide  
US-11-060-646-5

Query Match 23.8%; Score 25; DB 7; Length 16;  
Best Local Similarity 45.8%; Pred. No. 2.4e+02;  
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
QY 8 PGPVGEBCV 18  
DB 3 PDSYEVBCDV 13

RESULT 35  
US-11-193-512-47  
Sequence 47, Application US/11193512  
Publication No. US20050272918A1  
GENERAL INFORMATION:  
APPLICANT: KOIKE, Masaomi  
FURUYA, Akiho  
NAKAMURA, Kazuyasu  
IIDA, Akihiko  
ANAZAWA, Hideharu  
HANAI, Nobuo  
TAKATSU, Kiyoshi  
TITLE OF INVENTION: Antibody Against Human Interleukin-5  
Receptor Alpha Chain  
NUMBER OF SEQUENCES: 106  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennile & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: PatsSeq Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/11/193,512  
FILING DATE: 01-Aug-2005  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/10/283,349  
FILING DATE: 29-Oct-2002  
APPLICATION NUMBER: US/08/836,561  
FILING DATE: 09-MAY-1997  
APPLICATION NUMBER: JP 232384/95  
FILING DATE: 11-SEP-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Lawrence, III, Stanton T  
REGISTRATION NUMBER: 25,736  
REFERENCE/DOCKET NUMBER: 7005-115-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-790-9090  
TELEFAX: 212-869-9741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 47:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 47:  
US-11-193-512-47

Query Match 23.8%; Score 25; DB 7; Length 17;  
Best Local Similarity 53.8%; Pred. No. 2.5e+02;  
Matches 7; Conservative 0; Mismatches 4; Indels 2; Gaps 1;  
QY 1 DPAKG--MSPGCF 11  
DB 3 DPANGTKSDPKF 15

RESULT 36  
US-10-893-584-233  
Sequence 233, Application US/10893584  
Publication No. US20050272048A1  
GENERAL INFORMATION:  
APPLICANT: Borgford, Thor  
APPLICANT: Braun, Curtis  
APPLICANT: Purac, Admit  
APPLICANT: Scoll, Dominik  
TITLE OF INVENTION: Richin-Like Toxin Variants for Treatment of Cancer,  
Vital or Parasitic Infections  
FILE REFERENCE: 10447-025  
CURRENT APPLICATION NUMBER: US/10/893,584  
CURRENT FILING DATE: 2004-07-19  
PRIOR APPLICATION NUMBER: US 09/551,151  
PRIOR FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: US 09/403,752  
PRIOR FILING DATE: 1999-10-29  
PRIOR APPLICATION NUMBER: US 10/089,058  
PRIOR FILING DATE: 2000-10-04  
NUMBER OF SEQ ID NOS: 274  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 233  
LENGTH: 19  
TYPE: PRT  
ORGANISM: E. coli  
US-10-893-584-233

Query Match 23.8%; Score 25; DB 6; Length 19;  
Best Local Similarity 55.6%; Pred. No. 2.9e+02;  
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 9 PGPVGEBCV 17  
DB 5 PGRVGGG 13

RESULT 37  
US-10-623-155-414  
Sequence 414, Application US/10623155

```
/ Publication No. US20050261166A1
/ GENERAL INFORMATION:
/ APPLICANT: Wang, Tongtong
/ APPLICANT: Peckham, David W.
/ APPLICANT: Retter, Marc W.
/ APPLICANT: Fanger, Gary R.
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
/ FILE REFERENCE: 210121.455C20
/ CURRENT APPLICATION NUMBER: US/10/623,155
/ CURRENT FILING DATE: 2003-07-17
/ NUMBER OF SEQ ID NOS: 560
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 414
/ LENGTH: 20
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-623-155-414

Query Match      23.8%; Score 25; DB 6; Length 20;
Best Local Similarity 66.7%; Pred. No. 3e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      12 IVGEG 17
|:|:|
Db      1 IIGKEG 6

RESULT 38
US-10-623-155-525
/ Sequence 525, Application US/10623155
/ Publication No. US20050261166A1
/ GENERAL INFORMATION:
/ APPLICANT: Wang, Tongtong
/ APPLICANT: Peckham, David W.
/ APPLICANT: Retter, Marc W.
/ APPLICANT: Fanger, Gary R.
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
/ FILE REFERENCE: 210121.455C20
/ CURRENT APPLICATION NUMBER: US/10/623,155
/ CURRENT FILING DATE: 2003-07-17
/ NUMBER OF SEQ ID NOS: 560
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 525
/ LENGTH: 20
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-623-155-525

Query Match      23.8%; Score 25; DB 6; Length 20;
Best Local Similarity 66.7%; Pred. No. 3e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      12 IVGEG 17
|:|:|
Db      1 IIGKEG 6

RESULT 39
US-11-105-708-11
/ Sequence 11, Application US/11105708
/ Publication No. US20050261821A1
/ GENERAL INFORMATION:
/ APPLICANT: Pernaascti, Flavia
/ APPLICANT: Freimark, Bruce
/ APPLICANT: Van Egps, Dennis
/ APPLICANT: Brooks, Peter C
/ TITLE OF INVENTION: Method and Composition for Angiogenesis Inhibition
/ FILE REFERENCE: 30797-704.501
/ CURRENT APPLICATION NUMBER: US/11/105, 708
/ CURRENT FILING DATE: 2005-04-13
/ PRIOR APPLICATION NUMBER: 09/478, 977
```

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/ PRIOR FILING DATE: 2000-01-06
/ PRIOR APPLICATION NUMBER: 60/152,496
/ PRIOR FILING DATE: 1999-09-02
/ PRIOR APPLICATION NUMBER: 60/143,534
/ PRIOR FILING DATE: 1999-09-02
/ PRIOR APPLICATION NUMBER: 60/114,878
/ PRIOR FILING DATE: 1999-01-06
/ PRIOR APPLICATION NUMBER: 60/114,877
/ PRIOR FILING DATE: 1999-01-06
/ NUMBER OF SEQ ID NOS: 25
/ SOFTWARE: Patentin version 3.2
/ SEQ ID NO 11
/ LENGTH: 11
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-105-708-11

Query Match      23.3%; Score 24.5; DB 7; Length 11;
Best Local Similarity 66.7%; Pred. No. 1.9e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY      9 PGFIVGEG 17
|:|:|
Db      2 PGF-RGDEG 9

RESULT 40
US-10-986-501-338
/ Sequence 338, Application US/10986501
/ Publication No. US20050244845A1
/ GENERAL INFORMATION:
/ APPLICANT: Ruben et al.
/ TITLE OF INVENTION: 90 Human Secreted Proteins
/ FILE REFERENCE: P2013P2C1
/ CURRENT APPLICATION NUMBER: US/10/986,501
/ CURRENT FILING DATE: 2004-11-12
/ PRIOR APPLICATION NUMBER: US/10/621,363
/ PRIOR FILING DATE: 2003-07-18
/ PRIOR APPLICATION NUMBER: 09/969,730
/ PRIOR FILING DATE: 2001-10-06
/ PRIOR APPLICATION NUMBER: 09/774,639
/ PRIOR FILING DATE: 2001-02-01
/ PRIOR APPLICATION NUMBER: 60/238,291
/ PRIOR FILING DATE: 2000-10-06
/ PRIOR APPLICATION NUMBER: 09/244,112
/ PRIOR FILING DATE: 1999-02-04
/ PRIOR APPLICATION NUMBER: PCT/US98/16235
/ PRIOR FILING DATE: 1998-08-04
/ PRIOR APPLICATION NUMBER: 60/056,371
/ PRIOR FILING DATE: 1997-08-19
/ PRIOR APPLICATION NUMBER: 60/056,732
/ PRIOR FILING DATE: 1997-08-19
/ PRIOR APPLICATION NUMBER: 60/056,366
/ PRIOR FILING DATE: 1997-08-19
/ PRIOR APPLICATION NUMBER: 60/056,364
/ PRIOR FILING DATE: 1997-08-19
/ Remaining Prior Application data removed - See file wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 373
/ SOFTWARE: Patentin Ver. 2.0
/ SEQ ID NO 338
/ LENGTH: 7
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-986-501-338

Query Match      22.9%; Score 24; DB 6; Length 7;
Best Local Similarity 80.0%; Pred. No. 5.5e+04;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 DPAKG 5
|:|:|
Db      2 DPAKG 6
```

```
RESULT 41
US-11-045-024-1247
/ Sequence 1247, Application US/11045024
/ Publication No. US20050271676A1
/ GENERAL INFORMATION:
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Livingston, Brian
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Baker, Denise Marie
/ APPLICANT: Celis, Bateban
/ APPLICANT: Kubo, Ralph
/ APPLICANT: Grey, Howard M.
/ APPLICANT: BpImmune Inc.
/ TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
/ FILE REFERENCE: 2060.0040007
/ CURRENT APPLICATION NUMBER: US/11/045,024
/ CURRENT FILING DATE: 2005-01-28
/ PRIOR APPLICATION NUMBER: US 09/412,863
/ PRIOR FILING DATE: 1999-10-05
/ PRIOR APPLICATION NUMBER: US 08/027,146
/ PRIOR FILING DATE: 1993-03-05
/ PRIOR APPLICATION NUMBER: US 08/073,205
/ PRIOR FILING DATE: 1993-06-04
/ PRIOR APPLICATION NUMBER: US 08/103,396
/ PRIOR FILING DATE: 1993-08-06
/ PRIOR APPLICATION NUMBER: US 08/159,184
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/159,339
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/205,713
/ PRIOR FILING DATE: 1994-03-04
/ PRIOR APPLICATION NUMBER: US 08/347,610
/ PRIOR FILING DATE: 1994-12-01
/ NUMBER OF SEQ ID NOS: 14528
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 1247
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-1247

Query Match      22.9%; Score 24; DB 7; Length 9;
Best Local Similarity 50.0%; Pred. No. 5.5e+04;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      2 PAKGSP 9
      ||: ||
Db      1 PAKETAP 8

RESULT 42
US-11-045-024-8847
/ Sequence 8847, Application US/11045024
/ Publication No. US20050271676A1
/ GENERAL INFORMATION:
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Livingston, Brian
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Baker, Denise Marie
/ APPLICANT: Celis, Bateban
/ APPLICANT: Kubo, Ralph
/ APPLICANT: Grey, Howard M.
/ APPLICANT: BpImmune Inc.
/ TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
/ FILE REFERENCE: 2060.0040007
/ CURRENT APPLICATION NUMBER: US/11/045,024
```

```
CURRENT FILING DATE: 2005-01-28
/ PRIOR APPLICATION NUMBER: US 09/412,863
/ PRIOR FILING DATE: 1999-10-05
/ PRIOR APPLICATION NUMBER: US 08/027,146
/ PRIOR FILING DATE: 1993-03-05
/ PRIOR APPLICATION NUMBER: US 08/073,205
/ PRIOR FILING DATE: 1993-06-04
/ PRIOR APPLICATION NUMBER: US 08/103,396
/ PRIOR FILING DATE: 1993-08-06
/ PRIOR APPLICATION NUMBER: US 08/159,184
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/159,339
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/205,713
/ PRIOR FILING DATE: 1994-03-04
/ PRIOR APPLICATION NUMBER: US 08/347,610
/ PRIOR FILING DATE: 1994-12-01
/ NUMBER OF SEQ ID NOS: 14528
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 8847
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-8847

Query Match      22.9%; Score 24; DB 7; Length 9;
Best Local Similarity 50.0%; Pred. No. 5.5e+04;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      2 PAKGSP 9
      ||: ||
Db      1 PAKETAP 8

RESULT 43
US-10-919-492-35
/ Sequence 35, Application US/10919492
/ Publication No. US2005028249A1
/ GENERAL INFORMATION:
/ APPLICANT: STOUGAARD, PETER
/ APPLICANT: HANSEN, Ole Cai
/ TITLE OF INVENTION: RECOMBINANT HEXOSE OXIDASE, A METHOD OF PRODUCING
/ FILE REFERENCE: 14923.0014
/ CURRENT APPLICATION NUMBER: US/10/919,492
/ CURRENT FILING DATE: 2004-08-17
/ PRIOR APPLICATION NUMBER: 09/824,053
/ PRIOR FILING DATE: 2001-04-03
/ PRIOR APPLICATION NUMBER: 08/669,304
/ PRIOR FILING DATE: 1996-07-12
/ PRIOR APPLICATION NUMBER: PCT/DK96/00238
/ PRIOR FILING DATE: 1996-06-04
/ PRIOR APPLICATION NUMBER: 08/476,910
/ PRIOR FILING DATE: 1995-06-07
/ NUMBER OF SEQ ID NOS: 37
/ SOFTWARE: PatentIn Ver. 3.2
/ SEQ ID NO 35
/ LENGTH: 10
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-919-492-35

Query Match      22.9%; Score 24; DB 6; Length 10;
Best Local Similarity 80.0%; Pred. No. 2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      9 PGRTV 13
      ||: ||
Db      2 PGRTV 6
```

```
RESULT 44
US-11-045-024-5221
; Sequence 5221, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Cels, Steban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard W.
; APPLICANT: Eplimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5221
; LENGTH: 10
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-5221

Query Match          22.9%; Score 24; DB 7; Length 10;
Best Local Similarity 50.0%; Pred. No. 2e+02;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
```

```
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-129-104-61

Query Match          22.9%; Score 24; DB 7; Length 10;
Best Local Similarity 66.7%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      5 GMSPPG 10
DB      3 GAPPPG 8

RESULT 45
US-11-129-104-61
; Sequence 61, Application US/11129104
; Publication No. US20050287644A1
; GENERAL INFORMATION:
; APPLICANT: CHIU, YI-FANG
; APPLICANT: CHEN, LEE-HSIUAN
; APPLICANT: HUANG, JEN-PIN
; TITLE OF INVENTION: METHODS FOR PRODUCING AND CULTURING RABBIT-MOUSE
; TITLE OF INVENTION: HYBRIDOMAS AND MONOCLONAL ANTIBODIES SECRETED BY
; TITLE OF INVENTION: RABBIT-MOUSE HYBRIDOMAS
; FILE REFERENCE: 09468.0005-00000
; CURRENT APPLICATION NUMBER: US/11/129,104
; CURRENT FILING DATE: 2005-05-13
; PRIOR APPLICATION NUMBER: 60/571,440
; PRIOR FILING DATE: 2004-05-14
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 7
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Human, Mouse, or
US-11-129-104-7

Query Match          22.9%; Score 24; DB 7; Length 10;
Best Local Similarity 66.7%; Pred. No. 2e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      8 PPGKIV 13
DB      2 PPGKIV 7

RESULT 47
US-11-129-104-7
; Sequence 7, Application US/11129104
; Publication No. US20050287644A1
; GENERAL INFORMATION:
; APPLICANT: CHIU, YI-FANG
; APPLICANT: CHEN, LEE-HSIUAN
; APPLICANT: HUANG, JEN-PIN
; TITLE OF INVENTION: METHODS FOR PRODUCING AND CULTURING RABBIT-MOUSE
; TITLE OF INVENTION: HYBRIDOMAS AND MONOCLONAL ANTIBODIES SECRETED BY
; TITLE OF INVENTION: RABBIT-MOUSE HYBRIDOMAS
; FILE REFERENCE: 09468.0005-00000
; CURRENT APPLICATION NUMBER: US/11/129,104
; CURRENT FILING DATE: 2005-05-13
; PRIOR APPLICATION NUMBER: 60/571,440
; PRIOR FILING DATE: 2004-05-14
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 7
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Human, Mouse, or
US-11-129-104-7
```

Query Match 22.9%; Score 24; DB 7; Length 14;  
Best Local Similarity 66.7%; Pred. No. 2.9e+02;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 PPGFIV 13  
||:|  
Db 2 PPGKVV 7

## RESULT 48

US-10-866-120-4  
; Sequence 4, Application US/10866120  
; Publication No. US20050271173A1  
; GENERAL INFORMATION:  
; APPLICANT: Chin, Li-Te  
; APPLICANT: Hsu, Shu-Ching  
; TITLE OF INVENTION: METHOD FOR PRODUCING HUMAN ANTIBODIES OF AGONIST, ANTAGONIST, OR  
; TITLE OF INVENTION: INVERSE AGONIST  
; FILE REFERENCE: P7226/0600  
; CURRENT APPLICATION NUMBER: US/10/866,120  
; CURRENT FILING DATE: 2004-06-14  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 4  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: PEPTIDE  
; LOCATION: (1)..(15)  
US-10-866-120-4

Query Match 22.9%; Score 24; DB 6; Length 15;  
Best Local Similarity 44.4%; Pred. No. 3.1e+02;  
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 6 MSPPGFIVG 14  
||:|  
Db 5 MYPPPYVLG 13

## RESULT 49

US-10-919-492-6  
; Sequence 6, Application US/10919492  
; Publication No. US20050282249A1  
; GENERAL INFORMATION:  
; APPLICANT: STOUGAARD, PETER  
; APPLICANT: HANSEN, OLE CAI  
; TITLE OF INVENTION: RECOMBINANT HEXOSE OXIDASE, A METHOD OF PRODUCING  
; TITLE OF INVENTION: SAME AND USE OF SUCH ENZYME  
; FILE REFERENCE: 14923.0014  
; CURRENT APPLICATION NUMBER: US/10/919,492  
; CURRENT FILING DATE: 2004-08-17  
; PRIOR APPLICATION NUMBER: 09/824,053  
; PRIOR FILING DATE: 2001-04-03  
; PRIOR APPLICATION NUMBER: 08/669,304  
; PRIOR FILING DATE: 1996-07-12  
; PRIOR APPLICATION NUMBER: PCT/DK96/00238  
; PRIOR FILING DATE: 1996-06-04  
; PRIOR APPLICATION NUMBER: 08/476,910  
; PRIOR FILING DATE: 1995-06-07  
; NUMBER OF SEQ ID NOS: 37  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 6  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; FEATURE:  
; NAME/KEY: MOD\_RES

; LOCATION: (14)  
; OTHER INFORMATION: any naturally occurring amino acid, Asx or Glx  
US-10-919-492-6

Query Match 22.9%; Score 24; DB 6; Length 15;  
Best Local Similarity 80.0%; Pred. No. 3.1e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 9 PPGFIV 13  
||:|  
Db 2 PGGIV 6

## RESULT 50

US-10-919-492-13  
; Sequence 13, Application US/10919492  
; Publication No. US20050282249A1  
; GENERAL INFORMATION:  
; APPLICANT: STOUGAARD, PETER  
; APPLICANT: HANSEN, OLE CAI  
; TITLE OF INVENTION: RECOMBINANT HEXOSE OXIDASE, A METHOD OF PRODUCING  
; TITLE OF INVENTION: SAME AND USE OF SUCH ENZYME  
; FILE REFERENCE: 14923.0014  
; CURRENT APPLICATION NUMBER: US/10/919,492  
; CURRENT FILING DATE: 2004-08-17  
; PRIOR APPLICATION NUMBER: 09/824,053  
; PRIOR FILING DATE: 2001-04-03  
; PRIOR APPLICATION NUMBER: 08/669,304  
; PRIOR FILING DATE: 1996-07-12  
; PRIOR APPLICATION NUMBER: PCT/DK96/00238  
; PRIOR FILING DATE: 1996-06-04  
; PRIOR APPLICATION NUMBER: 08/476,910  
; PRIOR FILING DATE: 1995-06-07  
; NUMBER OF SEQ ID NOS: 37  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 13  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-10-919-492-13

Query Match 22.9%; Score 24; DB 6; Length 15;  
Best Local Similarity 80.0%; Pred. No. 3.1e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 9 PPGFIV 13  
||:|  
Db 2 PGGIV 6

## RESULT 51

US-10-503-575-119  
; Sequence 119, Application US/10503575  
; Publication No. US20050244823A1  
; GENERAL INFORMATION:  
; APPLICANT: Drifhout, Jan Moutier  
; APPLICANT: van Veele, Petrus Antonius  
; APPLICANT: Koning, Frits  
; TITLE OF INVENTION: NOVEL EPITOPES FOR CELIAC DISEASE AND AUTOIMMUNE DISEASES, METHOD  
; TITLE OF INVENTION: DETECTING THOSE AND NOVEL NON-ANTIGENIC FOOD COMPOUNDS  
; FILE REFERENCE: 2799/72843-PCT-US  
; CURRENT APPLICATION NUMBER: US/10/503,575  
; CURRENT FILING DATE: 2004-08-04  
; PRIOR APPLICATION NUMBER: PCT/NL03/00077  
; PRIOR FILING DATE: 2003-02-04  
; PRIOR APPLICATION NUMBER: EP 02075456.0  
; PRIOR FILING DATE: 2002-02-04  
; NUMBER OF SEQ ID NOS: 340  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 119

LENGTH: 19  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-503-575-119

Query Match 22.9%; Score 24; DB 6; Length 19;  
Best Local Similarity 42.9%; Pred. No. 4.1e+02;  
Matches 6; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 4 KGMSPGRVREG 17  
DB 4 KGPBPQGPAGEG 17

RESULT 52  
US-11-022-562-145  
Sequence 145, Application US/11022562  
Publication No. US20050249742A1  
GENERAL INFORMATION:  
APPLICANT: Rupprecht, Ruth M.  
APPLICANT: Shieong, Jlang  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING  
FILE REFERENCE: DFN-043CN  
CURRENT APPLICATION NUMBER: US/11/022,562  
CURRENT FILING DATE: 2004-12-22  
PRIOR APPLICATION NUMBER: PCT/US03/20322  
PRIOR FILING DATE: 2003-06-27  
PRIOR APPLICATION NUMBER: 60/392718  
PRIOR FILING DATE: 2002-06-27  
NUMBER OF SEQ ID NOS: 340  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 145  
LENGTH: 20  
TYPE: PRT  
ORGANISM: Simian Immunodeficiency Virus  
US-11-022-562-145

Query Match 22.9%; Score 24; DB 7; Length 20;  
Best Local Similarity 60.0%; Pred. No. 4.4e+02;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 7 SPPGP 11  
DB 14 APPGY 18

RESULT 53  
US-11-022-562-146  
Sequence 146, Application US/11022562  
Publication No. US20050249742A1  
GENERAL INFORMATION:  
APPLICANT: Rupprecht, Ruth M.  
APPLICANT: Shieong, Jlang  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING  
FILE REFERENCE: DFN-043CN  
CURRENT APPLICATION NUMBER: US/11/022,562  
CURRENT FILING DATE: 2004-12-22  
PRIOR APPLICATION NUMBER: PCT/US03/20322  
PRIOR FILING DATE: 2003-06-27  
PRIOR APPLICATION NUMBER: 60/392718  
PRIOR FILING DATE: 2002-06-27  
NUMBER OF SEQ ID NOS: 340  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 146  
LENGTH: 20  
TYPE: PRT  
ORGANISM: Simian Immunodeficiency Virus  
US-11-022-562-146

Query Match 22.9%; Score 24; DB 7; Length 20;  
Best Local Similarity 60.0%; Pred. No. 4.4e+02;

Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 7 SPPGP 11  
DB 4 APPGY 8

RESULT 54  
US-10-485-788A-79  
Sequence 79, Application US/10485788A  
Publication No. US20050282743A1  
GENERAL INFORMATION:  
APPLICANT: Lu, Peter S.  
APPLICANT: Rabinowitz, Joshua D.  
APPLICANT: Schweitzer, Johannes  
APPLICANT: Carrick, Deanna Marie  
APPLICANT: Arbor Vita Corporation  
TITLE OF INVENTION: Molecular Interactions in Cells  
FILE REFERENCE: 20054-00320US  
CURRENT APPLICATION NUMBER: US/10/485,788A  
CURRENT FILING DATE: 2004-02-03  
PRIOR APPLICATION NUMBER: US 60/309,841  
PRIOR FILING DATE: 2001-08-03  
PRIOR APPLICATION NUMBER: US 60/360,061  
PRIOR FILING DATE: 2002-02-25  
PRIOR APPLICATION NUMBER: WO PCT/US02/24655  
PRIOR FILING DATE: 2002-08-02  
NUMBER OF SEQ ID NOS: 841  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 79  
LENGTH: 7  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-485-788A-79

Query Match 21.9%; Score 23; DB 6; Length 7;  
Best Local Similarity 100.0%; Pred. No. 5.5e+04;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 MSP 9  
DB 1 MSP 4

RESULT 55  
US-10-485-788A-80  
Sequence 80, Application US/10485788A  
Publication No. US20050282743A1  
GENERAL INFORMATION:  
APPLICANT: Lu, Peter S.  
APPLICANT: Rabinowitz, Joshua D.  
APPLICANT: Schweitzer, Johannes  
APPLICANT: Carrick, Deanna Marie  
APPLICANT: Arbor Vita Corporation  
TITLE OF INVENTION: Molecular Interactions in Cells  
FILE REFERENCE: 20054-00320US  
CURRENT APPLICATION NUMBER: US/10/485,788A  
CURRENT FILING DATE: 2004-02-03  
PRIOR APPLICATION NUMBER: US 60/309,841  
PRIOR FILING DATE: 2001-08-03  
PRIOR APPLICATION NUMBER: US 60/360,061  
PRIOR FILING DATE: 2002-02-25  
PRIOR APPLICATION NUMBER: WO PCT/US02/24655  
PRIOR FILING DATE: 2002-08-02  
NUMBER OF SEQ ID NOS: 841  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 80  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-485-788A-80

Query Match 21.9%; Score 23; DB 6; Length 8;

Best Local Similarity 100.0%; Pred. No. 5.5e+04;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 MSPP 9  
|||  
Db 2 MSPP 5

## RESULT 56

US-10-850-635-26  
; Sequence 26; Application US/10850635  
; Publication No. US20050287149A1  
; GENERAL INFORMATION:  
; APPLICANT: Keler, Tibor  
; APPLICANT: Vitale, Laura  
; APPLICANT: Blaneset, Diane  
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES AGAINST  
; FILE REFERENCE: MXI-305  
; CURRENT APPLICATION NUMBER: US/10/850,635  
; CURRENT FILING DATE: 2004-05-21  
; PRIOR APPLICATION NUMBER: 60/472636  
; PRIOR FILING DATE: 2003-05-21  
; PRIOR APPLICATION NUMBER: 60/512336  
; PRIOR FILING DATE: 2003-10-16  
; NUMBER OF SEQ ID NOS: 72  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 26  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-850-635-26

Query Match 21.9%; Score 23; DB 6; Length 9;  
Best Local Similarity 80.0%; Pred. No. 5.5e+04;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GMSPP 9  
|||  
Db 4 GMSPP 8

## RESULT 57

US-11-010-748A-617  
; Sequence 617; Application US/11010748A  
; Publication No. US20050244421A1  
; GENERAL INFORMATION:  
; APPLICANT: Merck Patent GmbH  
; APPLICANT: STRITTMAYER, Wolfgang  
; APPLICANT: WOLL, Heidrun  
; APPLICANT: SCHAM, Burkhard  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING IMMUNE RESPONSE  
; FILE REFERENCE: MER-136  
; CURRENT APPLICATION NUMBER: US/11/010,748A  
; CURRENT FILING DATE: 2004-12-13  
; PRIOR APPLICATION NUMBER: PCT/EP03/06251  
; PRIOR FILING DATE: 2003-06-13  
; PRIOR APPLICATION NUMBER: EP02013423.5  
; PRIOR FILING DATE: 2002-06-13  
; NUMBER OF SEQ ID NOS: 926  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 617  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: HLA-binding peptide of Seq. No. 611  
US-11-010-748A-617

Query Match 21.9%; Score 23; DB 7; Length 9;  
Best Local Similarity 66.7%; Pred. No. 5.5e+04;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 9 PGFPLG 14  
|||  
Db 1 PGFPLG 6

## RESULT 58

US-11-010-748A-618  
; Sequence 618; Application US/11010748A  
; Publication No. US20050244421A1  
; GENERAL INFORMATION:  
; APPLICANT: Merck Patent GmbH  
; APPLICANT: STRITTMAYER, Wolfgang  
; APPLICANT: WOLL, Heidrun  
; APPLICANT: SCHAM, Burkhard  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING IMMUNE RESPONSE  
; FILE REFERENCE: MER-136  
; CURRENT APPLICATION NUMBER: US/11/010,748A  
; CURRENT FILING DATE: 2004-12-13  
; PRIOR APPLICATION NUMBER: PCT/EP03/06251  
; PRIOR FILING DATE: 2003-06-13  
; PRIOR APPLICATION NUMBER: EP02013423.5  
; PRIOR FILING DATE: 2002-06-13  
; NUMBER OF SEQ ID NOS: 926  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 618  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: HLA-binding peptide of Seq. No. 611  
US-11-010-748A-618

Query Match 21.9%; Score 23; DB 7; Length 9;  
Best Local Similarity 66.7%; Pred. No. 5.5e+04;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 9 PGFPLG 14  
|||  
Db 3 PGFPLG 8

## RESULT 59

US-11-010-748A-620  
; Sequence 620; Application US/11010748A  
; Publication No. US20050244421A1  
; GENERAL INFORMATION:  
; APPLICANT: Merck Patent GmbH  
; APPLICANT: STRITTMAYER, Wolfgang  
; APPLICANT: WOLL, Heidrun  
; APPLICANT: SCHAM, Burkhard  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING IMMUNE RESPONSE  
; FILE REFERENCE: MER-136  
; CURRENT APPLICATION NUMBER: US/11/010,748A  
; CURRENT FILING DATE: 2004-12-13  
; PRIOR APPLICATION NUMBER: PCT/EP03/06251  
; PRIOR FILING DATE: 2003-06-13  
; PRIOR APPLICATION NUMBER: EP02013423.5  
; PRIOR FILING DATE: 2002-06-13  
; NUMBER OF SEQ ID NOS: 926  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 620  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: HLA-binding peptide of Seq. No. 611  
US-11-010-748A-620

Query Match 21.9%; Score 23; DB 7; Length 9;  
Best Local Similarity 66.7%; Pred. No. 5.5e+04;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 9 PGFIVG 14  
||| : |  
Db 4 PGFPIG 9

RESULT 60  
US-11-010-748A-621  
/ Sequence 621, Application US/11010748A  
/ Publication No. US20050244421A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Merck Patent GmbH  
/ APPLICANT: STRITTMAYER, Wolfgang  
/ APPLICANT: MOLL, Heidrun  
/ APPLICANT: SCHARM, Burkhard  
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING IMMUNE RESPONSE  
/ FILE REFERENCE: MER-136  
/ CURRENT APPLICATION NUMBER: US/11/010,748A  
/ PRIOR FILING DATE: 2004-12-13  
/ PRIOR APPLICATION NUMBER: PCT/EP03/06251  
/ PRIOR FILING DATE: 2003-06-13  
/ PRIOR APPLICATION NUMBER: EP02013423.5  
/ NUMBER OF SEQ ID NOS: 926  
/ SOFTWARE: PatentIn version 3.1  
/ SEQ ID NO 621  
/ LENGTH: 9  
/ TYPE: PRT  
/ ORGANISM: Artificial Sequence  
/ FEATURE:  
/ OTHER INFORMATION: HLA-binding peptide of Seq. No. 611  
US-11-010-748A-621

Query Match 21.9%; Score 23; DB 7; Length 9;  
Best Local Similarity 66.7%; Pred. No. 5.5e+04;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 9 PGFIVG 14  
||| : |  
Db 2 PGFPIG 7

RESULT 61  
US-11-010-748A-625  
/ Sequence 625, Application US/11010748A  
/ Publication No. US20050244421A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Merck Patent GmbH  
/ APPLICANT: STRITTMAYER, Wolfgang  
/ APPLICANT: MOLL, Heidrun  
/ APPLICANT: SCHARM, Burkhard  
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING IMMUNE RESPONSE  
/ FILE REFERENCE: MER-136  
/ CURRENT APPLICATION NUMBER: US/11/010,748A  
/ PRIOR FILING DATE: 2004-12-13  
/ PRIOR APPLICATION NUMBER: PCT/EP03/06251  
/ PRIOR FILING DATE: 2003-06-13  
/ PRIOR APPLICATION NUMBER: EP02013423.5  
/ PRIOR FILING DATE: 2002-06-13  
/ NUMBER OF SEQ ID NOS: 926  
/ SOFTWARE: PatentIn version 3.1  
/ SEQ ID NO 625  
/ LENGTH: 9  
/ TYPE: PRT  
/ ORGANISM: Artificial Sequence  
/ FEATURE:  
/ OTHER INFORMATION: HLA-binding peptide of Seq. No. 611  
US-11-010-748A-625

Query Match 21.9%; Score 23; DB 7; Length 9;  
Best Local Similarity 66.7%; Pred. No. 5.5e+04;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 9 PGFIVG 14

Db 4 PGFPIG 9  
||| : |

RESULT 62  
US-11-010-748A-635  
/ Sequence 635, Application US/11010748A  
/ Publication No. US20050244421A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Merck Patent GmbH  
/ APPLICANT: STRITTMAYER, Wolfgang  
/ APPLICANT: MOLL, Heidrun  
/ APPLICANT: SCHARM, Burkhard  
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING IMMUNE RESPONSE  
/ FILE REFERENCE: MER-136  
/ CURRENT APPLICATION NUMBER: US/11/010,748A  
/ PRIOR FILING DATE: 2004-12-13  
/ PRIOR APPLICATION NUMBER: PCT/EP03/06251  
/ PRIOR FILING DATE: 2003-06-13  
/ PRIOR APPLICATION NUMBER: EP02013423.5  
/ NUMBER OF SEQ ID NOS: 926  
/ SOFTWARE: PatentIn version 3.1  
/ SEQ ID NO 635  
/ LENGTH: 9  
/ TYPE: PRT  
/ ORGANISM: Artificial Sequence  
/ FEATURE:  
/ OTHER INFORMATION: HLA-binding peptide of Seq. No. 611  
US-11-010-748A-635

Query Match 21.9%; Score 23; DB 7; Length 9;  
Best Local Similarity 66.7%; Pred. No. 5.5e+04;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 9 PGFIVG 14  
||| : |  
Db 1 PGFPIG 6

RESULT 63  
US-11-055-557-28  
/ Sequence 28, Application US/11055557  
/ Publication No. US20050255083A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Leppla, Stephen H.  
/ APPLICANT: Liu, Shi-Hui  
/ APPLICANT: Bugge, Thomas H.  
/ APPLICANT: The Government of the United States of America  
/ APPLICANT: as represented by The Secretary of the  
/ APPLICANT: Department of Health and Human Services  
/ TITLE OF INVENTION: Multimeric Protein Toxins to Target Cells Having  
/ TITLE OF INVENTION: Multiple Identifying Characteristics  
/ FILE REFERENCE: 015280-501100US  
/ CURRENT APPLICATION NUMBER: US/11/055,557  
/ PRIOR FILING DATE: 2005-02-09  
/ PRIOR APPLICATION NUMBER: US 60/543,417  
/ PRIOR FILING DATE: 2004-02-09  
/ NUMBER OF SEQ ID NOS: 42  
/ SOFTWARE: PatentIn Ver. 2.1  
/ SEQ ID NO 28  
/ LENGTH: 9  
/ TYPE: PRT  
/ ORGANISM: Artificial Sequence  
/ FEATURE:  
/ OTHER INFORMATION: Description of Artificial Sequence: Plasmidogen  
/ OTHER INFORMATION: activator cleavage site, uPA and tPA physiological  
/ OTHER INFORMATION: substrate sequence  
US-11-055-557-28

Query Match 21.9%; Score 23; DB 7; Length 9;  
Best Local Similarity 66.7%; Pred. No. 5.5e+04;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;



QY 9 PGFVIG 14  
||:|  
DB 3 PGRVVG 8

## RESULT 64

US-11-033-365-22  
Sequence 22, Application US/11033365  
GENERAL INFORMATION:  
APPLICANT: Neose Technologies Inc.  
APPLICANT: Defrees, Shawn  
APPLICANT: Zopf, David  
APPLICANT: Wang, ZhiGang  
APPLICANT: Clausen, Henrik  
TITLE OF INVENTION: O-Linked Glycosylation of peptides  
FILE REFERENCE: 040853-01-5138  
CURRENT APPLICATION NUMBER: US/11/033,365  
CURRENT FILING DATE: 2005-01-10  
PRIOR APPLICATION NUMBER: 60/535,284  
PRIOR FILING DATE: 2004-01-08  
PRIOR APPLICATION NUMBER: 60/544,411  
PRIOR FILING DATE: 2004-02-12  
PRIOR APPLICATION NUMBER: 60/546,631  
PRIOR FILING DATE: 2004-02-20  
PRIOR APPLICATION NUMBER: 60/555,813  
PRIOR FILING DATE: 2004-03-23  
PRIOR APPLICATION NUMBER: 60/570,891  
PRIOR FILING DATE: 2004-05-12  
NUMBER OF SEQ ID NOS: 213  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 22  
LENGTH: 11  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-11-033-365-22

Query Match 21.9%; Score 23; DB 7; Length 11;  
Best Local Similarity 42.9%; Pred. No. 3.2e+02;  
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 PAKMSP 8  
||:|  
DB 3 PTGGLCP 9

## RESULT 65

US-10-893-584-102  
Sequence 102, Application US/10893584  
GENERAL INFORMATION:  
APPLICANT: Borgford, Thor  
APPLICANT: Braun, Curtis  
APPLICANT: Purac, Adam  
APPLICANT: Stoll, Dominik  
TITLE OF INVENTION: Richn-like Toxin Variants for Treatment of Cancer,  
FILE REFERENCE: 10447-025  
CURRENT APPLICATION NUMBER: US/10/893,584  
CURRENT FILING DATE: 2004-07-19  
PRIOR APPLICATION NUMBER: US 09/551,151  
PRIOR FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: US 09/403,752  
PRIOR FILING DATE: 1999-10-29  
PRIOR APPLICATION NUMBER: US 10/089,058  
PRIOR FILING DATE: 2000-10-04  
NUMBER OF SEQ ID NOS: 274  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 102  
LENGTH: 12  
TYPE: PRT  
ORGANISM: Artificial Sequence

FEATURE:  
OTHER INFORMATION: Mutant preprotricin linker region for Urokinase-Type Plasmino  
US-10-893-584-102

Query Match 21.9%; Score 23; DB 6; Length 12;  
Best Local Similarity 66.7%; Pred. No. 3.5e+02;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 9 PGFVIG 14  
||:|  
DB 4 PGRVVG 9

## RESULT 66

US-10-893-584-198  
Sequence 198, Application US/10893584  
GENERAL INFORMATION:  
APPLICANT: Borgford, Thor  
APPLICANT: Braun, Curtis  
APPLICANT: Purac, Adam  
APPLICANT: Stoll, Dominik  
TITLE OF INVENTION: Richn-like Toxin Variants for Treatment of Cancer,  
FILE REFERENCE: 10447-025  
CURRENT APPLICATION NUMBER: US/10/893,584  
CURRENT FILING DATE: 2004-07-19  
PRIOR APPLICATION NUMBER: US 09/551,151  
PRIOR FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: US 09/403,752  
PRIOR FILING DATE: 1999-10-29  
PRIOR APPLICATION NUMBER: US 10/089,058  
PRIOR FILING DATE: 2000-10-04  
NUMBER OF SEQ ID NOS: 274  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 198  
LENGTH: 13  
TYPE: PRT  
ORGANISM: E. coli  
US-10-893-584-198

Query Match 21.9%; Score 23; DB 6; Length 13;  
Best Local Similarity 66.7%; Pred. No. 3.8e+02;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 9 PGFVIG 14  
||:|  
DB 2 PGRVVG 7

## RESULT 67

US-10-746-959C-5  
Sequence 5, Application US/10746959C  
GENERAL INFORMATION:  
APPLICANT: Los Alamos National Laboratory  
APPLICANT: Gupta, Goutam, et al.  
TITLE OF INVENTION: STRUCTURE-BASED RECEPTOR MIMICS TARGETED AGAINST BACTERIAL  
FILE REFERENCE: S-99,945  
CURRENT APPLICATION NUMBER: US/10/746,959C  
CURRENT FILING DATE: 2003-12-24  
NUMBER OF SEQ ID NOS: 22  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 5  
LENGTH: 14  
TYPE: PRT  
ORGANISM: Homo Sapiens  
US-10-746-959C-5

Query Match 21.9%; Score 23; DB 6; Length 14;  
Best Local Similarity 50.0%; Pred. No. 4.1e+02;  
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Oy 2 PAKGMSP 9  
|||  
Db 6 PAKSTAPP 13

RESULT 68  
US-10-939-890-200  
; Sequence 200, Application US/10939890  
; Publication No. US20050250700A1  
; GENERAL INFORMATION:  
; APPLICANT: Sato, Aaron K.  
; APPLICANT: Sexton, Daniel J.  
; APPLICANT: Dransfield, Daniel T.  
; APPLICANT: Ladner, Robert C.  
; APPLICANT: Arbogast, Christophe  
; APPLICANT: Bussac, Philippe  
; APPLICANT: Fan, Hong  
; APPLICANT: Khurana, Sudha  
; APPLICANT: Linder, Karen E.  
; APPLICANT: Marinelli, Edmund R.  
; APPLICANT: Nanjappa, Palanappa  
; APPLICANT: Nunn, Adrian D.  
; APPLICANT: Pillai, Radhakrishna  
; APPLICANT: Pochon, Sibylle  
; APPLICANT: Ramalingam, Kondareddiar  
; APPLICANT: Shrivastava, Ajay  
; APPLICANT: Song, Bo  
; APPLICANT: Swenson, Rolf E.  
; APPLICANT: Von Wronski, Mathew A.  
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES  
; FILE REFERENCE: D0617.70014US00  
; CURRENT APPLICATION NUMBER: US/10/939,890  
; PRIOR FILING DATE: 2004-09-13  
; PRIOR APPLICATION NUMBER: US 10/661,156  
; PRIOR FILING DATE: 2003-09-11  
; PRIOR APPLICATION NUMBER: US 10/382,082  
; PRIOR FILING DATE: 2003-03-03  
; PRIOR APPLICATION NUMBER: PCT/US03/06731  
; PRIOR FILING DATE: 2003-03-03  
; PRIOR APPLICATION NUMBER: US 60/440,411  
; PRIOR FILING DATE: 2003-01-15  
; PRIOR APPLICATION NUMBER: US 60/360,851  
; PRIOR FILING DATE: 2002-03-01  
; NUMBER OF SEQ ID NOS: 883  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 200  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Library Isolate  
US-10-939-890-200

Query Match 21.9%; Score 23; DB 6; Length 15;  
Best Local Similarity 57.1%; Pred. No. 4.5e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 2 PAKGMSP 8  
|||  
Db 3 PCKGMPP 9

RESULT 69  
US-10-939-890-202  
; Sequence 202, Application US/10939890  
; Publication No. US20050250700A1  
; GENERAL INFORMATION:  
; APPLICANT: Sato, Aaron K.  
; APPLICANT: Sexton, Daniel J.  
; APPLICANT: Dransfield, Daniel T.  
; APPLICANT: Ladner, Robert C.  
; APPLICANT: Arbogast, Christophe

; APPLICANT: Bussac, Philippe  
; APPLICANT: Fan, Hong  
; APPLICANT: Khurana, Sudha  
; APPLICANT: Linder, Karen E.  
; APPLICANT: Marinelli, Edmund R.  
; APPLICANT: Nanjappa, Palanappa  
; APPLICANT: Nunn, Adrian D.  
; APPLICANT: Pillai, Radhakrishna  
; APPLICANT: Pochon, Sibylle  
; APPLICANT: Ramalingam, Kondareddiar  
; APPLICANT: Shrivastava, Ajay  
; APPLICANT: Song, Bo  
; APPLICANT: Swenson, Rolf E.  
; APPLICANT: Von Wronski, Mathew A.  
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES  
; FILE REFERENCE: D0617.70014US00  
; CURRENT APPLICATION NUMBER: US/10/939,890  
; PRIOR FILING DATE: 2004-09-13  
; PRIOR APPLICATION NUMBER: US 10/661,156  
; PRIOR FILING DATE: 2003-09-11  
; PRIOR APPLICATION NUMBER: US 10/382,082  
; PRIOR FILING DATE: 2003-03-03  
; PRIOR APPLICATION NUMBER: PCT/US03/06731  
; PRIOR FILING DATE: 2003-03-03  
; PRIOR APPLICATION NUMBER: US 60/440,411  
; PRIOR FILING DATE: 2003-01-15  
; PRIOR APPLICATION NUMBER: US 60/360,851  
; PRIOR FILING DATE: 2002-03-01  
; NUMBER OF SEQ ID NOS: 883  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 202  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Library Isolate  
US-10-939-890-202

Query Match 21.9%; Score 23; DB 6; Length 15;  
Best Local Similarity 57.1%; Pred. No. 4.5e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 2 PAKGMSP 8  
|||  
Db 3 PCKGMPP 9

RESULT 70  
US-10-893-584-247  
; Sequence 247, Application US/10893584  
; Publication No. US20050272046A1  
; GENERAL INFORMATION:  
; APPLICANT: Borgford, Thor  
; APPLICANT: Braun, Curtis  
; APPLICANT: Puzac, Adamir  
; APPLICANT: Stoll, Dominik  
; TITLE OF INVENTION: Rac1-like Toxin Variants for Treatment of Cancer.  
; TITLE OF INVENTION: Viral or Parasitic Infections  
; FILE REFERENCE: 10447-025  
; CURRENT APPLICATION NUMBER: US/10/893,584  
; PRIOR FILING DATE: 2004-07-19  
; PRIOR APPLICATION NUMBER: US 09/551,151  
; PRIOR FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: US 09/403,752  
; PRIOR FILING DATE: 1999-10-29  
; PRIOR APPLICATION NUMBER: US 10/089,058  
; PRIOR FILING DATE: 2000-10-04  
; NUMBER OF SEQ ID NOS: 274  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 247  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: E. coli

US-10-893-584-247

Query Match 21.9%; Score 23; DB 6; Length 15;  
Best Local Similarity 66.7%; Pred. No. 4.5e+02;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 9 PGFVVG 14  
|||  
Db 3 PGFVVG 8

RESULT 71

US-11-187-558-4  
Sequence 4, Application US/11187558  
Publication No. US20050271655A1  
GENERAL INFORMATION:

APPLICANT: Huang, Xin-Yun  
TITLE OF INVENTION: METHODS FOR DESIGNING SPECIFIC ION CHANNEL BLOCKERS  
FILE REFERENCE: 19603/1454  
CURRENT APPLICATION NUMBER: US/11/187,558  
CURRENT FILING DATE: 2005-07-22  
PRIOR APPLICATION NUMBER: 60/079,268  
PRIOR FILING DATE: 1998-03-25  
PRIOR APPLICATION NUMBER: 09/273,217  
PRIOR FILING DATE: 1999-03-19  
NUMBER OF SEQ ID NOS: 4  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 4  
LENGTH: 15  
TYPE: PRT  
ORGANISM: rat  
US-11-187-558-4

Query Match 21.9%; Score 23; DB 7; Length 15;  
Best Local Similarity 57.1%; Pred. No. 4.5e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 DPAKGS 7  
|||  
Db 6 DPTSGFS 12

RESULT 72

US-10-919-492-3  
Sequence 3, Application US/10919492  
Publication No. US20050282249A1  
GENERAL INFORMATION:

APPLICANT: HANSEN, OLE CAT  
TITLE OF INVENTION: RECOMBINANT HEXOSE OXIDASE, A METHOD OF PRODUCING  
FILE REFERENCE: 14923.0014  
CURRENT APPLICATION NUMBER: US/10/919,492  
CURRENT FILING DATE: 2004-08-17  
PRIOR APPLICATION NUMBER: 09/824,053  
PRIOR FILING DATE: 2001-04-03  
PRIOR APPLICATION NUMBER: 08/669,304  
PRIOR FILING DATE: 1996-07-12  
PRIOR APPLICATION NUMBER: PCT/DK96/00238  
PRIOR FILING DATE: 1996-06-04  
PRIOR APPLICATION NUMBER: 08/476,910  
PRIOR FILING DATE: 1995-06-07  
NUMBER OF SEQ ID NOS: 37  
SOFTWARE: PatentIn Ver. 3.2  
SEQ ID NO 3  
LENGTH: 16  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURES:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
FEATURE:  
NAME/KEY: MOD\_RES

LOCATION: (15)  
OTHER INFORMATION: any naturally occurring amino acid, Asx or Glx  
US-10-919-492-3

Query Match 21.9%; Score 23; DB 6; Length 16;  
Best Local Similarity 71.4%; Pred. No. 4.8e+02;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 MSPPGFI 12  
|||  
Db 4 MSPRGVI 10

RESULT 73

US-10-919-492-10  
Sequence 10, Application US/10919492  
Publication No. US20050282249A1  
GENERAL INFORMATION:

APPLICANT: STOUGAARD, PETER  
TITLE OF INVENTION: RECOMBINANT HEXOSE OXIDASE, A METHOD OF PRODUCING  
FILE REFERENCE: 14923.0014  
CURRENT APPLICATION NUMBER: US/10/919,492  
CURRENT FILING DATE: 2004-08-17  
PRIOR APPLICATION NUMBER: 09/824,053  
PRIOR FILING DATE: 2001-04-03  
PRIOR APPLICATION NUMBER: 08/669,304  
PRIOR FILING DATE: 1996-07-12  
PRIOR APPLICATION NUMBER: PCT/DK96/00238  
PRIOR FILING DATE: 1996-06-04  
PRIOR APPLICATION NUMBER: 08/476,910  
PRIOR FILING DATE: 1995-06-07  
NUMBER OF SEQ ID NOS: 37  
SOFTWARE: PatentIn Ver. 3.2  
SEQ ID NO 10  
LENGTH: 16  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURES:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-10-919-492-10

Query Match 21.9%; Score 23; DB 6; Length 16;  
Best Local Similarity 71.4%; Pred. No. 4.8e+02;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 MSPPGFI 12  
|||  
Db 4 MSPRGVI 10

RESULT 74

US-11-108-185-42  
Sequence 42, Application US/11108185  
Publication No. US20050262591A1  
GENERAL INFORMATION:

APPLICANT: Debonte, Lorin R.  
APPLICANT: Fan, Zhigong  
APPLICANT: Mao, Guo-Hua  
TITLE OF INVENTION: FATTY ACID DESATURASES AND MUTANT SEQUENCES THEREOF  
FILE REFERENCE: 07148-063003  
CURRENT APPLICATION NUMBER: US/11/108,185  
CURRENT FILING DATE: 2005-04-18  
PRIOR APPLICATION NUMBER: US/09/771,904  
PRIOR FILING DATE: 2001-01-29  
PRIOR APPLICATION NUMBER: US 08/874,109  
PRIOR FILING DATE: 1997-06-12  
NUMBER OF SEQ ID NOS: 70  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 42  
LENGTH: 16

TYPE: PRT  
ORGANISM: Rictinus communis  
US-11-108-185-42

Query Match 21.9%; Score 23; DB 7; Length 16;  
Best Local Similarity 57.1%; Pred. No. 4.8e+02;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 7 SPFGFV 13  
DB 10 NPGKIM 16

RESULT 75  
US-10-880-238-107  
Sequence 107, Application US/10880238  
Publication No. US20050287538A1  
GENERAL INFORMATION:  
APPLICANT: Cheng, Ming-Tai  
TITLE OF INVENTION: FRAME-SHIFTING PCR FOR GERM-LINE  
FILE REFERENCE: 17329-003001  
CURRENT APPLICATION NUMBER: US/10/880,238  
CURRENT FILING DATE: 2004-06-29  
NUMBER OF SEQ ID NOS: 214  
SOFTWARE: PaateSeq for Windows Version 4.0  
SEQ ID NO 107  
LENGTH: 17  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetically generated peptide  
US-10-880-238-107

Query Match 21.9%; Score 23; DB 6; Length 17;  
Best Local Similarity 80.0%; Pred. No. 5.2e+02;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DPAKG 5  
DB 3 DPANG 7

RESULT 76  
US-10-880-238-109  
Sequence 109, Application US/10880238  
Publication No. US20050287538A1  
GENERAL INFORMATION:  
APPLICANT: Cheng, Ming-Tai  
TITLE OF INVENTION: FRAME-SHIFTING PCR FOR GERM-LINE  
FILE REFERENCE: 17329-003001  
CURRENT APPLICATION NUMBER: US/10/880,238  
CURRENT FILING DATE: 2004-06-29  
NUMBER OF SEQ ID NOS: 214  
SOFTWARE: PaateSeq for Windows Version 4.0  
SEQ ID NO 109  
LENGTH: 17  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetically generated peptide  
US-10-880-238-109

Query Match 21.9%; Score 23; DB 6; Length 17;  
Best Local Similarity 80.0%; Pred. No. 5.2e+02;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DPAKG 5  
DB 3 DPANG 7

RESULT 77  
US-11-010-748A-405  
Sequence 405, Application US/11010748A  
Publication No. US20050244421A1  
GENERAL INFORMATION:  
APPLICANT: Merck Patent GmbH  
APPLICANT: STRITTMAYER, Wolfgang  
APPLICANT: MOLL, Heidrun  
APPLICANT: SCHARM, Burkhard  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING IMMUNE RESPONSE  
FILE REFERENCE: MER-136  
CURRENT APPLICATION NUMBER: US/11/010,748A  
PRIOR APPLICATION NUMBER: PCT/EP03/06251  
PRIOR FILING DATE: 2003-06-13  
PRIOR APPLICATION NUMBER: EP02013423.5  
PRIOR FILING DATE: 2002-06-13  
NUMBER OF SEQ ID NOS: 926  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 405  
LENGTH: 17  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: CD42b peptide fragment  
US-11-010-748A-405

Query Match 21.9%; Score 23; DB 7; Length 17;  
Best Local Similarity 37.5%; Pred. No. 5.2e+02;  
Matches 6; Conservative 2; Mismatches 4; Indels 4; Gaps 1;

QY 2 PAKGSPFGFVGEERG 17  
DB 6 PAKGSPFGFVGEERG 17

RESULT 78  
US-11-033-039-1324  
Sequence 1324, Application US/11033039  
Publication No. US20060002947A1  
GENERAL INFORMATION:  
APPLICANT: HUMPHREYS, ROBERT  
APPLICANT: XU, MINZHEN  
TITLE OF INVENTION: LI-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES  
FILE REFERENCE: REH-2017US01  
CURRENT APPLICATION NUMBER: US/11/033,039  
CURRENT FILING DATE: 2005-01-11  
PRIOR APPLICATION NUMBER: 10/245,871  
PRIOR FILING DATE: 2002-09-17  
PRIOR APPLICATION NUMBER: 10/197,000  
PRIOR FILING DATE: 2002-07-17  
PRIOR APPLICATION NUMBER: 09/396,813  
PRIOR FILING DATE: 1999-09-14  
NUMBER OF SEQ ID NOS: 1452  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 1324  
LENGTH: 18  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
OTHER INFORMATION: Hybrid peptide  
NAME/KEY: MOD\_RES  
LOCATION: (5)..(5)  
OTHER INFORMATION: Ava  
US-11-033-039-1324

Query Match 21.9%; Score 23; DB 7; Length 18;  
Best Local Similarity 44.4%; Pred. No. 5.5e+02;  
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 9 PGPIVGEH 17  
|:|:|  
Db 8 PGLVAGWYG 16

RESULT 79  
US-10-503-575-224  
; Sequence 224, Application US/10503575  
; Publication No. US20050244823A1  
; GENERAL INFORMATION:  
; APPLICANT: Driffhout, Jan Wouter  
; APPLICANT: van Veelen, Petrus Antonius  
; TITLE OF INVENTION: NOVEL EPITOPES FOR CELIAC DISEASE AND AUTOIMMUNE DISEASES, METHOD  
; TITLE OF INVENTION: DETECTING THOSE AND NOVEL NON-ANTIGENIC FOOD COMPOUNDS  
; FILE REFERENCE: 2799/72843-PCT-US  
; CURRENT APPLICATION NUMBER: US/10/503,575  
; PRIOR FILING DATE: 2004-08-04  
; PRIOR APPLICATION NUMBER: PCT/NL03/00077  
; PRIOR FILING DATE: 2003-02-04  
; PRIOR FILING DATE: 2002-02-04  
; PRIOR FILING DATE: 2002-02-04  
; NUMBER OF SEQ ID NOS: 340  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 224  
; LENGTH: 19  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-503-575-224

Query Match 21.9%; Score 23; DB 6; Length 19;  
Best Local Similarity 45.5%; Pred. No. 5.8e+02;  
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 10 GFIYVGEVLS 20  
|:|:|:|  
Db 4 GYIVTDQKPLS 14

RESULT 80  
US-10-503-575-302  
; Sequence 302, Application US/10503575  
; Publication No. US20050244823A1  
; GENERAL INFORMATION:  
; APPLICANT: Driffhout, Jan Wouter  
; APPLICANT: van Veelen, Petrus Antonius  
; TITLE OF INVENTION: NOVEL EPITOPES FOR CELIAC DISEASE AND AUTOIMMUNE DISEASES, METHOD  
; TITLE OF INVENTION: DETECTING THOSE AND NOVEL NON-ANTIGENIC FOOD COMPOUNDS  
; FILE REFERENCE: 2799/72843-PCT-US  
; CURRENT APPLICATION NUMBER: US/10/503,575  
; CURRENT FILING DATE: 2004-08-04  
; PRIOR APPLICATION NUMBER: PCT/NL03/00077  
; PRIOR FILING DATE: 2003-02-04  
; PRIOR APPLICATION NUMBER: EP 02075456.0  
; PRIOR FILING DATE: 2002-02-04  
; NUMBER OF SEQ ID NOS: 340  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 302  
; LENGTH: 19  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-503-575-302

Query Match 21.9%; Score 23; DB 6; Length 19;  
Best Local Similarity 36.4%; Pred. No. 5.8e+02;  
Matches 4; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 4 KGMSPPGPIV 14  
|:|:|:|  
Db 8 EGDDPSGLQIG 18

RESULT 81  
US-10-503-575-303  
; Sequence 303, Application US/10503575  
; Publication No. US20050244823A1  
; GENERAL INFORMATION:  
; APPLICANT: Driffhout, Jan Wouter  
; APPLICANT: van Veelen, Petrus Antonius  
; TITLE OF INVENTION: NOVEL EPITOPES FOR CELIAC DISEASE AND AUTOIMMUNE DISEASES, METHO  
; TITLE OF INVENTION: DETECTING THOSE AND NOVEL NON-ANTIGENIC FOOD COMPOUNDS  
; FILE REFERENCE: 2799/72843-PCT-US  
; CURRENT APPLICATION NUMBER: US/10/503,575  
; CURRENT FILING DATE: 2004-08-04  
; PRIOR APPLICATION NUMBER: PCT/NL03/00077  
; PRIOR FILING DATE: 2003-02-04  
; PRIOR APPLICATION NUMBER: EP 02075456.0  
; PRIOR FILING DATE: 2002-02-04  
; NUMBER OF SEQ ID NOS: 340  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 303  
; LENGTH: 19  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-503-575-303

Query Match 21.9%; Score 23; DB 6; Length 19;  
Best Local Similarity 36.4%; Pred. No. 5.8e+02;  
Matches 4; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 4 KGMSPPGPIV 14  
|:|:|:|  
Db 2 EGDDPSGLQIG 12

RESULT 82  
US-10-623-155-533  
; Sequence 533, Application US/10623155  
; Publication No. US20050261166A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Tongtong  
; APPLICANT: Peckham, David W.  
; APPLICANT: Retter, Marc W.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER  
; FILE REFERENCE: 210121.455C20  
; CURRENT APPLICATION NUMBER: US/10/623,155  
; CURRENT FILING DATE: 2003-07-17  
; NUMBER OF SEQ ID NOS: 560  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 533  
; LENGTH: 20  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-623-155-533

Query Match 21.9%; Score 23; DB 6; Length 20;  
Best Local Similarity 50.0%; Pred. No. 6.2e+02;  
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 12 IVGEH 17  
|:|:|:|  
Db 2 LIGKEG 7

RESULT 83  
US-11-106-415-192  
; Sequence 192, Application US/11106415  
; Publication No. US20050287153A1  
; GENERAL INFORMATION:  
; APPLICANT: MARK S. DENNIS  
; TITLE OF INVENTION: Serum Albumin Binding Peptides for Tumor Targeting

```
/ FILE REFERENCE: P1774R1P2
/ CURRENT APPLICATION NUMBER: US/11/106,415
/ CURRENT FILING DATE: 2005-04-13
/ PRIOR APPLICATION NUMBER: US 10/186,229
/ PRIOR FILING DATE: 2002-06-28
/ NUMBER OF SEQ ID NOS: 425
/ SEQ ID NO 192
/ LENGTH: 20
/ TYPE: PRF
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: sequence is synthesized
US-11-106-415-192

Query Match
Best Local Similarity 21.9%; Score 23; DB 7; Length 20;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 14 GEEGVL 19
   |||||
Db 2 GEEGDL 7

RESULT 84
US-11-041-893-178
/ Sequence 178, Application US/11041893
/ Publication No. US20060002941A1
/ GENERAL INFORMATION:
/ APPLICANT: Mahaitas, Gregory G.
/ TITLE OF INVENTION: COMPOSITIONS COMPRISING IMMUNE RESPONSE
/ FILE REFERENCE: 100123.401
/ CURRENT APPLICATION NUMBER: US/11/041,893
/ PRIOR FILING DATE: 2005-01-24
/ PRIOR APPLICATION NUMBER: US 60/616,855
/ PRIOR FILING DATE: 2004-10-06
/ PRIOR APPLICATION NUMBER: US 60/538,713
/ PRIOR FILING DATE: 2004-01-23
/ NUMBER OF SEQ ID NOS: 295
/ SOFTWARE: PaateSeq for Windows Version 4.0
/ SEQ ID NO 178
/ LENGTH: 20
/ TYPE: PRF
/ ORGANISM: Toxoplasma gondii
US-11-041-893-178

Query Match
Best Local Similarity 21.9%; Score 23; DB 7; Length 20;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 PGFVGE 16
   ||:|
Db 3 PGDVIE 10

RESULT 85
US-11-107-029-11
/ Sequence 11, Application US/11107029
/ Publication No. US20050271667A1
/ GENERAL INFORMATION:
/ APPLICANT: NGUYEN, MAI H.
/ TITLE OF INVENTION: IDENTIFICATION OF A NOVEL ENDOTHELIAL-DERIVED GENE EG-1
/ FILE REFERENCE: 407T-30410US
/ CURRENT APPLICATION NUMBER: US/11/107,029
/ PRIOR FILING DATE: 2005-04-15
/ PRIOR APPLICATION NUMBER: US10/029,137
/ PRIOR FILING DATE: 2001-12-19
/ NUMBER OF SEQ ID NOS: 34
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 11
/ LENGTH: 17
/ TYPE: PRF
/ ORGANISM: Homo sapiens
```

```
US-11-107-029-11

Query Match
Best Local Similarity 21.4%; Score 22.5; DB 7; Length 17;
Matches 5; Conservative 4; Mismatches 3; Indels 1; Gaps 1;

QY 7 SPFGFVGEVGL 19
   |||:|:|
Db 1 APFG-LPGQASLL 12

RESULT 86
US-10-485-788A-120
/ Sequence 120, Application US/10485788A
/ Publication No. US20050282743A1
/ GENERAL INFORMATION:
/ APPLICANT: Lu, Peter S.
/ APPLICANT: Rabinowitz, Joshua D.
/ APPLICANT: Schweizer, Johannes
/ APPLICANT: Carrick, Deanna Marie
/ APPLICANT: Arbor Vita Corporation
/ TITLE OF INVENTION: Molecular Interactions in Cells
/ FILE REFERENCE: 20054-00320US
/ CURRENT APPLICATION NUMBER: US/10/485,788A
/ CURRENT FILING DATE: 2004-02-03
/ PRIOR APPLICATION NUMBER: US 60/309,841
/ PRIOR FILING DATE: 2001-08-03
/ PRIOR APPLICATION NUMBER: US 60/360,061
/ PRIOR FILING DATE: 2002-02-25
/ PRIOR APPLICATION NUMBER: WO PCT/US02/24655
/ PRIOR FILING DATE: 2002-08-02
/ NUMBER OF SEQ ID NOS: 841
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 120
/ LENGTH: 8
/ TYPE: PRF
/ ORGANISM: Homo sapiens
US-10-485-788A-120

Query Match
Best Local Similarity 21.0%; Score 22; DB 6; Length 8;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DPAKMS 7
   ||:|
Db 1 DPAKGS 7

RESULT 87
US-11-045-024-5161
/ Sequence 5161, Application US/11045024
/ Publication No. US20050271676A1
/ GENERAL INFORMATION:
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Livingston, Brian
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Baker, Denise Marie
/ APPLICANT: Kudo, Ralph
/ APPLICANT: Cells, Esteban
/ APPLICANT: Grey, Howard M.
/ APPLICANT: Epiimmune Inc.
/ TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
/ FILE REFERENCE: Vltus-1 Using Peptide and Nucleic Acid Compositions
/ FILE REFERENCE: 2060.0040007
/ CURRENT APPLICATION NUMBER: US/11/045,024
/ PRIOR FILING DATE: 2005-01-28
/ PRIOR APPLICATION NUMBER: US 09/412,863
/ PRIOR FILING DATE: 1999-10-05
/ PRIOR APPLICATION NUMBER: US 08/027,146
/ PRIOR FILING DATE: 1993-03-05
/ PRIOR APPLICATION NUMBER: US 08/073,205
```

PRIOR FILING DATE: 1993-06-04  
PRIOR APPLICATION NUMBER: US 08/103,396  
PRIOR FILING DATE: 1993-08-06  
PRIOR APPLICATION NUMBER: US 08/159,184  
PRIOR FILING DATE: 1993-11-29  
PRIOR APPLICATION NUMBER: US 08/159,339  
PRIOR FILING DATE: 1993-11-29  
PRIOR APPLICATION NUMBER: US 08/205,713  
PRIOR FILING DATE: 1994-03-04  
PRIOR APPLICATION NUMBER: US 08/347,610  
PRIOR FILING DATE: 1994-12-01  
NUMBER OF SEQ ID NOS: 14528  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 5161  
LENGTH: 8  
TYPE: PRT  
ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS  
US-11-045-024-5161

Query Match 21.0%; Score 22; DB 7; Length 8;  
Best Local Similarity 66.7%; Pred. No. 5.5e+04;  
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 GMSPPG 10  
| | | |  
Db 1 GPPIPG 6

## RESULT 88

US-11-045-024-7282  
Sequence 7282, Application US/11045024  
Publication No. US20050271676A1

## GENERAL INFORMATION:

APPLICANT: Sette, Alessandro  
APPLICANT: Sidney, John  
APPLICANT: Southwood, Scott  
APPLICANT: Livingston, Brian  
APPLICANT: Chesnut, Robert  
APPLICANT: Baker, Denise Marie  
APPLICANT: Celis, Ralphe  
APPLICANT: Kudo, Ralph  
APPLICANT: Grey, Howard M.  
APPLICANT: Bpimmune Inc.  
TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency  
TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions  
FILE REFERENCE: 2060.0040007  
CURRENT APPLICATION NUMBER: US/11/045,024  
CURRENT FILING DATE: 2005-01-28  
PRIOR APPLICATION NUMBER: US 09/412,863  
PRIOR FILING DATE: 1999-10-05  
PRIOR APPLICATION NUMBER: US 08/027,146  
PRIOR FILING DATE: 1993-03-05  
PRIOR APPLICATION NUMBER: US 08/073,205  
PRIOR FILING DATE: 1993-06-04  
PRIOR APPLICATION NUMBER: US 08/103,396  
PRIOR FILING DATE: 1993-08-06  
PRIOR APPLICATION NUMBER: US 08/159,184  
PRIOR FILING DATE: 1993-11-29  
PRIOR APPLICATION NUMBER: US 08/159,339  
PRIOR FILING DATE: 1993-11-29  
PRIOR APPLICATION NUMBER: US 08/205,713  
PRIOR FILING DATE: 1994-03-04  
PRIOR APPLICATION NUMBER: US 08/347,610  
PRIOR FILING DATE: 1994-12-01  
NUMBER OF SEQ ID NOS: 14528  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 7282  
LENGTH: 8  
TYPE: PRT  
ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS  
US-11-045-024-7282

Query Match 21.0%; Score 22; DB 7; Length 8;

Best Local Similarity 66.7%; Pred. No. 5.5e+04;  
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 GMSPPG 10  
| | | |  
Db 1 GPPIPG 6

## RESULT 89

US-11-045-024-13708  
Sequence 13708, Application US/11045024  
Publication No. US20050271676A1

## GENERAL INFORMATION:

APPLICANT: Sette, Alessandro  
APPLICANT: Sidney, John  
APPLICANT: Southwood, Scott  
APPLICANT: Livingston, Brian  
APPLICANT: Chesnut, Robert  
APPLICANT: Baker, Denise Marie  
APPLICANT: Celis, Ralphe  
APPLICANT: Kudo, Ralph  
APPLICANT: Grey, Howard M.  
APPLICANT: Bpimmune Inc.  
TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency  
TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions  
FILE REFERENCE: 2060.0040007  
CURRENT APPLICATION NUMBER: US/11/045,024  
CURRENT FILING DATE: 2005-01-28  
PRIOR APPLICATION NUMBER: US 09/412,863  
PRIOR FILING DATE: 1999-10-05  
PRIOR APPLICATION NUMBER: US 08/027,146  
PRIOR FILING DATE: 1993-03-05  
PRIOR APPLICATION NUMBER: US 08/073,205  
PRIOR FILING DATE: 1993-06-04  
PRIOR APPLICATION NUMBER: US 08/103,396  
PRIOR FILING DATE: 1993-08-06  
PRIOR APPLICATION NUMBER: US 08/159,184  
PRIOR FILING DATE: 1993-11-29  
PRIOR APPLICATION NUMBER: US 08/159,339  
PRIOR FILING DATE: 1993-11-29  
PRIOR APPLICATION NUMBER: US 08/205,713  
PRIOR FILING DATE: 1994-03-04  
PRIOR APPLICATION NUMBER: US 08/347,610  
PRIOR FILING DATE: 1994-12-01  
NUMBER OF SEQ ID NOS: 14528  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 13708  
LENGTH: 9  
TYPE: PRT  
ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS  
US-11-045-024-13708

Query Match 21.0%; Score 22; DB 7; Length 9;  
Best Local Similarity 66.7%; Pred. No. 5.5e+04;  
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 GMSPPG 10  
| | | |  
Db 4 GPPIPG 9

## RESULT 90

US-11-033-039-24  
Sequence 24, Application US/11033039  
Publication No. US20060002947A1

## GENERAL INFORMATION:

APPLICANT: HUMPHREYS, ROBERT  
APPLICANT: XU, MINZHEN  
TITLE OF INVENTION: LI-KEY/ANTIGENIC EPIPTOPE HYBRID PEPTIDE VACCINES  
FILE REFERENCE: REH-2017US01  
CURRENT APPLICATION NUMBER: US/11/033,039  
CURRENT FILING DATE: 2005-01-11  
PRIOR APPLICATION NUMBER: 10/245,871

```
/ PRIOR FILING DATE: 2002-09-17
/ PRIOR APPLICATION NUMBER: 10/197,000
/ PRIOR FILING DATE: 2002-07-17
/ PRIOR APPLICATION NUMBER: 09/396,813
/ PRIOR FILING DATE: 1999-09-14
/ NUMBER OF SEQ ID NOS: 1452
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 24
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Atacchia hypogaea
US-11-033-039-24

Query Match
Best Local Similarity 21.0%; Score 22; DB 7; Length 9;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      8 PGPGI 12
Db      4 PGPGI 8

RESULT 91
US-11-033-039-292
/ Sequence 292, Application US/11033039
/ Publication No. US20060002947A1
/ GENERAL INFORMATION:
/ APPLICANT: HUMPHREYS, ROBERT
/ APPLICANT: XU, MINZHEN
/ TITLE OF INVENTION: LI-KEY/ANTIGENIC EPIOTOPE HYBRID PEPTIDE VACCINES
/ FILE REFERENCE: REH-2017US01
/ CURRENT APPLICATION NUMBER: US/11/033,039
/ CURRENT FILING DATE: 2005-01-11
/ PRIOR APPLICATION NUMBER: 10/245,871
/ PRIOR FILING DATE: 2002-09-17
/ PRIOR APPLICATION NUMBER: 10/197,000
/ PRIOR FILING DATE: 2002-07-17
/ PRIOR APPLICATION NUMBER: 09/396,813
/ PRIOR FILING DATE: 1999-09-14
/ NUMBER OF SEQ ID NOS: 1452
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 292
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-033-039-292

Query Match
Best Local Similarity 21.0%; Score 22; DB 7; Length 9;
Matches 2; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy      10 GRIVGER 16
Db      3 GRIVGER 9

RESULT 92
US-11-045-024-1311
/ Sequence 1311, Application US/11045024
/ Publication No. US20050271676A1
/ GENERAL INFORMATION:
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Livingston, Brian
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Baker, Denise Marie
/ APPLICANT: Celis, Estebean
/ APPLICANT: Kubo, Ralph
/ APPLICANT: Grey, Howard M.
/ APPLICANT: EpiImmune Inc.
/ TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
/ TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
/ NUMBER OF SEQ ID NOS: 14528
```

```
/ FILE REFERENCE: 2060.0040007
/ CURRENT APPLICATION NUMBER: US/11/045,024
/ CURRENT FILING DATE: 2005-01-28
/ PRIOR APPLICATION NUMBER: US 09/412,863
/ PRIOR FILING DATE: 1999-10-05
/ PRIOR APPLICATION NUMBER: US 08/027,146
/ PRIOR FILING DATE: 1993-03-05
/ PRIOR APPLICATION NUMBER: US 08/073,205
/ PRIOR FILING DATE: 1993-06-04
/ PRIOR APPLICATION NUMBER: US 08/103,396
/ PRIOR FILING DATE: 1993-08-06
/ PRIOR APPLICATION NUMBER: US 08/159,184
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/159,339
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/205,713
/ PRIOR FILING DATE: 1994-03-04
/ PRIOR APPLICATION NUMBER: US 08/347,610
/ PRIOR FILING DATE: 1994-12-01
/ NUMBER OF SEQ ID NOS: 14528
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 1311
/ LENGTH: 10
/ TYPE: PRT
/ ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-1311

Query Match
Best Local Similarity 21.0%; Score 22; DB 7; Length 10;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      5 GMSPPG 10
Db      3 GMSPPG 8

RESULT 93
US-11-045-024-6377
/ Sequence 6377, Application US/11045024
/ Publication No. US20050271676A1
/ GENERAL INFORMATION:
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Livingston, Brian
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Baker, Denise Marie
/ APPLICANT: Celis, Estebean
/ APPLICANT: Kubo, Ralph
/ APPLICANT: Grey, Howard M.
/ APPLICANT: EpiImmune Inc.
/ TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
/ TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
/ FILE REFERENCE: 2060.0040007
/ CURRENT APPLICATION NUMBER: US/11/045,024
/ CURRENT FILING DATE: 2005-01-28
/ PRIOR APPLICATION NUMBER: US 09/412,863
/ PRIOR FILING DATE: 1999-10-05
/ PRIOR APPLICATION NUMBER: US 08/027,146
/ PRIOR FILING DATE: 1993-03-05
/ PRIOR APPLICATION NUMBER: US 08/073,205
/ PRIOR FILING DATE: 1993-06-04
/ PRIOR APPLICATION NUMBER: US 08/103,396
/ PRIOR FILING DATE: 1993-08-06
/ PRIOR APPLICATION NUMBER: US 08/159,184
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/159,339
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/205,713
/ PRIOR FILING DATE: 1994-03-04
/ PRIOR APPLICATION NUMBER: US 08/347,610
/ PRIOR FILING DATE: 1994-12-01
/ NUMBER OF SEQ ID NOS: 14528
```





Qy 11 FIVEGVLT 19  
|:|:|:|  
Db 2 FIVEDETVL 10

## RESULT 97

US-11-033-365-5  
Sequence 5, Application US/11033365  
Publication No. US20050250678A1  
GENERAL INFORMATION:  
APPLICANT: Neose Technologies Inc.  
APPLICANT: Defrees, Shawn  
APPLICANT: Zopf, David  
APPLICANT: Wang, Zhigang  
APPLICANT: Clausen, Henrik  
TITLE OF INVENTION: O-linked Glycosylation of peptides  
FILE REFERENCE: 040853-01-5138  
CURRENT FILING DATE: 2005-01-10  
PRIOR FILING DATE: 2004-02-20  
PRIOR APPLICATION NUMBER: 60/535,284  
PRIOR FILING DATE: 2004-01-08  
PRIOR APPLICATION NUMBER: 60/544,411  
PRIOR FILING DATE: 2004-02-12  
PRIOR APPLICATION NUMBER: 60/546,631  
PRIOR FILING DATE: 2004-02-20  
PRIOR APPLICATION NUMBER: 60/555,813  
PRIOR FILING DATE: 2004-03-23  
PRIOR APPLICATION NUMBER: 60/570,891  
PRIOR FILING DATE: 2004-05-12  
NUMBER OF SEQ ID NOS: 213  
SOFTWARE: Patent version 3.2  
SEQ ID NO 5  
LENGTH: 11  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-11-033-365-5

Query Match 21.0%; Score 22; DB 7; Length 11;  
Best Local Similarity 44.4%; Pred. No. 4.5e+02;  
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 2 PAKGMSPPG 10  
|:|:|:|  
Db 2 PTOGAMPTG 10

## RESULT 98

US-11-045-024-3056  
Sequence 3056, Application US/11045024  
Publication No. US20050271676A1  
GENERAL INFORMATION:  
APPLICANT: Sette, Alessandro  
APPLICANT: Sidney, John  
APPLICANT: Southwood, Scott  
APPLICANT: Livingston, Brian  
APPLICANT: Chesnut, Robert  
APPLICANT: Baker, Denise Marie  
APPLICANT: Cells, Esteban  
APPLICANT: Kubo, Ralph  
APPLICANT: Grey, Howard M.  
APPLICANT: EpiImmune Inc.  
TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency  
TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions  
FILE REFERENCE: 2060.0040007  
CURRENT FILING DATE: 2005-01-28  
PRIOR FILING DATE: 2005-01-28  
PRIOR APPLICATION NUMBER: US 09/412,863  
PRIOR FILING DATE: 1999-10-05  
PRIOR APPLICATION NUMBER: US 08/027,146  
PRIOR FILING DATE: 1993-03-05  
PRIOR APPLICATION NUMBER: US 08/073,205  
PRIOR FILING DATE: 1993-06-04

PRIOR APPLICATION NUMBER: US 08/103,396  
PRIOR FILING DATE: 1993-08-06  
PRIOR APPLICATION NUMBER: US 08/159,184  
PRIOR FILING DATE: 1993-11-29  
PRIOR APPLICATION NUMBER: US 08/159,339  
PRIOR FILING DATE: 1993-11-29  
PRIOR APPLICATION NUMBER: US 08/205,713  
PRIOR FILING DATE: 1994-03-04  
PRIOR APPLICATION NUMBER: US 08/347,610  
PRIOR FILING DATE: 1994-12-01  
NUMBER OF SEQ ID NOS: 14528  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 3056  
LENGTH: 11  
TYPE: PRT  
ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS  
US-11-045-024-3056

Query Match 21.0%; Score 22; DB 7; Length 11;  
Best Local Similarity 66.7%; Pred. No. 4.5e+02;  
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 GMSPPG 10  
|:|:|:|  
Db 3 GPIPPG 8

## RESULT 99

US-11-045-024-5702  
Sequence 5702, Application US/11045024  
Publication No. US20050271676A1  
GENERAL INFORMATION:  
APPLICANT: Sette, Alessandro  
APPLICANT: Sidney, John  
APPLICANT: Southwood, Scott  
APPLICANT: Livingston, Brian  
APPLICANT: Chesnut, Robert  
APPLICANT: Baker, Denise Marie  
APPLICANT: Cells, Esteban  
APPLICANT: Kubo, Ralph  
APPLICANT: Grey, Howard M.  
APPLICANT: EpiImmune Inc.  
TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency  
TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions  
FILE REFERENCE: 2060.0040007  
CURRENT FILING DATE: 2005-01-28  
PRIOR FILING DATE: 2005-01-28  
PRIOR APPLICATION NUMBER: US 09/412,863  
PRIOR FILING DATE: 1999-10-05  
PRIOR APPLICATION NUMBER: US 08/027,146  
PRIOR FILING DATE: 1993-03-05  
PRIOR APPLICATION NUMBER: US 08/073,205  
PRIOR FILING DATE: 1993-06-04  
PRIOR APPLICATION NUMBER: US 08/103,396  
PRIOR FILING DATE: 1993-08-06  
PRIOR APPLICATION NUMBER: US 08/159,184  
PRIOR FILING DATE: 1993-11-29  
PRIOR APPLICATION NUMBER: US 08/159,339  
PRIOR FILING DATE: 1993-11-29  
PRIOR APPLICATION NUMBER: US 08/205,713  
PRIOR FILING DATE: 1994-03-04  
PRIOR APPLICATION NUMBER: US 08/347,610  
PRIOR FILING DATE: 1994-12-01  
NUMBER OF SEQ ID NOS: 14528  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 5702  
LENGTH: 11  
TYPE: PRT  
ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS  
US-11-045-024-5702

Query Match 21.0%; Score 22; DB 7; Length 11;  
Best Local Similarity 66.7%; Pred. No. 4.5e+02;

Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 5 GMSPPG 10  
Db 4 GRIPPG 9

RESULT 100

US-11-045-024-9026  
Sequence 9026, Application US/11045024  
Publication No. US20050271676A1  
GENERAL INFORMATION:  
APPLICANT: Sette, Alessandro  
APPLICANT: Sidney, John  
APPLICANT: Southwood, Scott  
APPLICANT: Livingston, Brian  
APPLICANT: Chesnut, Robert  
APPLICANT: Baker, Denise Marie  
APPLICANT: Celis, Esben  
APPLICANT: Kubo, Ralph  
APPLICANT: Grey, Howard M.  
APPLICANT: Bpimmune Inc.  
TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency  
FILE REFERENCE: 2060.0040007  
CURRENT APPLICATION NUMBER: US/11/045,024  
CURRENT FILING DATE: 2005-01-28  
PRIOR APPLICATION NUMBER: US 09/412,863  
PRIOR FILING DATE: 1999-10-05  
PRIOR APPLICATION NUMBER: US 08/027,146  
PRIOR FILING DATE: 1993-03-05  
PRIOR APPLICATION NUMBER: US 08/073,205  
PRIOR FILING DATE: 1993-06-04  
PRIOR APPLICATION NUMBER: US 08/103,396  
PRIOR FILING DATE: 1993-08-06  
PRIOR APPLICATION NUMBER: US 08/159,184  
PRIOR FILING DATE: 1993-11-29  
PRIOR APPLICATION NUMBER: US 08/159,339  
PRIOR FILING DATE: 1993-11-29  
PRIOR APPLICATION NUMBER: US 08/205,713  
PRIOR FILING DATE: 1994-03-04  
PRIOR APPLICATION NUMBER: US 08/347,610  
PRIOR FILING DATE: 1994-12-01  
NUMBER OF SEQ ID NOS: 14528  
SOFTWARE: FASTSEQ for Windows Version 4.0  
SEQ ID NO 9026  
LENGTH: 11  
TYPE: PR1  
ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS  
US-11-045-024-9026

Query Match 21.0%; Score 22; DB 7; Length 11;  
Best Local Similarity 44.4%; Pred. No. 4.5e+02;  
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
Qy 9 PGRIVSEG 17  
Db 1 PGULETSEG 9

Search completed: January 20, 2006, 19:46:30  
Job time : 9.07692 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 20, 2006, 18:55:50 ; Search time 11.3462 Seconds  
(without alignments)  
169.602 Million cell updates/sec

Title: US-09-662-293-4  
Perfect score: 105  
Sequence: 1 DPAKGMSPGFIVGSEGVLS 20

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 3886

Minimum DB seq length: 0  
Maximum DB seq length: 20

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database :  
1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the change being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	32	30.5	15	2	F57789
2	31	29.5	17	2	PH0082
3	28	26.7	10	2	S26506
4	28	26.7	15	2	S54712
5	28	26.7	20	2	B60801
6	27	25.7	16	2	C49048
7	27	25.7	16	2	PS0210
8	26	24.8	9	2	S65433
9	26	24.8	9	2	A43065
10	26	24.8	9	2	B60246
11	26	24.8	9	2	A26744
12	26	24.8	9	2	A61057
13	26	24.8	9	2	A60579
14	26	24.8	9	2	A61363
15	26	24.8	9	2	A61358
16	26	24.8	11	2	S13379
17	26	24.8	11	2	B26744
18	26	24.8	11	2	A61365
19	26	24.8	12	2	A61360
20	26	24.8	12	2	A61359
21	26	24.8	13	2	A61361
22	26	24.8	14	2	A61362
23	26	24.8	15	2	A36279
24	26	24.8	17	1	A61339
25	26	24.8	20	2	S39380
26	25	23.8	10	2	A36454
27	25	23.8	10	2	C60527
28	25	23.8	12	2	T46794
29	25	23.8	20	2	A33878

30	25	23.8	20	2	A61576	insulin-like growth
31	25	23.8	20	2	A46644	temperature-labile
32	24	22.9	10	2	B60588	sperm-activating p
33	24	22.9	10	2	B60788	sperm-activating p
34	24	22.9	15	2	I65478	c-Ki-ras - hamster
35	24	22.9	15	2	PT0097	glutathione peroxi
36	24	22.9	17	2	S77834	DNA-directed RNA p
37	24	22.9	18	2	S57518	T cell receptor be
38	24	22.9	19	2	C37072	proteoglycan 65k c
39	24	22.9	19	2	S11611	ribosomal protein
40	24	22.9	20	2	PQ0688	photosystem I 14.0
41	24	22.9	20	2	PQ0687	photosystem I 14.1
42	23	21.9	9	2	S35538	ribosomal protein
43	23	21.9	10	2	C60588	sperm-activating p
44	23	21.9	10	2	B60527	sperm-activating p
45	23	21.9	10	2	I60588	sperm-activating p
46	23	21.9	12	2	C36201	1-aminocyclopropan
47	23	21.9	13	2	A59387	VCAM-1 5'UTR bindi
48	23	21.9	18	2	S13974	chlorophyll a/b-bi
49	23	21.9	19	2	S29766	cytochrome c (EDH)
50	23	21.9	19	2	B28457	proteoglycan II, b
51	23	21.9	20	2	B39108	lipoprotein Acld p
52	23	21.9	20	2	A31516	lectin, galactose/
53	23	21.9	20	2	S38288	50K allergen - per
54	23	21.9	20	2	S06150	photosystem I chal
55	22.5	21.4	15	2	PA0040	malate dehydrogena
56	22	21.0	9	2	PA0033	protein QA300033 -
57	22	21.0	10	2	D60527	sperm-activating p
58	22	21.0	12	2	PS0213	28K protein 4412 -
59	22	21.0	12	2	S65409	histone H2B - huma
60	22	21.0	14	2	A35377	GTP-binding protei
61	22	21.0	14	2	PS0255	20K protein 5503 -
62	22	21.0	15	2	PA0110	translation elonga
63	22	21.0	16	2	A59042	alpha-conotoxin Ep
64	22	21.0	18	2	A36133	hypothetical prote
65	22	21.0	18	2	I59649	human leukocyte an
66	22	21.0	20	2	S19240	histone H2B (clone
67	22	21.0	20	2	B33290	histone H2B - huma
68	22	21.0	20	2	C56385	nitrophorin 3 - Rh
69	21	20.0	8	2	A35768	T-cell receptor al
70	21	20.0	9	2	PD0027	pev-tachykinin - p
71	21	20.0	10	2	F60527	sperm-activating p
72	21	20.0	10	2	S39030	lysyl-bradykinin -
73	21	20.0	11	2	A40693	transgelin - sheep
74	21	20.0	12	2	S39762	cytochrome P450 U7
75	21	20.0	12	2	B58502	43.2K bile stone p
76	21	20.0	14	2	B60683	malate dehydrogena
77	21	20.0	15	2	B39109	hypothetical 1.5K
78	21	20.0	15	2	S05700	insulin-like growth
79	21	20.0	15	2	PL0110	complement factor
80	21	20.0	16	2	S55307	glutathione transf
81	21	20.0	16	2	A31963	pyruvate dehydroge
82	21	20.0	17	2	S01104	hypothetical prote
83	21	20.0	17	2	I55612	thyroid hormone re
84	21	20.0	17	2	I51203	myosin heavy chain
85	21	20.0	18	2	A39997	group III allergen
86	21	20.0	18	2	A35678	hypothetical prote
87	21	20.0	19	2	B29501	fibriopeptide A -
88	21	20.0	19	2	A48400	phosphocarrier pro
89	21	20.0	19	2	S23233	vitronectin - ghee
90	21	20.0	19	2	S02808	vitronectin - ghee
91	21	20.0	19	2	S22232	vitronectin - bovine
92	21	20.0	20	2	B48400	phosphocarrier pro
93	21	20.0	20	2	S65399	immunodeficiency v
94	21	20.0	20	2	A61414	chymotrypsin (EC 3
95	21	20.0	20	2	I53671	neurofilament heav
96	20.5	19.5	20	2	S05411	carboxylesterase (
97	20.5	19.5	20	2	A39543	collagen alpha 1(I
98	20	19.0	8	2	PT0559	T-cell receptor be
99	20	19.0	8	2	PT0554	T-cell receptor be
100	20	19.0	9	2	B41983	orf downstream to b

## ALIGNMENTS

## RESULT 1

F57789  
galbladder stone matrix protein 2, 41K - human (fragment)  
CjSpecies: Homo sapiens (man)  
CjDate: 23-Feb-1996 #sequence\_revision 23-Feb-1996 #text\_change 09-Jul-2004  
CjAccession: F57789  
R.Binette, J.P.; Binette, M.B.  
submitted to the Protein Sequence Database, February 1996  
AjDescription: The proteins of galbladder stones.  
AjReference number: A57789  
AjAccession: F57789  
AjStatus: preliminary  
AjMolecule type: protein  
AjResidues: 1-15 <BIN>  
AjCross-references: UNIPROT:Q7M4P9; UNIPARC:UPI000017C122  
AjNote: 9-Phe was also found

Query Match 30.5%; Score 32; DB 2; Length 15;  
Best Local Similarity 60.0%; Pred. No. 79;  
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 8 PPGFVGEERG 17  
| | | | |  
Db 5 PDGFIEGSG 14

## RESULT 2

PH0082  
neuroglian protein, short form - fruit fly (Drosophila sp.) (fragment)  
CjSpecies: Drosophila sp.  
CjDate: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 16-Jul-1999  
CjAccession: PH0082  
R.Hortsch, M.; Bieber, A.J.; Patel, N.H.; Goodman, C.S.  
Neuron 4, 697-709, 1990  
AjTitle: Differential splicing generates a nervous system-specific form of Drosophila ne  
AjReference number: PH0082; MUID:90262720; PMID:1693086  
AjAccession: PH0082  
AjStatus: preliminary  
AjMolecule type: mRNA  
AjResidues: 1-17 <HOR>  
AjCross-references: UNIPARC:UPI000017BEEF

Query Match 29.5%; Score 31; DB 2; Length 17;  
Best Local Similarity 40.0%; Pred. No. 1.3e+02;  
Matches 6; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 5 GMSPPGFVGEERGVL 19  
| | | | |  
Db 1 GMSPPGFVGEERGVL 15

## RESULT 3

S26506  
collagen alpha 1(VI) chain - bovine (fragment)  
CjSpecies: Bos primigenius taurus (cattle)  
CjDate: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 09-Jul-2004  
CjAccession: S26506  
R.Jander, R.; Rautenberg, J.; Glanville, R.W.  
Eur. J. Biochem. 133, 39-46, 1983  
AjTitle: Further characterization of the three polypeptide chains of bovine and human sh  
AjReference number: S26506; MUID:83209648; PMID:6652033  
AjAccession: S26506  
AjStatus: preliminary  
AjMolecule type: protein  
AjResidues: 1-10 <JAN>  
AjCross-references: UNIPROT:Q7M2N0; UNIPARC:UPI000017C4R3  
CjKeywords: hydroxyproline  
F19/Modified site: hydroxyproline (Pro) #status experimental  
Query Match 26.7%; Score 28; DB 2; Length 10;

Best Local Similarity 66.7%; Pred. No. 2.1e+02;  
Matches 6; Conservative 1; Mismatches 0; Indels 2; Gaps 1;

QY 2 PAKGMSPPG 10  
| | | | |  
Db 4 PARG--PPG 10

## RESULT 4

SS4712  
zein Zp22/6 protein - maize  
CjSpecies: Zea mays (maize)  
CjDate: 23-Aug-1995 #sequence\_revision 19-Oct-1995 #text\_change 09-Jul-2004  
CjAccession: SS4712  
R.Chandhuri, S.; Messing, J.  
Mol. Gen. Genet. 246, 707-715, 1995  
AjTitle: RFLP mapping of the maize dzr1 locus, which regulates methionine-rich 10 kDa ze  
AjReference number: SS4712; MUID:95206245; PMID:7898438  
AjAccession: SS4712  
AjStatus: preliminary  
AjMolecule type: protein  
AjResidues: 1-15 <CHA>  
AjCross-references: UNIPROT:Q7M1F8; UNIPARC:UPI000017B16A

Query Match 26.7%; Score 28; DB 2; Length 15;  
Best Local Similarity 36.4%; Pred. No. 3.4e+02;  
Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 PAKGMSPPGFI 12  
| | | | |  
Db 4 PQOSLAPPAIL 14

## RESULT 5

B60801  
acrosome stabilizing factor small chain - rabbit (fragment)  
CjSpecies: Oryctolagus cuniculus (domestic rabbit)  
CjDate: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999  
CjAccession: B60801  
R.Wilson, W.L.; Oliphant, G.  
Biol. Reprod. 37, 159-169, 1987  
AjTitle: Isolation and biochemical characterization of the subunits of the rabbit sperm  
AjReference number: A60801; MUID:88000873; PMID:1651543  
AjAccession: B60801  
AjMolecule type: protein  
AjResidues: 1-20 <WIL>  
AjCross-references: UNIPARC:UPI000017C5B4  
AjComment: spermatozoa must undergo capacitation and the acrosome reaction to become cap  
CjKeywords: glycoprotein, semen

Query Match 26.7%; Score 28; DB 2; Length 20;  
Best Local Similarity 50.0%; Pred. No. 4.7e+02;  
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 DPAKMSPPG 10  
| | | | |  
Db 1 DTKRAAEPPG 10

## RESULT 6

C49048  
T-cell receptor beta chain V region (CDR3 junction, clone Vbeta20.1) - human (fragment)  
CjSpecies: Homo sapiens (man)  
CjDate: 21-Jan-1994 #sequence\_revision 18-Nov-1994 #text\_change 30-May-1997  
CjAccession: C49048  
R.Stoud, M.; Kjeldsen-Kragh, J.; Suleyman, S.; Vinje, O.; Natvig, J.B.; Forre, O.  
Eur. J. Immunol. 22, 2413-2418, 1992  
AjTitle: Limited heterogeneity of T cell receptor variable region gene usage in juvenile  
AjReference number: A49048; MUID:92387250; PMID:1387614  
AjAccession: C49048  
AjStatus: preliminary; not compared with conceptual translation  
AjMolecule type: mRNA  
AjResidues: 1-16 <SIO>

A/Cross-references: UNIPARC:UPI000017C3A9  
 A/Experimental source: patient EV, IL-2R+ synovial T-cells  
 A/Note: sequence extracted from NCBI backbone (NCBIP:113265)  
 C/Keywords: T-cell receptor

Query Match 25.7%; Score 27; DB 2; Length 16;  
 Best Local Similarity 57.1%; Pred. No. 5.2e+02;  
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 8 PGFV 14  
 DB 10 PGFVFG 16

## RESULT 7

PS0210  
 28K protein 4209 - rice (strain Nihonbare) (fragment)

C/Species: Oryza sativa (rice)  
 C/Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 09-Jul-2004  
 C/Accession: PS0210

R/Tsugita, A.; Miyake, N.

Submitted to JIPID, April 1993

A/Reference number: PS0208

A/Accession: PS0210

A/Molecule type: protein

A/Residues: 1-16 <TSA>

A/Cross-references: UNIPROT:Q7M281; UNIPARC:UPI000017B0F9

A/Experimental source: germ, brain, strain Nihonbare

C/Comment: molecular weight 28K, pI 7.3.

Query Match 25.7%; Score 27; DB 2; Length 16;  
 Best Local Similarity 42.9%; Pred. No. 5.2e+02;  
 Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 9 PGFV 15  
 DB 1 PGLVIGD 7

## RESULT 8

865433  
 bradykinin - horn fly (fragment)

C/Species: Haematobia irritans (horn fly)

C/Date: 28-Oct-1996 #sequence\_revision 13-Mar-1997 #text\_change 13-Mar-1997

C/Accession: 865433

R/Wiffels, G.; Fitzgerald, C.; Gough, J.; Riding, G.; Elvin, C.; Kemp, D.; Willadsen, F.

Bur. J. Biochem. 237, 414-423, 1996

A/Title: Cloning and characterisation of angiotensin-converting enzyme from the dipteran

A/Reference number: 865431; PMID:96215437; PMID:8647080

A/Accession: 865433

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-9 <MID>

A/Cross-references: UNIPARC:UPI000002CF4A

A/Note: the source is designated as Haematobia irritans exigua

Query Match 24.8%; Score 26; DB 2; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PGFV 11  
 DB 2 PGFV 5

## RESULT 9

A43065  
 hydroxyproline-3-bradykinin - frog (Helleophryne purcellii)

C/Species: Helleophryne purcellii

C/Date: 07-Oct-1994 #sequence\_revision 07-Oct-1994 #text\_change 09-Jul-2004

C/Accession: A43065

R/Nakajima, T.; Yasuhara, T.; Bragmar, G.F.; Vissler, J.

Experientia 35, 1133, 1979

A/Title: Occurrence of Hrp(3)-bradykinin in methanol extracts of the skin of the South

A/Reference number: A43065; PMID:80024576; PMID:488255

A/Accession: A43065

A/Molecule type: protein

A/Residues: 1-9 <NA>

A/Cross-references: UNIPROT:Q7L217; UNIPARC:UPI000002CF4A

C/Keywords: bradykinin; hydroxyproline; skin

F3/Modified site: hydroxyproline (Pro) #status experimental

Query Match 24.8%; Score 26; DB 2; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PGFV 11  
 DB 2 PGFV 5

## RESULT 10

B60246  
 ornitho-kinin - chicken

C/Species: Gallus gallus (chicken)

C/Date: 11-Dec-1992 #sequence\_revision 11-Dec-1992 #text\_change 16-Aug-2004

C/Accession: B60246

R/Kimura, M.; Sueyoshi, T.; Morita, T.; Tanaka, K.; Iwanaga, S.

Adv. Exp. Med. Biol. 247A, 359-367, 1989

A/Title: Ornitho-kininogen and ornitho-kinin: isolation, characterization and chemical

A/Reference number: A60246; PMID:90102072; PMID:2603803

A/Accession: B60246

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-9 <KIM>

A/Cross-references: UNIPROT:Q7L250; UNIPARC:UPI000017A4F8

Query Match 24.8%; Score 26; DB 2; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PGFV 11  
 DB 2 PGFV 5

## RESULT 11

A26744  
 bradykinin-like peptide - garden dagger wasp

N/Alternate names: Thr-6-bradykinin

C/Species: Megascolla flavifrons (garden dagger wasp)

C/Date: 08-Mar-1989 #sequence\_revision 08-Mar-1989 #text\_change 05-Oct-2004

C/Accession: A26744

R/Yasuhara, T.; Mantel, P.; Nakajima, T.; Plek, T.

Toxicol 25, 527-535, 1987

A/Title: Two kinins isolated from an extract of the venom reservoirs of the solitary wa

A/Reference number: A94322; PMID:87293024; PMID:3617088

A/Accession: A26744

A/Molecule type: protein

A/Residues: 1-9 <YAS>

A/Cross-references: UNIPARC:UPI000012DF29

Query Match 24.8%; Score 26; DB 2; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PGFV 11  
 DB 2 PGFV 5

## RESULT 12

A61057  
 Thr-6 bradykinin - scollid wasp (Colpa interrupta)

C/Species: Colpa interrupta

C/Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 05-Oct-2004

C/Accession: A61057  
 R.Piek, T.; Hue, B.; Mantel, P.; Nakajima, T.; Peihare, M.; Yasuhara, T.  
 Comp. Biochem. Physiol. C 96, 157-162, 1990  
 A/Title: Thrombin(6)-bradykinin in the venom of the wasp Colpa interrupta (F.) presynap  
 A/Reference number: A61057; PMID:91130217; PMID:1980872  
 A/Accession: A61057  
 A/Molecule type: protein  
 A/Residues: 1-9 <PIR>  
 A/Cross-references: UNIPARC:UPI000012DP29  
 C/Keywords: bradykinin; presynaptic neurotoxin; venom

Query Match 24.8%; Score 26; DB 2; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PPGF 11  
 ||||  
 Db 2 PPGF 5

## RESULT 13

A60579  
 bradykinin-like peptide - slider turtle  
 C/Species: Pseudemys scripta (slider)  
 C/Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 05-Oct-2004  
 C/Accession: A60579  
 R.Conlon, J.M.; Hicks, J.W.; Smith, D.D.  
 Endocrinology 126, 985-991, 1990  
 A/Title: Isolation and biological activity of a novel kinin ([Thr(6)]bradykinin) from th  
 A/Reference number: A60579; PMID:9012625; PMID:2298179  
 A/Accession: A60579  
 A/Molecule type: protein  
 A/Residues: 1-9 <CON>  
 A/Cross-references: UNIPARC:UPI000012DP29  
 C/Comment: This peptide increases aortic blood flow but, unlike bradykinin in mammalian  
 C/Keywords: plasma

Query Match 24.8%; Score 26; DB 2; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PPGF 11  
 ||||  
 Db 2 PPGF 5

## RESULT 14

A61363  
 bradykinin - common frog  
 C/Species: Rana temporaria (common frog)  
 C/Date: 09-Sep-1994 #sequence\_revision 09-Sep-1994 #text\_change 05-Oct-2004  
 C/Accession: A61363  
 R.Anaestasi, A.; Brepamer, V.; Bertaccini, G.  
 Comp. Biochem. Physiol. A 14, 43-52, 1965  
 A/Title: Occurrence of bradykinin in the skin of Rana temporaria.  
 A/Reference number: A61363  
 A/Accession: A61363  
 A/Status: preliminary  
 A/Molecule type: protein  
 A/Residues: 1-9 <ANA>  
 A/Cross-references: UNIPROT:Q7LZJ8; UNIPARC:UPI000002CF4A  
 C/Keywords: skin

Query Match 24.8%; Score 26; DB 2; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PPGF 11  
 ||||  
 Db 2 PPGF 5

## RESULT 15

A61358  
 bradykinin-like peptide I - Japanese pond frog  
 C/Species: Rana nigromaculata (Japanese pond frog)  
 C/Date: 09-Sep-1994 #sequence\_revision 09-Sep-1994 #text\_change 05-Oct-2004  
 C/Accession: A61358  
 R.Nakajima, T.  
 Chem. Pharm. Bull. 16, 769-770, 1968  
 A/Title: Occurrence of a new active peptide on smooth muscle and bradykinin in the skin  
 A/Reference number: A61358; PMID:68412013; PMID:5677638  
 A/Accession: A61358  
 A/Status: preliminary  
 A/Molecule type: protein  
 A/Residues: 1-9 <NAK>  
 A/Cross-references: UNIPROT:Q7LZ54; UNIPARC:UPI000017A4F0  
 C/Keywords: skin

Query Match 24.8%; Score 26; DB 2; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PPGF 11  
 ||||  
 Db 2 PPGF 5

## RESULT 16

S13279  
 Ile-Ser-bradykinin - human (fragment)  
 N/Alternate names: T-kinin  
 C/Species: Homo sapiens (man)  
 C/Date: 02-Dec-1993 #sequence\_revision 13-Mar-1997 #text\_change 09-Jul-2004  
 C/Accession: S13279  
 R.Wunderer, G.; Walter, I.; Eschenbacher, B.; Lang, M.; Kellermann, J.; Kindermann, G.  
 Biol. Chem. Hoppe-Seyler 371, 977-981, 1990  
 A/Title: Ile-Ser-bradykinin is an aberrant permeability factor in various human malignan  
 A/Reference number: S13279; PMID:9116748; PMID:2076202  
 A/Accession: S13279  
 A/Molecule type: protein  
 A/Residues: 1-11 <WUN>  
 A/Cross-references: UNIPROT:Q7MAP1; UNIPARC:UPI0000148EBE  
 C/Keywords: bradykinin

Query Match 24.8%; Score 26; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 4.9e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PPGF 11  
 ||||  
 Db 4 PPGF 7

## RESULT 17

B26744  
 megascollakinin - garden dagger wasp  
 N/Alternate names: 6-Thr-bradykinin-Iys-Ala  
 C/Species: Megascollia flavifrons (garden dagger wasp)  
 C/Date: 08-Mar-1989 #sequence\_revision 08-Mar-1989 #text\_change 05-Oct-2004  
 C/Accession: B26744; A28609  
 R.Yasuhara, T.; Mantel, P.; Nakajima, T.; Piek, T.  
 Toxicon 25, 527-535, 1987  
 A/Title: Two kinins isolated from an extract of the venom reservoirs of the solitary wa-  
 A/Reference number: A94322; PMID:87293024; PMID:5617088  
 A/Accession: B26744  
 A/Molecule type: protein

Query Match 24.8%; Score 26; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 4.9e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

A/Residues: 1-11 <YAS>  
 A/Cross-references: UNIPROT:P12797; UNIPARC:UPI0000126AD6  
 R.Nakajima, T.; Piek, T.; Yasuhara, T.; Mantel, P.  
 Toxicon 26, 34, 1988  
 A/Title: Two kinins isolated from the venom of Megascollia flavifrons.  
 A/Accession: A28609  
 A/Molecule type: protein  
 A/Residues: 1-11 <NAK>



A/Cross-references: UNIPARC:UPI0000126AD6  
C/Keywords: bradykinin, presynaptic neurotoxin, venom

Query Match 24.8%; Score 26; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 4.9e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PPGF 11  
Db 2 PPGF 5

## RESULT 18

A61365  
phyllotoxin - Rohde's leaf frog  
N/Alternate names: bradykinin-1-iso-leucyl-tyrosine O-sulfate  
C/Species: Phyllomedusa rohdei (Rohde's leaf frog)  
C/Date: 09-Sep-1994 #sequence\_revision 09-Sep-1994 #text\_change 05-Oct-2004  
C/Accession: A61365  
R/Author: A.; Bertaccini, G.; Bergamer, V.  
A/Title: Pharmacological data on phyllotoxin (bradykinin-1-iso-leucyl-tyrosine O-sulphate)  
A/Reference number: A61365; PMID:5970899  
A/Accession: A61365  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-11 <ANA>  
A/Cross-references: UNIPROT:Q7L252; UNIPARC:UPI000017A4F2  
C/Keywords: sulfoprotein  
P/1/Binding site: sulfate (Tyr) (covalent) #status experimental

Query Match 24.8%; Score 26; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 4.9e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PPGF 11  
Db 2 PPGF 5

## RESULT 19

A61360  
vespakinin M - hornet (Vespa mandarinia)  
C/Species: Vespa mandarinia  
C/Date: 09-Sep-1994 #sequence\_revision 09-Sep-1994 #text\_change 05-Oct-2004  
C/Accession: A61360  
R/Kishimura, H.; Yasuhara, T.; Yoshida, H.; Nakajima, T.  
Chem. Pharm. Bull. 24, 2896-2897, 1976  
A/Title: Vespakinin-M, a novel bradykinin analogue containing hydroxyproline, in the ven  
A/Reference number: A61360; PMID:7714342; PMID:1017116  
A/Accession: A61360  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-12 <KRS>  
A/Cross-references: UNIPROT:Q7M373; UNIPARC:UPI000017A4F3  
C/Keywords: hydroxyproline, venom  
P/1/Modified site: 4-hydroxyproline (Pro) #status experimental

Query Match 24.8%; Score 26; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 5.4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PPGF 11  
Db 3 PPGF 6

## RESULT 20

A61359  
vespakinin X - hornet (Vespa xanthoptera)  
C/Species: Vespa xanthoptera  
C/Date: 09-Sep-1994 #sequence\_revision 09-Sep-1994 #text\_change 05-Oct-2004  
C/Accession: A61359

R/Yasuhara, T.; Yoshida, H.; Nakajima, T.

Chem. Pharm. Bull. 25, 936-941, 1977

A/Title: Chemical investigation of the hornet (Vespa xanthoptera Cameron) venom. The st

A/Reference number: A61359; PMID:87187853; PMID:264186

A/Accession: A61359

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-12 <YAS>

A/Cross-references: UNIPROT:Q7M372; UNIPARC:UPI000017A4F4

C/Keywords: venom

Query Match 24.8%; Score 26; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 5.4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PPGF 11  
Db 3 PPGF 6

## RESULT 21

A61361  
bradykinin-like peptide - Bombina orientalis  
C/Species: Bombina orientalis  
C/Date: 09-Sep-1994 #sequence\_revision 09-Sep-1994 #text\_change 05-Oct-2004  
C/Accession: A61361  
R/Yasuhara, T.; Hira, M.; Nakajima, T.; Yanaihara, N.; Yanaihara, C.; Hashimoto, T.; Sa  
Chem. Pharm. Bull. 21, 1388-1391, 1973  
A/Title: Active peptide on smooth muscle in the skin of Bombina orientalis Boulenger a  
A/Reference number: A61361; PMID:73256822; PMID:4732297  
A/Accession: A61361  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-13 <YAS>  
A/Cross-references: UNIPROT:P63060; UNIPARC:UPI000017A4F5  
C/Keywords: skin

Query Match 24.8%; Score 26; DB 2; Length 13;  
Best Local Similarity 100.0%; Pred. No. 6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PPGF 11  
Db 2 PPGF 5

## RESULT 22

A61362  
bradykinin-like peptide III - Japanese pond frog  
C/Species: Rana nigromaculata (Japanese pond frog)  
C/Date: 09-Sep-1994 #sequence\_revision 09-Sep-1994 #text\_change 05-Oct-2004  
C/Accession: A61362  
R/Nakajima, T.  
Chem. Pharm. Bull. 16, 2088-2089, 1968  
A/Title: On the third active peptide on smooth muscle in the skin of Rana nigromaculata  
A/Reference number: A61362; PMID:69117202; PMID:5751736  
A/Accession: A61362  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-14 <NAK>  
A/Cross-references: UNIPROT:Q7L253; UNIPARC:UPI000017A4F1  
C/Keywords: skin

Query Match 24.8%; Score 26; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 6.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PPGF 11  
Db 2 PPGF 5

## RESULT 23

A36279  
chemoattractant protease - earthworm (Lumbricus terrestris) (fragment)  
C:Species: Lumbricus terrestris (Common earthworm)  
C>Date: 18-Jan-1991 #sequence\_revision 18-Jan-1991 #text\_change 09-Jul-2004  
C/Accession: A36279  
R:Jiang, X.C.; Inouchi, J.; Wang, D.; Halpern, M.  
J. Biol. Chem. 265, 8736-8744, 1990  
A>Title: Purification and characterization of a chemoattractant from electric shock-induced snakes.  
A/Reference number: A36279; MUID:90256800; PMID:2160465  
A/Accession: A36279  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-15 <UIA>  
A/Cross-references: UNIPROT:O44335; UNIPARC:UPI000017BD77

Query Match 24.8%; Score 26; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PGPF 11  
| | | |  
Db 5 PGPF 8

RESULT 24  
A61339  
vespulinin 1 - eastern yellowjacket  
N/Contains: vespulinin 2  
C:Species: Vespula maculifrons (eastern yellowjacket)  
C>Date: 17-Jul-1994 #sequence\_revision 07-Oct-1994 #text\_change 09-Jul-2004  
C/Accession: A61339  
R:Yoshida, H.; Geller, R.G.; Pisano, J.J.  
Biochemistry 15, 61-64, 1976  
A>Title: Vespulinins: new carbohydrate-containing bradykinin derivatives.  
A/Reference number: A61339; MUID:76114777; PMID:1247511  
A/Accession: A61339  
A/Molecule type: protein  
A/Residues: 1-17 <YOS>  
A/Cross-references: UNIPROT:P57672; UNIPARC:UPI0000138459  
C/Superfamily: vespulinin  
C/Keywords: antihypertensive; bradykinin; glycoprotein; venom  
F:1-17/Product: vespulinin 1 #status experimental <MARI>  
F:3-17/Product: vespulinin 2 #status experimental <MARI>  
F:9-17/Region: bradykinin-like  
F:3,4/Binding site: carbohydrate (Thr) (covalent) #status experimental

Query Match 24.8%; Score 26; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 8.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PGPF 11  
| | | |  
Db 10 PGPF 13

RESULT 25  
S39380  
pectinesterase (EC 3.1.1.11) - papaya  
N/Alternate names: pectin methylsterase  
C:Species: Carica papaya (papaya)  
C>Date: 19-Mar-1997 #sequence\_revision 25-Apr-1997 #text\_change 17-Mar-1999  
C/Accession: S39380  
R:Lim, Y.M.; Chung, M.C.M.  
Arch. Biochem. Biophys. 307, 15-20, 1993  
A>Title: Isolation and characterization of pectin methylsterase from Papaya.  
A/Reference number: S39380; MUID:94058247; PMID:8239653  
A/Accession: S39380  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-20 <LIM>  
A/Cross-references: UNIPARC:UPI000017AF3D  
C/Keywords: carboxylic ester hydrolase

Query Match 24.8%; Score 26; DB 2; Length 20;  
Best Local Similarity 40.0%; Pred. No. 9.7e+02;  
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 9 PGFVGEBCV 18  
| : : : |  
Db 5 PAAVADGV 14

RESULT 26  
A36454  
trypsin-modulating oostatic factor - yellow fever mosquito  
C:Species: Aedes aegypti (yellow fever mosquito)  
C>Date: 12-Apr-1991 #sequence\_revision 12-Apr-1991 #text\_change 09-Jul-2004  
C/Accession: A36454; A61630  
R:Borovsky, D.; Carlson, D.A.; Griffin, P.R.; Shabanowitz, J.; Hunt, D.F.  
FASEB J. 4, 3015-3020, 1990  
A>Title: Mosquito oostatic factor: a novel decapeptide modulating trypsin-like enzyme bi  
A/Reference number: A36454; MUID:90367888; PMID:2394318  
A/Accession: A36454  
A/Molecule type: protein  
A/Residues: 1-10 <BOR>  
A/Cross-references: UNIPROT:P19425; UNIPARC:UPI0000034259  
R:Borovsky, D.; Carlson, D.A.; Griffin, P.R.; Shabanowitz, J.; Hunt, D.F.  
Insect Biochem. Mol. Biol. 23, 703-712, 1993  
A>Title: Mass spectrometry and characterization of Aedes aegypti trypsin modulating oost  
A/Reference number: A61630; MUID:93357794; PMID:8335526  
A/Accession: A61630  
A/Molecule type: protein  
A/Residues: 1-10 <BOS>  
A/Cross-references: UNIPARC:UPI0000034259  
A/Note: none of the amino acids is modified  
C/Function: inhibits synthesis of trypsin- and chymotrypsin-like enzymes by midgut ep  
A/Description: inhibits synthesis of trypsin- and chymotrypsin-like enzymes by midgut ep  
C/Keywords: hormone

Query Match 23.8%; Score 25; DB 2; Length 10;  
Best Local Similarity 55.6%; Pred. No. 6.4e+02;  
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 DEAKGMSPP 9  
| | | | |  
Db 2 DEAPPPPP 10

RESULT 27  
C60527  
sperm-activating peptide (Ser-3, Ile-4, Gly-5 SAB-I) - sea urchin (Tripneustes gratilla)  
N/Alternate names: speract homolog TG-4  
C:Species: Tripneustes gratilla  
C>Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 16-Aug-2004  
C/Accession: C60527; D39572  
R:Yoshino, K.I.; Kajitara, H.; Nomura, K.; Takao, T.; Shimonishi, Y.; Kurita, M.; Yamaguchi  
Comp. Biochem. Physiol. B 94, 739-751, 1989  
A>Title: A halogenated amino acid-containing sperm activating peptide and its related pe  
ctus nudus, Echinometra mathaei and Heterocentrotus mammillatus.  
A/Reference number: A60527  
A/Accession: C60527  
A/Molecule type: protein  
A/Residues: 1-10 <YOS>  
A/Cross-references: UNIPROT:Q7M376; UNIPARC:UPI000017A4E5  
A/Note: this peptide did not contain bromophenylalanine  
R:Yoshino, K.; Takao, T.; Suhara, M.; Kitai, T.; Hori, H.; Nomura, K.; Yamaguchi, M.; Si  
Biochemistry 30, 6203-6209, 1991  
A>Title: Identification of a novel amino acid, o-bromo-L-phenylalanine, in egg-associated  
A/Reference number: A39572; MUID:91283461; PMID:2059627  
A/Accession: D39572  
A/Molecule type: protein  
A/Residues: 1-10 <YOS>  
A/Cross-references: UNIPARC:UPI000017A4E5  
A/Note: this peptide contained bromophenylalanine  
C/Keywords: bromine

F/2/Modified site: 2'-bromophenylalanine (Phe) (partial) #status experimental

Query Match 23.8%; Score 25; DB 2; Length 10;

Best Local Similarity 55.6%; Pred. No. 6.4e+02;

Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 10 GPTVGEV 18

|||:|:|

1 GFTSGGGV 9

RESULT 28

T46794

hypothetical protein [imported] - Haloarcula marismortui (fragment)

C/Species: Haloarcula marismortui

C/Date: 17-Mar-2000 #sequence\_revision 17-Mar-2000 #text\_change 09-Jul-2004

C/Accession: T46794

R/Arndt, E.

PEBB Lett. 267, 193-198, 1990

A/Title: Nucleotide sequence of four genes encoding ribosomal proteins from the 'S10 and

A/Reference number: S10731; MUID:90356772; PMID:2133141

A/Accession: T46794

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-12 <ARN>

A/Cross-references: UNIPROT:P10971, UNIPARC:UPI000016F7C4, EMBL:X55311, NID:943610; PIDD

Query Match 23.8%; Score 25; DB 2; Length 12;

Best Local Similarity 75.0%; Pred. No. 7.8e+02;

Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 12 IVGEGVL 19

|||||

1 IQGEGDL 8

RESULT 29

A33878

myosin light chain kinase, smooth muscle - turkey (fragment)

C/Species: Melospiza gallopavo (common turkey)

C/Date: 27-Feb-1990 #sequence\_revision 27-Feb-1990 #text\_change 09-Jul-2004

C/Accession: A33878

R/Ikebe, M.; Maruta, S.; Reardon, S.

J. Biol. Chem. 264, 6967-6971, 1989

A/Title: Location of the inhibitory region of smooth muscle myosin light chain kinase.

A/Reference number: A33878; MUID:9214114; PMID:2708351

A/Accession: A33878

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-20 <IKES>

A/Cross-references: UNIPROT:Q7LZH3, UNIPARC:UPI00001755C

C/Superfamily: myosin-light-chain kinase, nonmuscle; fibronectin type III repeat homolog

C/Keywords: smooth muscle

Query Match 23.8%; Score 25; DB 2; Length 20;

Best Local Similarity 50.0%; Pred. No. 1.4e+03;

Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 PAKGSP 9

|||:|:|

8 PPKATRP 15

RESULT 30

A61576

Insulin-like growth factor I - unidentified organism (fragment)

N/Alternate names: Microtetraspora glauca ribosomal protein L30 [misidentification]

C/Species: unidentified organism

C/Date: 28-Oct-1994 #sequence\_revision 28-Oct-1994 #text\_change 04-Feb-2000

C/Accession: A61576

R/Ochi, K.; Miyadoh, S.; Tamura, T.

Int. J. Syst. Bacteriol. 41, 234-239, 1991

A/Title: Polyacrylamide gel electrophoresis analysis of ribosomal protein AT-L30 as a nd

A/Reference number: A61576; MUID:91307971; PMID:1854638

A/Accession: A61576

A/Molecule type: protein

A/Residues: 1-20 <OCH>

A/Cross-references: UNIPARC:UPI0000176668

A/Note: the species was designated Microtetraspora glauca and the protein called ribosc

gests an error

C/Superfamily: Insulin

Query Match 23.8%; Score 25; DB 2; Length 20;

Best Local Similarity 57.1%; Pred. No. 1.4e+03;

Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 11 FTVGEG 17

|||:|:|

10 FVXGERG 16

RESULT 31

A46644

temperature-labile cholesterol ester hydrolase - rat (fragment)

C/Species: Rattus norvegicus (Norway rat)

C/Date: 21-Sep-1993 #sequence\_revision 18-Nov-1994 #text\_change 28-Apr-1995

C/Accession: A46644

R/Wee, S.; Grogan, W.M.

J. Biol. Chem. 268, 8158-8163, 1993

A/Title: Testicular temperature-labile cholesterol ester hydrolase. Relationship to iso-

divalent cations.

A/Reference number: A46644; MUID:93216794; PMID:8463327

A/Accession: A46644

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-20 <WEB>

A/Cross-references: UNIPARC:UPI000006581

A/Experimental source: testis

A/Note: sequence extracted from NCBI backbone (NCBIP:129155)

Query Match 23.8%; Score 25; DB 2; Length 20;

Best Local Similarity 50.0%; Pred. No. 1.4e+03;

Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 6 MSPGPRVGB 15

|||||

6 VSPPAVVB 15

RESULT 32

B60588

sperm-activating peptide (Ala-3, Gly-5 SAP-I) - sea urchin (Strongylocentrotus nudus)

N/Alternate names: speract homolog

C/Species: Strongylocentrotus nudus

C/Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 16-Aug-2004

C/Accession: B60588

R/Yoshino, K.I.; Kajitara, H.; Nomura, K.; Takao, T.; Shimonishi, Y.; Kurita, M.; Yamagu

Comp. Biochem. Physiol. B 94, 733-751, 1989

A/Title: A halogenated amino acid-containing sperm activating peptide and its related p-

otus nudus, Schinometra mathaei and Heterocentrotus mammillatus.

A/Reference number: A60527

A/Accession: B60588

A/Molecule type: protein

A/Residues: 1-10 <YOS>

A/Cross-references: UNIPROT:Q7M4B6, UNIPARC:UPI000017A4DA

Query Match 22.9%; Score 24; DB 2; Length 10;

Best Local Similarity 55.6%; Pred. No. 9.2e+02;

Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 10 GPTVGEV 18

|||:|:|

1 GFTSGGGV 9

RESULT 33

E60788  
 sperm-activating peptide (Ala-3, Gly-5 speract) - sea urchin (Pseudocentrotus depressus)  
 C/Species: Pseudocentrotus depressus  
 C/Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-2004  
 C/Accession: E60788  
 R/Suzuki, N.; Kajitara, H.; Nomura, K.; Garbere, D.L.; Yoshino, K.; Kurita, M.; Tanaka, H  
 Comp. Biochem. Physiol. B 89, 687-693, 1988  
 A/Title: Some more speract derivatives associated with eggs of sea urchins, Pseudocentrotus  
 A/Reference number: A60787; PMID:88242184; PMID:3378407  
 A/Accession: E60788  
 A/Molecule type: protein  
 A/Residues: 1-10 <SUZ>  
 A/Cross-references: UNIPROT:Q7M4D4; UNIPARC:UPI000017A4DA  
 A/Comment: This oligopeptide from egg jelly is one of several from this species, all of  
 at shows some, but not absolute, species restriction.

Query Match 22.9%; Score 24; DB 2; Length 10;  
 Best Local Similarity 55.6%; Pred. No. 9.2e+02;  
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 10 GFIVGEGV 18  
 |||:|  
 Db 1 GFALGGGV 9

RESULT 34  
 165478  
 c-Ki-ras - hamster (fragment)  
 C/Species: Cricetinae gen. sp. (hamster)  
 C/Date: 12-Aug-1996 #sequence\_revision 12-Aug-1996 #text\_change 28-Feb-1997  
 C/Accession: 165478  
 R/Takahashi, T.; Moyer, M.P.; Cano, M.; Wang, Q.J.; Mountjoy, C.P.; Sanger, W.; Adrian,  
 Carcinogenesis 16, 931-939, 1995  
 A/Title: Differences in molecular biological, biological and growth characteristics betw  
 A/Reference number: 152734; PMID:95246257; PMID:7728976  
 A/Accession: 165478  
 A/Status: preliminary; translated from GB/EMBL/DBJ  
 A/Molecule type: DNA  
 A/Residues: 1-15 <RNS>  
 A/Cross-references: UNIPARC:UPI000017C607; GB:S77069; NID:g914177  
 C/Genetics:  
 A/Gene: c-Ki-ras

Query Match 22.9%; Score 24; DB 2; Length 15;  
 Best Local Similarity 57.1%; Pred. No. 1.5e+03;  
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 12 IVGEGV 18  
 |||:|  
 Db 8 VVGADGV 14

RESULT 35  
 PT0097  
 glutathione peroxidase, non-selenium containing - mouse (fragment)  
 N/Alternate names: antioxidant protein 2  
 C/Species: Mus musculus (house mouse)  
 C/Date: 21-Aug-1998 #sequence\_revision 21-Aug-1998 #text\_change 24-Nov-1999  
 C/Accession: PT0097  
 R/Kawakami, T.; Uchida, T.; Sakai, T.; Kamo, M.; Morimasa, T.; Taugite, A.  
 submitted to JIPIID, July 1998  
 A/Description: Proteome analysis of mouse brain.  
 A/Reference number: PT0091  
 A/Accession: PT0097  
 A/Molecule type: protein  
 A/Residues: 1-15 <KAW>  
 A/Cross-references: UNIPARC:UPI000017C66B  
 A/Experimental source: brain, striatum

Query Match 22.9%; Score 24; DB 2; Length 15;  
 Best Local Similarity 44.4%; Pred. No. 1.5e+03;  
 Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 8 PPGFVIGEE 16  
 |||:|  
 Db 1 PGGLLGKE 9

RESULT 36  
 577834  
 DNA-directed RNA polymerase (EC 2.7.7.6) beta' chain - Mycoplasma capricolum (fragment)  
 N/Alternate names: hypothetical protein mc396  
 C/Species: Mycoplasma capricolum  
 C/Date: 09-Oct-1997 #sequence\_revision 07-Nov-1997 #text\_change 09-Jul-2004  
 C/Accession: 577834; S46904  
 R/Bork, P.; Ouzounis, C.; Casari, G.; Schneider, R.; Sander, C.; Dolan, M.; Gilbert, W.,  
 Mol. Microbiol. 16, 955-967, 1995  
 A/Title: Exploring the Mycoplasma capricolum genome: a minimal cell reveals its physiolo  
 A/Reference number: 577739; PMID:96059641; PMID:7476192  
 A/Accession: 577834  
 A/Status: nucleic acid sequence not shown; translation not shown  
 A/Molecule type: DNA  
 A/Residues: 1-17 <BOR>  
 A/Cross-references: UNIPROT:Q49077; UNIPARC:UPI00000BAD53; EMBL:233297; NID:g516238; P  
 A/Experimental source: ATCC 27343  
 A/Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1994  
 C/Genetics:  
 A/genetic code: SGC3  
 C/Keywords: nucleotidyltransferase; transcription

Query Match 22.9%; Score 24; DB 2; Length 17;  
 Best Local Similarity 45.5%; Pred. No. 1.7e+03;  
 Matches 5; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 MSPGFVIGEE 16  
 |||:|  
 Db 1 MGAPSIIVNE 11

RESULT 37  
 557518  
 T cell receptor beta chain V region - human (fragment)  
 C/Species: Homo sapiens (man)  
 C/Date: 10-Oct-1995 #sequence\_revision 17-Nov-1995 #text\_change 05-Nov-1999  
 C/Accession: 557518  
 R/Burrows, S.R.; Silling, S.L.; Moss, D.J.; Khanna, R.; Misko, I.S.; Argact, V.P.  
 submitted to the EMBL Data Library, June 1995  
 A/Description: T cell receptor repertoire for a viral epitope in humans is diversified  
 A/Reference number: 557494  
 A/Accession: 557518  
 A/Status: preliminary  
 A/Molecule type: mRNA  
 A/Residues: 1-18 <BUR>  
 A/Cross-references: UNIPARC:UPI0000116735; EMBL:249920; NID:g887490; PIDN:CAA90166.1; P  
 C/Keywords: T-cell receptor

Query Match 22.9%; Score 24; DB 2; Length 18;  
 Best Local Similarity 38.5%; Pred. No. 1.8e+03;  
 Matches 5; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 3 AKGMPPIVIGE 15  
 |||:|  
 Db 2 ASLPPPTSTAGE 14

RESULT 38  
 C37072  
 proteoglycan 65k core peptide KS-C - chicken (fragment)  
 C/Species: Gallus gallus (chicken)  
 C/Date: 15-Feb-1991 #sequence\_revision 15-Feb-1991 #text\_change 30-Sep-1993  
 C/Accession: C37072  
 R/Krueger Jr., R.C.; Fields, T.A.; Hildreth IV, J.; Schwartz, N.B.  
 J. Biol. Chem. 265, 12075-12087, 1990  
 A/Title: Chick cartilage chondroitin sulfate proteoglycan core protein. I. Generation a  
 A/Reference number: A37072; PMID:90307743; PMID:2365711  
 A/Accession: C37072

A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-19 <PRO>  
A:Cross-references: UNIPARC:UPI000017C02E

Query Match 22.9%; Score 24; DB 2; Length 19;  
Best Local Similarity 75.0%; Pred. No. 1.9e+03;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 13 VGEGLVS 20  
| | | | |  
DB 5 VGEGLVS 12

## RESULT 39

S11611  
ribosomal protein S2 [validated] - Halobacterium salinarum (fragment)  
N/Alternate names: ribosomal protein H55A  
C/Species: Halobacterium salinarum

C/Date: 31-Dec-1990 #sequence\_revision 31-Dec-1990 #text\_change 09-Jul-2004  
C/Accession: S11611

R/Yaguchi, M.; Visentin, L.P.; Zuker, M.; Matheson, A.T.; Roy, C.; Strom, A.R.  
Zbl. Bakt. Hyg. I. Abt. Orig. C 3, 200-208, 1982

A/Title: Amino-terminal sequences of ribosomal proteins from the 30S subunit of archaea  
A/Reference number: S11609

A/Accession: S11611

A:Molecule type: protein

A:Residues: 1-19 <YMS>

A:Cross-references: UNIPROT:Q7M546; UNIPARC:UPI000017CB39

A/Note: the protein is designated as ribosomal protein H55A

C/Keywords: protein biosynthesis; ribosome

Query Match 22.9%; Score 24; DB 2; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.9e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 SPFG 10  
| | | | |  
DB 15 SPFG 18

## RESULT 40

P00688  
photosystem I 14.0K B4 chain - common tobacco (fragment)  
C/Species: Nicotiana tabacum (common tobacco)

C/Date: 19-May-1994 #sequence\_revision 19-May-1994 #text\_change 17-Mar-1999  
C/Accession: P00688

R/Ookata, J.; Mikami, K.; Hayashida, N.; Nakamura, M.; Sugitara, M.  
Plant Physiol. 102, 1259-1267, 1993

A/Title: Molecular heterogeneity of photosystem I, psad, psab, psaf, psah and psal are

A/Reference number: P00667; PMID:94105345; PMID:8278548

A/Accession: P00688

A:Molecule type: protein

A:Residues: 1-20 <OBO>

A:Cross-references: UNIPARC:UPI000008D0B5

C/Keywords: chloroplast; photosynthesis; photosystem I

Query Match 22.9%; Score 24; DB 2; Length 20;  
Best Local Similarity 57.1%; Pred. No. 2e+03;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 AKGMSP 9  
| | | | |  
DB 13 AKGMSP 19

## RESULT 41

P00687  
photosystem I 14.1K B3 chain - common tobacco (fragment)  
C/Species: Nicotiana tabacum (common tobacco)

C/Date: 19-May-1994 #sequence\_revision 19-May-1994 #text\_change 17-Mar-1999  
C/Accession: P00687; P00675  
R/Ookata, J.; Mikami, K.; Hayashida, N.; Nakamura, M.; Sugitara, M.

Plant Physiol. 102, 1259-1267, 1993

A/Title: Molecular heterogeneity of photosystem I, psad, psab, psaf, psah and psal are

A/Reference number: P00667; PMID:94105345; PMID:8278548

A/Accession: P00687

A:Molecule type: protein

A:Residues: 1-20 <OBO>

A:Cross-references: UNIPARC:UPI00000972B7

A/Note: this peptide was designated photosystem I 14.1K B3 chain

A/Accession: P00675

A:Molecule type: protein

A:Residues: 2-11 <OB2>

A:Cross-references: UNIPARC:UPI000017B0AB

A/Note: this peptide was designated photosystem I 14.0K B4 chain

C/Keywords: chloroplast; photosynthesis; photosystem I; thylakoid

Query Match 22.9%; Score 24; DB 2; Length 20;  
Best Local Similarity 57.1%; Pred. No. 2e+03;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

## RESULT 42

S35538  
ribosomal protein S7 - Mycobacterium intracellulare (fragment)  
C/Species: Mycobacterium intracellulare

C/Date: 09-Dec-1993 #sequence\_revision 14-Nov-1997 #text\_change 12-Jul-2004  
C/Accession: S35538

R/Nair, J.; Rouse, D.; Morris, S.

Nucleic Acids Res. 21, 1039, 1993

A/Title: Nucleotide sequence analysis of the ribosomal S12 gene of Mycobacterium intrac

A/Reference number: S35537; PMID:93197130; PMID:8451173

A/Accession: S35538

A>Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-9 <NAT>

A:Cross-references: UNIPROT:P33564; UNIPARC:UPI000016FA77; EMBL:L08171; NID:9149994; PI

A/Note: the nucleotide sequence was submitted to the EMBL data library, February 1993

C/Superfamily: ribosomal protein S7/S5

C/Keywords: protein biosynthesis; ribosome

Query Match 21.9%; Score 23; DB 2; Length 9;  
Best Local Similarity 57.1%; Pred. No. 2.8e+05;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 PAKGMSP 8  
| | | | |  
DB 2 PAKGMSP 8

## RESULT 43

C60588  
sperm-activating peptide (Ser-3, Gly-5 SAP-I) - sea urchin (Strongylocentrotus nudus)

N/Alternate names: speract homolog

C/Species: Strongylocentrotus nudus

C/Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 16-Aug-2004  
C/Accession: C60588

R/Ioshino, K.I.; Kajitara, H.; Nomura, K.; Takao, T.; Shimonishi, Y.; Kurita, M.; Yamaguchi

Comp. Biochem. Physiol. B 94, 739-751, 1989

A/Title: A halogenated amino acid-containing sperm activating peptide and its related p

A/Reference number: A60527

A/Accession: C60588

A:Molecule type: protein

A:Residues: 1-10 <YOS>

A:Cross-references: UNIPROT:Q7M4B4; UNIPARC:UPI000017A4B4

Query Match 21.9%; Score 23; DB 2; Length 10;  
Best Local Similarity 55.6%; Pred. No. 1.3e+03;  
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 10 GFVGEV 18  
 ||:|  
 Db 1 GFSLGCGGV 9

## RESULT 44

E60527

sperm-activating peptide (Ser-3, Gly-5 SAP-I) - sea urchin (Tripneustes gratilla)

N.Alternate names: speract homolog TG-7

C.Species: Tripneustes gratilla

C.Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 16-Aug-2004

C.Accession: E60527, G39572

R.Yoshino, K.I.; Kajitani, H.; Nomura, K.; Takao, T.; Shimomishi, Y.; Kurita, M.; Yamaguchi, M.

A.Title: A halogenated amino acid-containing sperm activating peptide and its related pe

ctus nudus, Echinosmetra mathaei and Heterocentrotus mammillatus.

A.Reference number: A60527

A.Accession: E60527

A.Molecule type: protein

A.Residues: 1-10 <YOS>

A.Cross-references: UNIPROT:Q7M3T7; UNIPARC:UPI000017A4E4

A.Note: This peptide did not contain bromophenylalanine

R.Yoshino, K.; Takao, T.; Suhara, M.; Kikui, T.; Hori, H.; Nomura, K.; Yamaguchi, M.; Sh

Biochemistry 30, 6203-6209, 1991

A.Title: Identification of a novel amino acid, o-bromo-L-phenylalanine, in egg-associated

A.Reference number: A39572; PMID:91283461; PMID:2059627

A.Accession: G39572

A.Molecule type: protein

A.Residues: 1-10 <YOS>

A.Cross-references: UNIPARC:UPI000017A4E4

A.Note: This peptide contained bromophenylalanine

A.Keyword: bromine

F.2/Modified site: 2'-bromophenylalanine (Phe) (partial) #status experimental

Query Match 21.9%; Score 23; DB 2; Length 10;  
 Best Local Similarity 55.6%; Pred. No. 1.3e+03;  
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 10 GFVGEV 18  
 ||:|  
 Db 1 GFSLGCGGV 9

## RESULT 45

I60588

sperm-activating peptide (Glu-3, Met-4, Gly-5, Thr-7 SAP-I) - slate-pencil urchin (Hetero

C.Species: Heterocentrotus mammillatus

C.Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 16-Aug-2004

C.Accession: I60588

R.Yoshino, K.I.; Kajitani, H.; Nomura, K.; Takao, T.; Shimomishi, Y.; Kurita, M.; Yamaguchi

Comp. Biochem. Physiol. B 94, 739-751, 1989

A.Title: A halogenated amino acid-containing sperm activating peptide and its related pe

ctus nudus, Echinosmetra mathaei and Heterocentrotus mammillatus.

A.Reference number: A60527

A.Accession: I60588

A.Molecule type: protein

A.Residues: 1-10 <YOS>

A.Cross-references: UNIPROT:Q7M4C0; UNIPARC:UPI000017A4E4

Query Match 21.9%; Score 23; DB 2; Length 10;  
 Best Local Similarity 55.6%; Pred. No. 1.3e+03;  
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 10 GFVGEV 18  
 ||:|  
 Db 1 GFSLGCGGV 9

## RESULT 46

C36201

1-aminocyclopropane-1-carboxylate synthase (EC 4.4.1.14) - apple tree (fragment)

C.Species: Malus domestica (apple tree)

C.Date: 28-Mar-1991 #sequence\_revision 28-Mar-1991 #text\_change 09-Jul-2004

C.Accession: C36201

A.Title: 1-aminocyclopropane-1-carboxylate synthase (EC 4.4.1.14) - apple tree (fragment)

A.Keyword: Malus domestica (apple tree)

A.Reference number: A36201; PMID:91045911; PMID:2122449

A.Accession: C36201

A.Molecule type: protein

A.Residues: 1-12 <YIP>

A.Cross-references: UNIPROT:Q9FUC3; UNIPROT:Q9SB01; UNIPROT:Q9SB94; UNIPROT:Q24062; UNIP

A.Experimental source: strain Golden delicious

C.Superfamily: 1-aminocyclopropane-1-carboxylate synthase

C.Keywords: carbon-sulfur lyase; ethylene biosynthesis; phosphoprotein; pyridoxal phosph

F.4/Binding site: pyridoxal phosphate (Lys) (covalent) #status experimental

C.Accession: C36201; C33103

R.Yip, W.K.; Dong, J.G.; Kenny, J.W.; Thompson, G.A.; Yang, S.F.

Proc. Natl. Acad. Sci. U.S.A. 87, 7930-7934, 1990

A.Title: Characterization and sequencing of the active site of 1-aminocyclopropane-1-car

A.Reference number: A36201; PMID:91045911; PMID:2122449

A.Accession: C36201

A.Molecule type: protein

A.Residues: 1-12 <YIP>

A.Cross-references: UNIPROT:Q9FUC3; UNIPROT:Q9SB01; UNIPROT:Q9SB94; UNIPROT:Q24062; UNIP

A.Experimental source: strain Golden delicious

C.Superfamily: 1-aminocyclopropane-1-carboxylate synthase

C.Keywords: carbon-sulfur lyase; ethylene biosynthesis; phosphoprotein; pyridoxal phosph

F.4/Binding site: pyridoxal phosphate (Lys) (covalent) #status experimental

Query Match 21.9%; Score 23; DB 2; Length 12;  
 Best Local Similarity 44.4%; Pred. No. 1.6e+03;  
 Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 AKGMPGPF 11  
 ||:|  
 Db 3 SKDLGLPGF 11

## RESULT 47

A59387

VCAM-1 5'UTR binding protein - Rana pipiens (fragment)

C.Species: Rana pipiens

C.Date: 24-May-2001 #sequence\_revision 24-May-2001 #text\_change 09-Jul-2004

C.Accession: A59387

R.BANERJEE, H.

submitted to the Protein Sequence Database, February 2001

A.Description: Identification and characterization of a novel VCAM-1 5'UTR.

A.Reference number: A59387

A.Accession: A59387

A.Molecule type: preliminary

A.Residues: 1-13 <BAN>

A.Cross-references: UNIPROT:P82866; UNIPARC:UPI00000PDEZD

A.Experimental source: CCL-145

A.Note: VCAM-1 5' untranslated region binding protein with a probable translation inhibi

Query Match 21.9%; Score 23; DB 2; Length 13;  
 Best Local Similarity 44.4%; Pred. No. 1.8e+03;  
 Matches 4; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 DPAKMSPP 9  
 ||:|  
 Db 4 DPVAGYKBP 12

## RESULT 48

S13974

chlorophyll a/b-binding protein type I - garden pea (fragment)

C.Species: Pisum sativum (garden pea)

C.Date: 19-Mar-1997 #sequence\_revision 24-Mar-1999 #text\_change 24-Mar-1999

C.Accession: S13974

R.Jahns, P.; Junge, W.

Bur. U. Biochem. 193, 731-736, 1990

A.Title: Dicyclohexylcarbodiimide-binding proteins related to the short circuit of the F

A.Reference number: S13973; PMID:91065379; PMID:2174365

A.Accession: S13974

A.Molecule type: protein

A.Residues: 1-18 <TAH>

A.Cross-references: UNIPARC:UPI000017B061

A.Genetics: nuclear

C.Keywords: chlorophyll; chloroplast; light-harvesting complex; photosystem I; thylakoi

Query Match 21.9%; Score 23; DB 2; Length 18;  
 Best Local Similarity 40.0%; Pred. No. 2.6e+03;  
 Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 6 MSPPGFVGE 15

Db 1 LAVGILVPS 10

## RESULT 49

S29766  
Cytochrome c(EDH) - Pseudomonas aeruginosa  
C/Species: Pseudomonas aeruginosa  
C/Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 09-Jul-2004  
C/Accession: S29766  
R/Schrover, J.M.; Frank, J.; van Melink, J.B.; Duine, J.A.  
Biochem. J. 290, 123-127, 1993  
A/Title: Quaternary structure of quinoprotein ethanol dehydrogenase from Pseudomonas aer  
A/Reference number: S29766; PMID:93176105; PMID:8382472  
A/Accession: S29766  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-19 <SCH>  
A/Cross-references: UNIPROT:Q9R5C8; UNIPARC:UPI000008913D

## Query Match

Best Local Similarity 21.9%; Score 23; DB 2; Length 19;  
Pred. No. 2.7e+03;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 KGMSPPG 10  
Db 12 KGLEPLG 18

## RESULT 50

B28457  
proteoglycan II, bone - human (tentative sequence) (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 19-May-1989 #sequence\_revision 19-May-1989 #text\_change 09-Jul-2004  
C/Accession: B28457  
R/Fisher, L.W.; Hawkins, G.R.; Tyros, N.; Terline, J.D.  
J. Biol. Chem. 262, 9702-9708, 1987  
A/Title: Purification and partial characterization of small proteoglycans I and II, bone  
A/Reference number: A92656; PMID:87250639; PMID:3597437  
A/Accession: B28457  
A/Molecule type: protein  
A/Residues: 1-19 <FIS>  
A/Cross-references: UNIPROT:P07585; UNIPARC:UPI000017C328

## Query Match

Best Local Similarity 21.9%; Score 23; DB 2; Length 19;  
Pred. No. 2.7e+03;  
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 DPAKMSPP 8  
Db 1 DPAKGIAP 8

## RESULT 51

B39108  
lipoprotein AcFd precursor - Vibrio cholerae (fragment)  
C/Species: Vibrio cholerae  
C/Date: 18-Oct-1991 #sequence\_revision 18-Oct-1991 #text\_change 13-Sep-1996  
C/Accession: B39108  
R/Parrot, C.; Taxman, B.; Mekalanos, J.J.;  
Proc. Natl. Acad. Sci. U.S.A. 88, 1641-1645, 1991  
A/Title: TokR regulates the production of lipoproteins and the expression of serum resist  
A/Reference number: A39108; PMID:91156664; PMID:200374  
A/Accession: B39108  
A/Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra  
A/Molecule type: DNA  
A/Residues: 1-20 <PAR>  
A/Cross-references: UNIPARC:UPI000017AAD2  
C/Keywords: lipid binding; lipoprotein

Query Match 21.9%; Score 23; DB 2; Length 20;  
Best Local Similarity 60.0%; Pred. No. 2.9e+03;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 10 GPVIG 14  
Db 12 GFLIG 16

## RESULT 52

A31516  
lectin, galactose/N-acetylgalactosamine-specific - rat (fragment)  
C/Species: Rattus norvegicus (Norway rat)  
C/Date: 28-Feb-1990 #sequence\_revision 28-Feb-1990 #text\_change 18-Jun-1993  
C/Accession: A31516  
R/Ii, M.; Kawasaki, T.; Yamashina, I.  
Biochem. Biophys. Res. Commun. 155, 720-725, 1988  
A/Title: Structural similarity between the macrophage lectin specific for galactose/N-a  
A/Reference number: A31516; PMID:8833956; PMID:3421964  
A/Accession: A31516  
A/Molecule type: protein  
A/Residues: 1-20 <IIX>  
A/Cross-references: UNIPARC:UPI000017C946

## Query Match

Best Local Similarity 21.9%; Score 23; DB 2; Length 20;  
Pred. No. 2.9e+03;  
Matches 5; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 DPAKMSPPGF 11  
Db 10 DEAGKAPPSF 20

## RESULT 53

S38288  
50K allergen - perennial ryegrass (fragment)  
C/Species: Lolium perenne (perennial ryegrass)  
C/Date: 19-Mar-1997 #sequence\_revision 25-Apr-1997 #text\_change 09-Jul-2004  
C/Accession: S38288  
R/Petersen, A.; Schramm, G.; Becker, W.M.; Schlaak, M.  
Biol. Chem. Hoppe-Seyler 374, 855-861, 1993  
A/Title: Comparison of four grass pollen species concerning their allergens of grass gr  
A/Reference number: S38288; PMID:94092339; PMID:7505588  
A/Accession: S38288  
A/Molecule type: protein  
A/Residues: 1-20 <PER>  
A/Cross-references: UNIPROT:Q7M264; UNIPARC:UPI000017B086

## Query Match

Best Local Similarity 21.9%; Score 23; DB 2; Length 20;  
Pred. No. 2.9e+03;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 PAKMSPP 8  
Db 13 PAKGATP 19

## RESULT 54

S06150  
photosystem I chain III - maize (fragment)  
C/Species: Zea mays (maize)  
C/Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 09-Jul-2004  
C/Accession: S06150  
R/Andaman, S.; Vainstein, A.; Thorber, J.P.  
FEBS Lett. 256, 150-154, 1989  
A/Title: Correlation of some published amino acid sequences for photosystem I polypepti  
A/Reference number: S06149; PMID:90033290; PMID:2680596  
A/Accession: S06150  
A/Molecule type: protein  
A/Residues: 1-20 <ANA>  
A/Cross-references: UNIPROT:P13193; UNIPARC:UPI0000132514  
A/Note: the authors identified this protein as light-harvesting complex I 17K protein  
C/Keywords: chloroplast; photosynthesis; photosystem I; thylakoid

Query Match 21.9%; Score 23; DB 2; Length 20;  
Best Local Similarity 60.0%; Pred. No. 2.9e+03;

Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 GMSPP 9  
|:|:|  
Db 4 GURPP 8

RESULT 55  
PA0040  
malate dehydrogenase (EC 1.1.1.37) glyoxysomal - Arabidopsis thaliana (fragment)

C/Species: Arabidopsis thaliana (mouse-ear cress)  
C/Date: 30-Jun-1992 #sequence\_revision 06-Jan-1995 #text\_change 31-Dec-2004

C/Accession: PA0040

R/Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.

submitted to JPIID, July 1994

A/Description: Separation and characterization of Arabidopsis proteins by two-dimensions

A/Reference number: PA0001

A/Accession: PA0040

A/Molecule type: protein

A/Residues: 1-15 <KAM>

A/Cross-references: UNIPROT:Q93ZA7; UNIPARC:UPI000017AFD0

C/Superfamily: L-lactate dehydrogenase

C/Keywords: glyoxysome; NAD; oxidoreductase

Query Match 21.4%; Score 22.5; DB 2; Length 15;  
Best Local Similarity 63.6%; Pred. No. 2.5e+03;  
Matches 7; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 3 AKGMSPPGIV 13  
|:|:|  
Db 2 AKG-GNPGFKV 11

RESULT 56  
PA0033

protein Q930033 - Arabidopsis thaliana (fragment)

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 30-Jun-1992 #sequence\_revision 06-Jan-1995 #text\_change 06-Jun-1997

C/Accession: PA0033

R/Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.

submitted to JPIID, July 1994

A/Description: Separation and characterization of Arabidopsis proteins by two-dimensions

A/Reference number: PA0001

A/Accession: PA0033

A/Molecule type: protein

A/Residues: 1-9 <KAM>

A/Cross-references: UNIPARC:UPI000017AF66

A/Experimental source: leaf

Query Match 21.0%; Score 22; DB 2; Length 9;  
Best Local Similarity 62.5%; Pred. No. 2.8e+05;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 12 IYVBEQV 19  
|:|:|  
Db 2 IYVEXXV 9

RESULT 57  
D60527

sperm-activating peptide (Gly-5 SAP-I) - sea urchin (Tripneustes gratilla)

N/Alternate names: speract homolog TG-6

C/Species: Tripneustes gratilla

C/Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 16-Aug-2004

C/Accession: D60527; F39572

R/Yoshino, K.; Kajiura, H.; Nomura, K.; Takao, T.; Shimonishi, Y.; Kurita, M.; Yamaguchi, M.

Camp. Biochem. Physiol. B 94, 739-751, 1989

A/Title: A halogenated amino acid-containing sperm activating peptide and its related products

A/Reference number: A60527

A/Accession: D60527

A/Molecule type: protein

A/Residues: 1-10 <YOS>  
A/Cross-references: UNIPROT:Q7M3T9; UNIPARC:UPI000017A4E3  
A/Note: this peptide did not contain bromophenylalanine

R/Yoshino, K.; Takao, T.; Sahara, M.; Kitai, T.; Hori, H.; Nomura, K.; Yamaguchi, M.; Sh

Biochemistry 30, 6203-6209, 1991

A/Title: Identification of a novel amino acid, o-bromo-L-phenylalanine, in egg-associate

A/Reference number: A39572; PMID:91283461; PMID:2059627

A/Accession: F39572

A/Molecule type: protein

A/Residues: 1-10 <YOS>

A/Cross-references: UNIPARC:UPI000017A4E3

A/Note: this peptide contained bromophenylalanine

C/Keywords: bromine

F.2/Modified site: 2'-bromophenylalanine (Phe) (partial) #status experimental

Query Match 21.0%; Score 22; DB 2; Length 10;  
Best Local Similarity 55.6%; Pred. No. 1.9e+03;  
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 10 GPVGEQV 18  
|:|:|  
Db 1 GPDLAGGV 9

RESULT 58  
P80213

28K protein 4412 - rice (strain Nihonbare) (fragment)

C/Species: Oryza sativa (rice)

C/Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 09-Jul-2004

C/Accession: P80213

R/Tsugita, A.; Kamo, M.

submitted to JPIID, April 1993

A/Reference number: P80209

A/Accession: P80213

A/Molecule type: protein

A/Residues: 1-12 <TSU>

A/Cross-references: UNIPROT:Q7M280; UNIPARC:UPI000017B0FA

A/Experimental source: callus

C/Comment: molecular weight 28K, pI 4.6.

Query Match 21.0%; Score 22; DB 2; Length 12;  
Best Local Similarity 50.0%; Pred. No. 2.3e+03;  
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 8 PPGFVBEQ 17  
|:|:|  
Db 3 PPGFVTTEG 12

RESULT 59  
S65409

histone H2B - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 28-Oct-1996 #sequence\_revision 13-Mar-1997 #text\_change 31-Dec-2004

C/Accession: S65409

R/Frohman, M.; Gunne, H.; Bergman, A.C.; Agerberth, B.; Bergman, T.; Boman, A.; Lidén, S.,

Burr, J. Biochem. 237, 86-92, 1996

A/Title: Biochemical and antibacterial analysis of human wound and blister fluid.

A/Reference number: S65409; PMID:96203912; PMID:8620898

A/Accession: S65409

A/Molecule type: protein

A/Residues: 1-12 <PRO>

A/Cross-references: UNIPROT:Q96CF4; UNIPROT:Q60814; UNIPARC:UPI00001771AE

C/Keywords: chromosomal protein; DNA binding; nucleosome core

Query Match 21.0%; Score 22; DB 2; Length 12;  
Best Local Similarity 44.4%; Pred. No. 2.3e+03;  
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 DPAGMSPP 9  
|:|:|  
Db 2 DPAGSAPP 10



```
RESULT 60
A35377
GTP-binding protein G-alpha-11 chain - rat (fragment)
C/Species: Rattus norvegicus (Norway rat)
C/Date: 17-Aug-1990 #sequence_revision 17-Aug-1990 #text_change 31-Oct-1997
C/Accession: A35377
R/Linder, M.E.; Ewald, D.A.; Miller, R.J.; Gilman, A.G.
J. Biol. Chem. 265, 8243-8251, 1990
A/Title: Purification and characterization of G-alpha and three types of G-beta after
A/Reference number: A35377; PMID:90243707; PMID:2159473
A/Accession: A35377
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-14 <LTI>
A/Cross-references: UNIPARC:UPI0000177872
C/Superfamily: GTP-binding regulatory protein Gs alpha chain

Query Match          21.0%; Score 22; DB 2; Length 14;
Best Local Similarity 36.4%; Pred. No. 2.8e+03;
Matches 4; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY          5 GMSPPPTVGE 15
| : | : |
Db          2 GAEEGFMFAE 12

RESULT 61
PS0255
20K protein 5503 - rice (strain Nihonbare) (fragment)
C/Species: Oryza sativa (rice)
C/Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Mar-1995
C/Accession: PS0255
R/Tsugita, A.
submitted to JIPID, April 1993
A/Reference number: PS0206
A/Accession: PS0255
A/Molecule type: protein
A/Residues: 1-14 <TIS>
A/Cross-references: UNIPARC:UPI000017B0F2
A/Experimental source: leaf, chlorophyll, strain Nihonbare
A/Note: molecular weight 20K, pI 4.3

Query Match          21.0%; Score 22; DB 2; Length 14;
Best Local Similarity 44.4%; Pred. No. 2.8e+03;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY          12 IVGESEGLS 20
| : | : | : |
Db          3 IAKKGVIT 11

RESULT 62
PA0110
translational elongation factor eEF-1 beta' chain - Arabidopsis thaliana (fragment)
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 07-Apr-1995 #sequence_revision 26-May-1995 #text_change 31-Dec-2004
C/Accession: PA0110
R/Kamo, M.; Kawakami, T.; Tsugita, A.
submitted to JIPID, March 1995
A/Reference number: PA0109
A/Accession: PA0110
A/Molecule type: protein
A/Residues: 1-15 <KAM>
A/Cross-references: UNIPROT:Q9SCX3; UNIPARC:UPI000017B0LC
C/Superfamily: translational elongation factor eEF-1 beta chain

Query Match          21.0%; Score 22; DB 2; Length 15;
Best Local Similarity 83.3%; Pred. No. 3e+03;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY          15 EEGVLS 20
| | | | |

RESULT 63
A59042
alpha-conotoxin Epi - cone shell (Conus episcopatus)
C/Species: Conus episcopatus (blehop's cone)
C/Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 09-Jul-2004
C/Accession: A59042
R/Loughnan, M.; Bond, T.; Atkins, A.; Cuevas, J.; Adams, D.J.; Broxton, N.M.; Livett, B
J. Biol. Chem. 273, 15667-15674, 1998
A/Title: Alpha-conotoxin Epi, a novel sulfated peptide from Conus episcopatus that sele
A/Reference number: A59042; PMID:98288307; PMID:9624161
A/Accession: A59042
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-16 <LOU>
A/Cross-references: UNIPROT:P56638; UNIPARC:UPI00001287BF
C/Superfamily: alpha-conotoxin
C/Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; postsynaptic neuro
P/1-16/Product: alpha-conotoxin Epi #status experimental <MAT>
P/2-8-3-16/Disulfide bonds: #status experimental
P/15/Binding site: sulfate (Tyr) (covalent) #status experimental
P/16/Modified site: amidated carboxyl end (Cys) #status experimental

Query Match          21.0%; Score 22; DB 2; Length 16;
Best Local Similarity 36.4%; Pred. No. 3.2e+03;
Matches 4; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY          1 DPAKMSPPGF 11
| | | : |
Db          5 DPKMNNDY 15

RESULT 64
A36133
hypothetical protein (bkd 5' region) - Pseudomonas putida (fragment)
C/Species: Pseudomonas putida
C/Date: 30-Nov-1990 #sequence_revision 30-Nov-1990 #text_change 09-Jul-2004
C/Accession: A36133
R/Madhusudan, K.T.; Huang, G.; Burns, G.; Sokatch, J.R.
J. Bacteriol. 172, 5655-5663, 1990
A/Title: Transcriptional analysis of the promoter region of the Pseudomonas putida bran
A/Reference number: A36133; PMID:91008935; PMID:2211503
A/Accession: A36133
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-18 <MAD>
A/Cross-references: UNIPROT:Q00360; UNIPARC:UPI000017A993; GB:M33715

Query Match          21.0%; Score 22; DB 2; Length 18;
Best Local Similarity 44.4%; Pred. No. 3.7e+03;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY          6 MSPPPTVGE 14
| : | : | : |
Db          1 MTABGLEG 9

RESULT 65
I59649
human leukocyte antigen alpha chain - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C/Accession: I59649
R/Fogdell, A.; Olerup, O.
Tissue Antigens 44, 19-24, 1994
A/Title: The DQA1*0104 allele is carried by DRB1*1001- and DRB1*1401-positive haplotypes;
A/Reference number: I59649; PMID:95064785; PMID:7974465
A/Accession: I59649
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-18 <RES>
```

A:Cross-references: UNIPROT:Q30216; UNIPARC:UPI00008A43F; GB:S75685; NID:9913771; PIDN:  
 C:Gene: GDB:HLA-DOA1  
 A:Cross-references: GDB:120638; OMIM:146880  
 A:Map position: 6p21.3-6p21.3

Query Match 21.0%; Score 22; DB 2; Length 18;  
 Best Local Similarity 42.9%; Pred. No. 3.7e+03;  
 Matches 6; Conservative 2; Mismatches 2; Indels 4; Gaps 1;  
 QY 6 MSPPGTIVGEGVL 19  
 |||  
 |||  
 Db 9 MSP----CGEGGIV 18

RESULT 66  
 S19240  
 histone H2B (clone pCH1.0ER) - chicken (fragment)  
 C:Species: Gallus gallus (chicken)  
 C:Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 09-Jul-2004  
 A:Accession: I50648; S19240  
 R:Sturm, R.A.; Dalton, S.; Wells, J.R.  
 Nucleic Acids Res. 16, 8571-8586, 1988  
 A:Title: Conservation of histone H2B/H2B intergene regions: a role for the H2B specific  
 A:Reference number: I50647; MUID:88335608; PMID:3267232  
 A:Accession: I50648  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-20 <S12>  
 A:Cross-references: UNIPROT:Q90859; UNIPARC:UPI00000FD2CA; EMBL:X07765; NID:963429; PIDN  
 C:Superfamily: histone H2B  
 C:Keywords: chromosomal protein; nucleosome core

Query Match 21.0%; Score 22; DB 2; Length 20;  
 Best Local Similarity 44.4%; Pred. No. 4.2e+03;  
 Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 DPAKGMSP 9  
 |||  
 |||  
 Db 3 EPAKSNAP 11

RESULT 67  
 B33290  
 histone H2B - human (fragments)  
 C:Species: Homo sapiens (man)  
 C:Date: 20-Dec-1989 #sequence\_revision 20-Dec-1989 #text\_change 18-Jun-1993  
 A:Accession: B33290  
 R:Baxter, G.D.; Smith, P.J.; Lavin, M.F.  
 Biochem. Biophys. Res. Commun. 162, 30-37, 1989  
 A:Title: Molecular changes associated with induction of cell death in a human T-cell leu  
 A:Reference number: A33290; MUID:89322258; PMID:2546549  
 A:Accession: B33290  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-20 <BAK>  
 A:Cross-references: UNIPARC:UPI000017C15D

Query Match 21.0%; Score 22; DB 2; Length 20;  
 Best Local Similarity 44.4%; Pred. No. 4.2e+03;  
 Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 DPAKGMSP 9  
 |||  
 |||  
 Db 2 EPAKSNAP 10

RESULT 68  
 C56385  
 nitrophorin 3 - Rhodnius prolixus (fragment)  
 N:Alternate names: nitric oxide-carry protein NP3  
 C:Species: Rhodnius prolixus  
 C:Date: 21-Jul-1995 #sequence\_revision 21-Jul-1995 #text\_change 09-Jul-2004

C:Accession: C56385  
 R:Champagne, D.B.; Nussenzveig, R.H.; Ribeiro, J.M.C.  
 J. Biol. Chem. 270, 8691-8695, 1995  
 A:Title: Purification, partial characterization, and cloning of nitric oxide-carrying he  
 A:Reference number: A56385; MUID:95238361; PMID:7721773  
 A:Accession: C56385  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-20 <CHA>  
 A:Cross-references: UNIPROT:Q77000; UNIPROT:Q9T55; UNIPARC:UPI000017BE29  
 C:Keywords: heme; salivary gland; vasodilator

Query Match 21.0%; Score 22; DB 2; Length 20;  
 Best Local Similarity 30.8%; Pred. No. 4.2e+03;  
 Matches 4; Conservative 2; Mismatches 7; Indels 0; Gaps 0;  
 QY 2 PAKGMSPPGTVG 14  
 |||  
 |||  
 Db 8 PKKGIDKAKYFSG 20

RESULT 69  
 A35768  
 T-cell receptor alpha chain V-J region (34S-281) - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C:Date: 05-Oct-1990 #sequence\_revision 05-Oct-1990 #text\_change 30-May-1997  
 A:Accession: A35768  
 R:Kosbetli, H.; Imai, K.; Nakayama, F.; Sado, T.; Moriwaki, K.; Taniguchi, M.  
 Proc. Natl. Acad. Sci. U.S.A. 87, 5248-5252, 1990  
 A:Title: Homogeneous junctional sequence of the VJ4+ T-cell antigen receptor alpha chain  
 A:Reference number: A35768; MUID:90319089; PMID:2371269  
 A:Accession: A35768  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-8 <KOS>  
 A:Cross-references: UNIPARC:UPI000017C78B  
 A:Note: the sequence shown follows the authors' translation at position 1 of TGT  
 C:Keywords: T-cell receptor

Query Match 20.0%; Score 21; DB 2; Length 8;  
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 QY 12 IYGEKG 17  
 |||  
 |||  
 Db 2 VVGDRG 7

RESULT 70  
 P00027  
 pcv-tachykinin - penaeid shrimp (Penaeus vannamei) (fragment)  
 C:Species: Penaeus vannamei  
 C:Date: 21-Aug-1998 #sequence\_revision 21-Aug-1998 #text\_change 09-Jul-2004  
 A:Accession: P00027  
 R:Nieto, J.; Veelaert, D.; Derna, R.; Waelkens, B.; Ceraciens, A.; Coast, G.; Devreese,  
 Biochem. Biophys. Res. Commun. 248, 406-411, 1998  
 A:Title: Identification of one tachykinin- and two kinin-related peptides in the brain c  
 A:Reference number: P00027; MUID:98342103; PMID:9675150  
 A:Accession: P00027  
 A:Molecule type: protein  
 A:Residues: 1-9 <NIB>  
 A:Cross-references: UNIPROT:Q7M3L3; UNIPARC:UPI000017CB0C  
 C:Comment: This peptide belongs to myotropic neuropeptides.

Query Match 20.0%; Score 21; DB 2; Length 9;  
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 QY 7 SPGRF 12  
 |||  
 |||  
 Db 1 AFSGPL 6

```

RESULT 71
P60527
sperm-activating peptide (Gly-3,5 SAP-I) - sea urchin (Tripneustes gratilla)
N:Alternate names: speract homolog TG-8
C:Species: Tripneustes gratilla
C>Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-2004
C:Accession: P60527; H39572
R:Yoshino, K.I.; Kajitani, H.; Nomura, K.; Takao, T.; Shimomishi, Y.; Kurita, M.; Yamaguchi, Comp. Biochem. Physiol. B 94, 739-751, 1989
A>Title: A halogenated amino acid-containing sperm activating peptide and its related peptides nuda, Echinomera machael and Heterocentrotus mammillatus.
A:Reference number: A60527
A:Accession: P60527
A:Molecule type: protein
A:Residues: 1-10 <YOS>
A:Cross-references: UNIPROT:Q7M3T9, UNIPARC:UPI000017A4E2
A>Note: this peptide did not contain bromophenylalanine
R:Yoshino, K.I.; Takao, T.; Suhara, M.; Kitai, T.; Horii, H.; Nomura, K.; Yamaguchi, M.; Shiohama, Biochemistry 30 6203-6209, 1991
A>Title: Identification of a novel amino acid, o-bromo-L-phenylalanine, in egg-associated proteins
A:Reference number: A39572; MUID:91283461; PMID:2059627
A:Accession: H39572
A:Molecule type: protein
A:Residues: 1-10 <YO2>
A:Cross-references: UNIPARC:UPI000017A4E2
A>Note: this peptide contained bromophenylalanine
C:Keywords: bromine
F:2/Modified site: 2'-bromophenylalanine (Phe) (partial) #status experimental

Query Match          20.0%; Score 21; DB 2; Length 10;
Beet Local Similarity 55.6%; Pred. No. 2.7e+03;
Matches      5; Conservative      1; Mismatches      3; Indels      0; Gaps      0;

Cy       10 GFVGGEGV 18
        ||| |
        1 GFGLGGCGV 9

RESULT 72
S39030
lysyl-bradykinin - rainbow trout
C:Species: Oncorhynchus mykiss (rainbow trout)
C>Date: 19-May-1994 #sequence_revision 19-Apr-1996 #text_change 16-Aug-2004
C:Accession: S39030
R:Conlon, J.M.; Olson, K.R.
FEBS Lett. 334, 75-78, 1993
A>Title: Purification of a vasopressin-like peptide related to lysyl-bradykinin from trout plasma
A:Reference number: S39030; MUID:94038817; PMID:8224232
A:Accession: S39030
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-10 <CON>
A:Cross-references: UNIPROT:Q9PRZ1, UNIPARC:UPI0000126AD7

Query Match          20.0%; Score 21; DB 2; Length 10;
Beet Local Similarity 75.0%; Pred. No. 2.7e+03;
Matches      3; Conservative      1; Mismatches      0; Indels      0; Gaps      0;

Cy       8 PRGF 11
        |||
        3 PRGM 6

RESULT 73
A40693
transgelin - sheep (fragment)
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C>Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 09-Jul-2004
C:Accession: A40693
R:Shapland, C.J.; Hansen, J.J.; Totty, N.F.; Lawson, D.
A:Cell Biol. 121, 1065-1073, 1993
A>Title: Purification and properties of transgelin: a transformation and shape change sensitive reference number: A40693; MUID:93273790; PMID:8501116

```

A:Accession: A40693  
 A:Molecule type: protein  
 A:Residues: 1-11 <SHA>  
 A:Cross-references: UNIPROT:Q7M2V7; UNIPARC:UPI00001776A2  
 A:Experimental source: aorta  
 C:Comment: This protein gets actin and is down regulated by transformation or loss of C.  
 C:Superfamily: smooth muscle protein Sm22; calponin repeat homology; smooth muscle prot.  
 C:Keywords: actin binding; cytoskeleton  
  
 Query Match  
 Best Local Similarity 66.7%; Score 21; DB 2; Length 11;  
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
  
 QY 2 PAKGMS 7  
 ||: |||  
 DB 3 PSYGMS 8  
  
 RESULT 74  
 S39762  
 cytochrome P450 U7-7b - rat (fragment)  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 19-May-1994 #sequence\_revision 10-Nov-1995 #text\_change 10-Nov-1995  
 C:Accession: S39762  
 R:Ohishi, N.; Imoka, S.; Suzuki, T.; Funae, Y.  
 B:Biochim. Biophys. Acta 1158, 227-236, 1993  
 A:Title: Characterization of two P-450 isozymes placed in the rat CYP2D subfamily.  
 A:Reference number: S39761; PMID:94072607; PMID:8251521  
 A:Accession: S39762  
 A:Molecule type: protein  
 A:Residues: 1-12 <OHI>  
 A:Cross-references: UNIPARC:UPI000017C8F7  
  
 Query Match  
 Best Local Similarity 28.6%; Score 21; DB 2; Length 12;  
 Matches 2; Conservative 4; Mismatches 1; Indels 0; Gaps 0;  
  
 QY 10 GRVGEV 16  
 ||: ||: ||:  
 DB 1 GLLIGDD 7  
  
 RESULT 75  
 S58502  
 43.2K bile stone protein - unidentified bacterium (fragment)  
 C:Species: unidentified bacterium  
 C:Date: 07-Feb-1997 #sequence\_revision 07-Feb-1997 #text\_change 09-Jul-2004  
 C:Accession: S58502  
 R:Binette, J.P.; Binette, M.B.  
 A:Submitted to the Protein Sequence Database, October 1996  
 A:Description: The proteins of kidney and gallbladder stones.  
 A:Reference number: A58501  
 A:Accession: S58502  
 A:Status: Preliminary  
 A:Molecule type: protein  
 A:Residues: 1-12 <BIN>  
 A:Cross-references: UNIPROT:Q7M1D0; UNIPARC:UPI000017A8D4  
 A:Note: A secondary sequence DVKIGVAGS was also found  
  
 Query Match  
 Best Local Similarity 44.4%; Score 21; DB 2; Length 12;  
 Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
  
 QY 10 GRVGEV 18  
 ||: ||: ||:  
 DB 2 GFALNEQPV 10  
  
 RESULT 76  
 S60683  
 malate dehydrogenase (decarboxylating) (EC 1.1.1.39) - millet (fragment)  
 A:Species: Panicum sp. (millet)

CjDate: 24-Feb-1994 #sequence\_revision 24-Feb-1994 #text\_change 09-Jul-2004

CjAccession: B60683

R.Murata, T.; Ikeda, Y.; Takano, M.; Ohnagi, R.

Plant Cell Physiol. 30, 429-437, 1989

AjTitle: Comparative studies of NAD-malic enzyme from leaves of various C-4 plants.

AjReference number: A60683

AjAccession: B60683

AjMolecule type: protein

AjResidues: 1-14 <MUR>

AjCross-references: UNIPROT:Q7MT9; UNIPARC:UPI000017B12F

CjKeywords: oxidoreductase; photosynthesis

Query Match 20.0%; Score 21; DB 2; Length 14;

Best Local Similarity 75.0%; Pred. No. 4e+03;

Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 SPPG 10

DB 4 APPG 7

#### RESULT 77

B39109

hypothetical 1.5K protein - hepatitis C virus

NjAlternate names: hypothetical protein 2

CjSpecies: hepatitis C virus

CjDate: 18-Oct-1991 #sequence\_revision 18-Oct-1991 #text\_change 07-May-1999

CjAccession: B39109; J01585

R.Han, J.H.; Shyamala, V.; Richman, K.H.; Brauer, M.J.; Irvine, B.; Urdea, M.S.; Tekamp-

Proc. Natl. Acad. Sci. U.S.A. 88, 1711-1715, 1991

AjTitle: Characterization of the terminal region of hepatitis C viral RNA: identification

AjReference number: A39109; MUID:91156678; PMID:1705704

AjAccession: B39109

AjStatus: not compared with conceptual translation

AjMolecule type: mRNA

AjResidues: 1-15 <HAN>

AjCross-references: UNIPARC:UPI000014E546; GB:M58406

R.Kumar, U.; Cheng, D.; Thomas, H.; Monjardino, J.

J. Gen. Virol. 73, 1521-1525, 1992

AjTitle: Cloning and sequencing of the structural region and expression of putative core

AjReference number: J01584; MUID:92300349; PMID:1318944

AjAccession: J01585

AjMolecule type: genomic RNA

AjResidues: 1-15 <KUM>

AjCross-references: UNIPARC:UPI000014E546

AjExperimental source: strain U.K.

Query Match 20.0%; Score 21; DB 2; Length 15;

Best Local Similarity 60.0%; Pred. No. 4.3e+03;

Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 MSPG 10

DB 4 VQPG 8

#### RESULT 78

S05700

insulin-like growth factor-binding protein, adult - human (fragment)

CjSpecies: Homo sapiens (man)

CjDate: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 18-Jun-1993

CjAccession: S05700

R.Roghan, M.; Hosenlopp, P.; LePage, P.; Ballard, A.; Binoux, M.

FEBS Lett. 255, 253-258, 1989

AjTitle: Isolation from human cerebrospinal fluid of a new insulin-like growth factor-bi

AjReference number: S05699; MUID:90005986; PMID:2551732

AjAccession: S05700

AjMolecule type: protein

AjResidues: 1-15 <ROG>

AjCross-references: UNIPARC:UPI000017C274

Query Match

Best Local Similarity 20.0%; Score 21; DB 2; Length 15;

Matches 30.8%; Pred. No. 4.3e+03;

Matches 4; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 2 PAKGMSPPGFIY 14

DB 3 PEGGQGVQALLPG 15

#### RESULT 79

P10110

complement factor B1-Bb and B2-Bb - guinea pig (fragment)

CjSpecies: Cavia porcellus (guinea pig)

CjDate: 31-Mar-1990 #sequence\_revision 31-Mar-1990 #text\_change 15-Nov-1996

CjAccession: P10110

R.Matushita, M.; Okada, H.

Mol. Immunol. 26, 669-676, 1989

AjTitle: Two forms of guinea pig factor B of the alternative complement pathway with dif

AjReference number: A31136; MUID:89384686; PMID:279589

AjAccession: P10110

AjMolecule type: protein

AjResidues: 1-15 <MAT>

AjCross-references: UNIPARC:UPI000017CA2B

CjKeywords: complement alternate pathway; glycoprotein

Query Match

Best Local Similarity 20.0%; Score 21; DB 2; Length 15;

Matches 57.1%; Pred. No. 4.3e+03;

Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DPAKMS 7

DB 5 DPAGSMN 11

#### RESULT 80

S55307

glutathione transferase 3-3 - rat (fragments)

CjSpecies: Rattus norvegicus (Norway rat)

CjDate: 27-Oct-1995 #sequence\_revision 03-Nov-1995 #text\_change 07-May-1999

CjAccession: S55307

R.Cooke, R.J.; Bjornstedt, R.; Douglas, K.T.; McKie, J.H.; King, M.D.; Coles, B.; Kett

Biochem. J. 302, 383-390, 1994

AjTitle: Photolability labelling of the active site of the rat glutathione transferases

AjReference number: S55307; MUID:94379965; PMID:8092989

AjAccession: S55307

AjStatus: preliminary

AjMolecule type: protein

AjResidues: 1-16 <COO>

AjCross-references: UNIPARC:UPI000017C91E

Query Match 20.0%; Score 21; DB 2; Length 16;

Best Local Similarity 37.5%; Pred. No. 4.6e+03;

Matches 6; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 5 GMSPPGFIYGBGVIS 20

DB 1 GLTHPSQIMRFKXYLS 16

#### RESULT 81

A31963

pyruvate dehydrogenase (lipoamide) (EC 1.2.4.1) alpha chain type I - pig roundworm (frag

CjSpecies: Ascaris suum (pig roundworm)

CjDate: 29-Jun-1989 #sequence\_revision 29-Jun-1989 #text\_change 09-Jul-2004

CjAccession: A31963

R.Thissen, J.; Komnicki, R.

J. Biol. Chem. 263, 19092-19097, 1988

AjTitle: Phosphorylation and inactivation of the pyruvate dehydrogenase from the anaerob

AjReference number: A31963; MUID:89066711; PMID:3198613

AjAccession: A31963

AjStatus: preliminary

AjMolecule type: protein

AjResidues: 1-16 <THI>

AjCross-references: UNIPROT:P26267; UNIPARC:UPI000017B69C

CjKeywords: mitochondrion; oxidoreductase; phosphoprotein

Query Match 20.0%; Score 21; DB 2; Length 16;  
Best Local Similarity 80.0%; Pred. No. 4.6e+03;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 MSPPG 10  
| | |  
| | |  
Db 7 MSDPG 11

## RESULT 82

S01104

hypothetical protein 3 - fruit fly (Drosophila melanogaster)

C/Species: Drosophila melanogaster

C/Date: 30-Jun-1989 #sequence\_revision 30-Jun-1989 #text\_change 09-Jul-2004

C/Accession: S01104

R/Evelech, D.D.; Marsh, J.L.

Mol. Gen. Genet. 209, 290-298, 1987

A/Title: Overlapping transcription units in Drosophila: sequence and structure of the C

A/Reference number: S01102; MUID:88038375; PMID:3478553

A/Accession: S01104

A/Molecule type: DNA

A/Residues: 1-16 &lt;EVS&gt;

A/Cross-references: UNIPROT:Q18378; UNIPARC:UPI0000835F4; EMBL:X05991; NID:G7759; PIDN:

C/Genetic:

A/Genes: C8

A/Cross-references: FlyBase:FBgn0002036

Query Match 20.0%; Score 21; DB 2; Length 16;  
Best Local Similarity 30.0%; Pred. No. 4.6e+03;  
Matches 3; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 3 AKGMSPPGF 12  
| | | | |  
| | | | |  
Db 2 AAGLTRPALV 11

## RESULT 83

I55612

thyroid hormone receptor beta - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 05-Nov-1999

C/Accession: I55612

R/Adams, M.; Matthews, C.; Collingwood, T.N.; Tone, Y.; Beck-Peccoz, P.; Chatterjee, K.K.

J. Clin. Invest. 94, 506-515, 1994

A/Title: Genetic analysis of 29 kindreds with generalized and pituitary resistance to th

A/Reference number: I55612; MUID:94314950; PMID:8040303

A/Accession: I55612

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-17 &lt;RBS&gt;

A/Cross-references: UNIPARC:UPI00011F7B5; GB:S72623; NID:G633779; PIDN:AAB31420.1; PID:

C/Genetic:

A/Genes: TRbeta

Query Match 20.0%; Score 21; DB 2; Length 17;  
Best Local Similarity 50.0%; Pred. No. 5e+03;  
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 9 PGFVIG 14  
| | | | |  
| | | | |  
Db 6 PPVVLG 11

## RESULT 84

I51203

myosin heavy chain - chicken (fragment)

C/Species: Gallus gallus (chicken)

C/Date: 04-Sep-1997 #sequence\_revision 07-Nov-1997 #text\_change 09-Jul-2004

C/Accession: I51203

R/Kelley, C.A.; Takahashi, M.; Yu, J.H.; Adelstein, R.S.

J. Biol. Chem. 268, 12848-12854, 1993

A/Title: An insert of seven amino acids confers functional differences between smooth mu

A/Reference number: I51203; MUID:93286132; PMID:8509418

A/Accession: I51203

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-17 &lt;KRL&gt;

A/Cross-references: UNIPROT:Q91352; UNIPARC:UPI00000FD367; GB:S62578; NID:G386220; PIDN:

Query Match 20.0%; Score 21; DB 2; Length 17;  
Best Local Similarity 57.1%; Pred. No. 5e+03;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 9 PGFVIG 15  
| | | | |  
| | | | |  
Db 10 PSFVIG 16

## RESULT 85

A39997

group III allergen - house-dust mite (Dermatophagoides pteronyssinus)

C/Species: Dermatophagoides pteronyssinus

C/Date: 18-Oct-1991 #sequence\_revision 18-Oct-1991 #text\_change 30-Sep-1993

C/Accession: A39997

R/Stewart, G.A.; Ward, L.D.; Simpson, R.J.; Thompson, P.J.

submitted to the Protein Sequence Database, September 1991

A/Reference number: A39997

A/Accession: A39997

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-18 &lt;STR&gt;

A/Cross-references: UNIPARC:UPI000017BE12

Query Match 20.0%; Score 21; DB 2; Length 18;  
Best Local Similarity 55.6%; Pred. No. 5.3e+03;  
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 12 IVGEGVLS 20  
| | | | |  
| | | | |  
Db 1 IVGEXALA 9

## RESULT 86

A35678

hypothetical protein (proenkephalin 5' region) - mouse

C/Species: Mus musculus (house mouse)

C/Date: 28-Sep-1990 #sequence\_revision 28-Sep-1990 #text\_change 09-Jul-2004

C/Accession: A35678

R/Kilpatrick, D.L.; Zinn, S.A.; Fitzgerald, M.; Higuchi, H.; Sabol, S.L.; Meyerhardt, J

Mol. Cell. Biol. 10, 3717-3726, 1990

A/Title: Transcription of the rat and mouse proenkephalin genes is initiated at distinct

A/Reference number: A35678; MUID:90287163; PMID:2355920

A/Accession: A35678

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-18 &lt;KTL&gt;

Query Match 20.0%; Score 21; DB 2; Length 18;  
Best Local Similarity 44.4%; Pred. No. 5.3e+03;  
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 PAKMSPPG 10  
| | | | |  
| | | | |  
Db 9 PWDRIIPG 17

## RESULT 87

B29501

fibriinopeptide A - European moose

C/Species: Alces alces alces (European moose, elk)

C/Date: 21-Nov-1987 #sequence\_revision 21-Nov-1987 #text\_change 09-Jul-2004

C/Accession: B29501

R/Blomback, B.; Blomback, M.; Hann, C.

unpublished results, cited by Blomback, B., and Blomback, M., in Chemotaxonomy and Ser

A:Reference number: A29501

A:Accession: B29501

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-19 <BIO>

A:Cross-references: UniProt:Q7M315; UNIPARC:UPI0000177781

C:Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disulfide

Query Match 20.0%; Score 21; DB 2; Length 19;

Best Local Similarity 80.0%; Pred. No. 5.6e+03;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DPAKG 5

DB 5 DPAKG 9

RESULT 88

A48400

phosphocarrier protein 1, HPr-1 - Streptococcus salivarius (fragment)

C:Species: Streptococcus salivarius

C:Date: 19-Nov-1993 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004

C:Accession: A48400

R:Vadboncoeur, C.; Konishi, Y.; Dumas, F.; Gauthier, L.; Frenette, M.

Biochimie 73, 1427-1430, 1991

A:Title: HPr polymorphism in oral streptococci is caused by the partial removal of the N

A:Reference number: A48400; PMID:92190346; PMID:1799636

A:Accession: A48400

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-19 <VAD>

A:Note: sequence extracted from NCBI backbone (NCBIP:88289)

C:Superfamily: phosphotransferase system phosphotransferase-containing protein; phosphotransferase

Query Match 20.0%; Score 21; DB 2; Length 19;

Best Local Similarity 57.1%; Pred. No. 5.6e+03;

Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 12 IVGEGV 18

DB 7 IVAGTGI 13

RESULT 89

S22233

Vitronectin - sheep (fragment)

C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C:Date: 22-Nov-1993 #sequence\_revision 29-Aug-1997 #text\_change 29-Aug-1997

C:Accession: S22233

R:Nakashima, N.; Miyazaki, K.; Ishikawa, M.; Yatchgo, T.; Ogawa, H.; Uchibori, H.; Matsui

Biochim. Biophys. Acta 1120, 1-10, 1992

A:Title: Vitronectin diversity in evolution but uniformly in ligand binding and size of

A:Reference number: S21768; PMID:92207982; PMID:1372829

A:Accession: S22233

A:Molecule type: protein

A:Residues: 1-19 <NAK>

A:Cross-references: UNIPARC:UPI000017C5A9

Query Match 20.0%; Score 21; DB 2; Length 19;

Best Local Similarity 36.4%; Pred. No. 5.6e+03;

Matches 4; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 DPAKMSPPGF 11

DB 3 ESXKGRXTEGF 13

RESULT 90

S02808

nucleolin - bovine (fragment)

C:Species: Bos primigenius taurus (cattle)

C:Date: 28-Feb-1990 #sequence\_revision 28-Feb-1990 #text\_change 09-Jul-2004

C:Accession: S02808

R:Sapp, M.; Richter, A.; Welshart, K.; Calzergues-Ferrer, M.; Amalric, F.; Wallace, M.C.

Bur. J. Biochem. 179, 541-548, 1989

A:Title: Characterization of a 48-kDa nucleic-acid-binding fragment of nucleolin.

A:Reference number: S02808; PMID:89153087; PMID:2920725

A:Accession: S02808

A:Molecule type: protein

A:Residues: 1-19 <SAP>

A:Cross-references: UniProt:Q7M2L8; UNIPARC:UPI000017C5A8

Query Match 20.0%; Score 21; DB 2; Length 19;

Best Local Similarity 57.1%; Pred. No. 5.6e+03;

Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 AKGMSPP 9

DB 4 AKQKAP 10

RESULT 91

S22232

Vitronectin - goat (fragment)

C:Species: Capra aegagrus hircus (domestic goat)

C:Date: 22-Nov-1993 #sequence\_revision 29-Aug-1997 #text\_change 09-Jul-2004

C:Accession: S22232

R:Nakashima, N.; Miyazaki, K.; Ishikawa, M.; Yatchgo, T.; Ogawa, H.; Uchibori, H.; Matsui

Biochim. Biophys. Acta 1120, 1-10, 1992

A:Title: Vitronectin diversity in evolution but uniformly in ligand binding and size of

A:Reference number: S21768; PMID:92207982; PMID:1372829

A:Accession: S22232

A:Molecule type: protein

A:Residues: 1-19 <NAK>

A:Cross-references: UniProt:Q9TR55; UNIPARC:UPI000017C591

Query Match 20.0%; Score 21; DB 2; Length 19;

Best Local Similarity 36.4%; Pred. No. 5.6e+03;

Matches 4; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 DPAKMSPPGF 11

DB 3 ESXKGRXTEGF 13

RESULT 92

B48400

phosphocarrier protein 2, HPr-2 - Streptococcus salivarius (fragment)

C:Species: Streptococcus salivarius

C:Date: 19-Nov-1993 #sequence\_revision 18-Nov-1994 #text\_change 23-May-1997

C:Accession: B48400

R:Vadboncoeur, C.; Konishi, Y.; Dumas, F.; Gauthier, L.; Frenette, M.

Biochimie 73, 1427-1430, 1991

A:Title: HPr polymorphism in oral streptococci is caused by the partial removal of the N

A:Reference number: A48400; PMID:92190346; PMID:1799636

A:Accession: B48400

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-20 <VAD>

A:Cross-references: UNIPARC:UPI0000177FCA

A:Note: sequence extracted from NCBI backbone (NCBIP:88290)

C:Superfamily: phosphotransferase system phosphotransferase-containing protein; phosphotransferase

C:Keywords: phosphoprotein

Query Match 20.0%; Score 21; DB 2; Length 20;

Best Local Similarity 57.1%; Pred. No. 6e+03;

Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 12 IVGEGV 18

DB 8 IVAGTGI 14

RESULT 93

S65399

Immunodeficiency virus type 1, HIV-1 gp120 - human (fragments)  
 C/Species: Homo sapiens (man)  
 C/Date: 28-Oct-1996 #sequence\_revision 13-Mar-1997 #text\_change 17-Mar-1999  
 C/Accession: S65399  
 R/Niwa, Y.; Yano, M.; Futaki, S.; Okumura, Y.; Kido, H.  
 Eur. J. Biochem. 237, 64-70, 1996  
 A/Title: T-cell membrane-associated serine protease, tryptase TL(2), binds human immunodeficiency virus type 1 inhibits cleavage of gp120.  
 A/Reference number: S65399; PMID:96203909; PMID:8620895  
 A/Accession: S65399  
 A/Status: preliminary  
 A/Molecule type: protein  
 A/Residues: 1-10; 11-20 <NIM>  
 A/Cross-references: UNIPROT:Q10000030087; UNIPARC:UP10000178619  
 C/Superfamily: type B retrovirus env polyprotein

Query Match 20.0%; Score 21; DB 2; Length 20;  
 Best Local Similarity 28.6%; Pred. No. 6e+03;  
 Matches 4; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 2 PAKMSPPRTVGE 15  
 DB 3 PGRAPVTGRIGD 16

## RESULT 94

A61414  
 Chymotrypsin (EC 3.4.21.1) - snapping turtle (fragment)  
 C/Species: Chelydra serpentina (snapping turtle)  
 C/Date: 09-Sep-1994 #sequence\_revision 09-Sep-1994 #text\_change 09-Jul-2004  
 C/Accession: A61414  
 R/Bhargava, A.K.; Barnard, E.A.  
 J. Mol. Evol. 2, 187-198, 1973  
 A/Title: Evolution in the pancreatic chymotrypsinogen series: N-terminal sequence determination  
 A/Reference number: A61414; PMID:76146602; PMID:4807189  
 A/Accession: A61414  
 A/Status: preliminary  
 A/Molecule type: protein  
 A/Residues: 1-20 <BRH>  
 A/Cross-references: UNIPROT:Q7L234; UNIPARC:UP10000178FBS  
 C/Keywords: hydrolase; protein digestion; serine proteinase

Query Match 20.0%; Score 21; DB 2; Length 20;  
 Best Local Similarity 80.0%; Pred. No. 6e+03;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 12 IVGGE 16  
 DB 16 IVGDE 20

## RESULT 95

I53671  
 neurofilament heavy subunit - human (fragment)  
 C/Species: Homo sapiens (man)  
 C/Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 09-Jul-2004  
 C/Accession: I53671  
 R/Figlewicz, D.A.; Rouleau, G.A.; Krizus, A.; Julien, J.P.  
 Gene 132, 297-300, 1993  
 A/Title: Polymorphism in the multi-phosphorylation domain of the human neurofilament heavy subunit  
 A/Reference number: I53671; PMID:94040777; PMID:8224877  
 A/Accession: I53671  
 A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA  
 A/Residues: 1-20 <RES>  
 A/Cross-references: UNIPROT:Q16070; UNIPARC:UP10000072AP9; GB:S66488; NID:G452861; PIND: C/genetics:  
 A/Genes: GDB:NEFH  
 A/Cross-references: GDB:120225; OMIM:162230  
 A/Map position: 22q12.1-22q13.1

Query Match 20.0%; Score 21; DB 2; Length 20;  
 Best Local Similarity 57.1%; Pred. No. 6e+03;

Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 2 PAKMSPP 8  
 DB 2 PERAKSP 8

## RESULT 96

S05411  
 carboxylesterase (EC 3.1.1.1) - Sulfolobus acidocaldarius (fragment)  
 N/Alternate names: serine esterase  
 C/Species: Sulfolobus acidocaldarius  
 C/Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 09-Jul-2004  
 C/Accession: S05411  
 R/Sodex, H.; Goerlich, H.  
 Biochem. J. 261, 993-998, 1989  
 A/Title: Further kinetic and molecular characterization of an extremely heat-stable carboxylesterase  
 A/Reference number: S05411; PMID:90026296; PMID:2508625  
 A/Accession: S05411  
 A/Molecule type: protein  
 A/Residues: 1-20 <SOB>  
 A/Cross-references: UNIPROT:Q7M529; UNIPARC:UP1000017ABE3  
 A/Note: 1-Ala and 1-Ser were also found  
 C/Keywords: carboxylic ester hydrolase; tetramer

Query Match 19.5%; Score 20.5; DB 2; Length 20;  
 Best Local Similarity 35.7%; Pred. No. 7.1e+03;  
 Matches 5; Conservative 3; Mismatches 5; Indels 1; Gaps 1;

QY 1 DPA-KGMSPPGFIV 13  
 DB 3 DPTIKCLBSGFVI 16

## RESULT 97

A39543  
 collagen alpha 1(I) chain - bovine (fragment)  
 C/Species: Bos primigenius taurus (cattle)  
 C/Date: 28-Feb-1992 #sequence\_revision 28-Feb-1992 #text\_change 09-Jul-2004  
 C/Accession: A39543  
 R/Wu, J.J.; Lark, M.W.; Chun, L.R.; Eyre, D.R.  
 J. Biol. Chem. 266, 5625-5628, 1991  
 A/Title: Sites of bromelain cleavage in collagen types II, IX, X, and XI of cartilage  
 A/Reference number: A39543; PMID:91170231; PMID:2005102  
 A/Accession: A39543  
 A/Status: preliminary  
 A/Molecule type: protein  
 A/Residues: 1-20 <WUA>  
 A/Cross-references: UNIPROT:Q7M2Q7; UNIPARC:UP1000017AL5C  
 C/Keywords: coiled coil; extracellular matrix; glycoprotein; trimer

Query Match 19.5%; Score 20.5; DB 2; Length 20;  
 Best Local Similarity 37.5%; Pred. No. 7.1e+03;  
 Matches 6; Conservative 0; Mismatches 3; Indels 7; Gaps 1;

QY 2 PAKMS-----PPG 10  
 DB 4 PDGAGAGLPGRPQPPG 19

## RESULT 98

PT0559  
 T-cell receptor beta chain V-D-J region (126-1BH) - mouse (fragment)  
 C/Species: Mus musculus (house mouse)  
 C/Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
 C/Accession: PT0559  
 R/Feeney, A.V.  
 J. Exp. Med. 174, 115-124, 1991  
 A/Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
 A/Reference number: PT0509; PMID:91277601; PMID:1711558  
 A/Accession: PT0559  
 A/Status: translation not shown  
 A/Molecule type: mRNA

A/Residues: 1-8 <PBE>  
A/Cross-references: UNIPARC:UPI000017C80B  
A/Experimental source: day 18 fetal thymus, strain BALB/c  
C/Keywords: T-cell receptor

Query Match 19.0%; Score 20; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 8 PPG 10  
DB 4 PPG 6

RESULT 99  
PT0554  
T-cell receptor beta chain V-D-J region (126-1G) - mouse (fragment)  
C/Species: Mus musculus (house mouse)  
C/Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
C/Accession: PT0554  
R/Peeney, A.J.  
J. Exp. Med. 174, 115-124, 1991  
A/Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
A/Reference number: PT0509; MUID:91277601; PMID:1711558  
A/Accession: PT0554  
A/Status: translation not shown  
A/Molecule type: mRNA  
A/Residues: 1-8 <PBE>  
A/Cross-references: UNIPARC:UPI000017C815  
A/Experimental source: day 18 fetal thymus, strain BALB/c  
C/Keywords: T-cell receptor

Query Match 19.0%; Score 20; DB 2; Length 8;  
Best Local Similarity 60.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 14 GEGV 18  
DB 3 GDEGL 7

RESULT 100  
B41983  
orf downstream to bacterioferritin - Azorobacter vinelandii (fragment)  
C/Species: Azorobacter vinelandii  
C/Date: 04-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004  
C/Accession: B41983  
R/Grossman, M.J.; Hinton, S.M.; Minak-Bernero, V.; Slaughter, C.; Stiefel, E.I.  
Proc. Natl. Acad. Sci. U.S.A. 89, 2419-2423, 1992  
A/Title: Unification of the ferritin family of proteins.  
A/Reference number: A41983; MUID:92196129; PMID:1549605  
A/Accession: B41983  
A/Status: preliminary; not compared with conceptual translation  
A/Molecule type: nucleic acid; protein  
A/Residues: 1-9 <GRO>  
A/Cross-references: UNIPROT:P25825; UNIPARC:UPI000013A327; GB:M83692; NID:g142297; PIDN:  
A/Note: sequence extracted from NCBI backbone (NCBIP:88442)

Query Match 19.0%; Score 20; DB 2; Length 9;  
Best Local Similarity 75.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 6 MSPP 9  
DB 1 MAPP 4

Search completed: January 20, 2006, 19:12:12  
Job time : 12.3462 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 20, 2006, 18:54:54 ; Search time 66.5385 Seconds

(without alignments)  
212.066 Million cell updates/sec

Title: US-09-662-293-4

Perfect score: 105  
Sequence: 1 DPAKGMSPGFVGESEGLS 20

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 14590

Minimum DB seq length: 0  
Maximum DB seq length: 20

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 100 summaries

Database : Uniprot\_05.80:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysts of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	32	30.5	15	Q7MA99_HUMAN	Q7MA99 homo sapien
2	30	28.6	17	Q6N669_VITRV	Q6N669 vitis vinif
3	28	28.6	18	Q8NFB4_HUMAN	Q8NFB4 homo sapien
4	28	26.7	10	Q7M2N0_BOVIN	Q7M2N0 bos taurus
5	28	26.7	15	Q7M1F8_MAIZE	Q7M1F8 zea mays (m
6	28	26.7	16	Q7SM54_GDELA	Q7SM54 human t-lym
7	28	26.7	20	Q71HR5_LACDL	Q71HR5 lactobacilli
8	28	26.7	20	Q79CF0_RHILB	Q79CF0 rhizobium l
9	27	25.7	16	Q7M281_ORISA	Q7M281 oryza sativ
10	27	25.7	16	Q9T2Q4_BRANA	Q9T2Q4 brassica na
11	27	25.7	19	Q9N195_BOVIN	Q9N195 bos taurus
12	26	24.8	9	BRK1_RANNI	BRK154 rana nigrom
13	26	24.8	9	KNL3_BOMVA	P83058 bombyx var
14	26	24.8	9	KNL3_CYPDO	P83659 cyphonomyx
15	26	24.8	9	P84497_TRASC	P84497 trachemys s
16	26	24.8	9	Q7LZ50_CHICK	Q7LZ50 gallus gall
17	26	24.8	9	Q7LZJ8_RANTR	Q7LZJ8 rana tempor
18	26	24.8	9	Q7LZ17_9NEOB	Q7LZ17 helesophrys
19	26	24.8	11	BRKP_PHYRO	Q71552 phyllomedus
20	26	24.8	11	BRK1_MEGFL	P12797 megalocolla
21	26	24.8	11	Q7SB11_HUMAN	Q7SB11 homo sapien
22	26	24.8	11	Q7M4P1_HUMAN	Q7M4P1 homo sapien
23	26	24.8	12	VESP_VESXA	Q7M3C2 vespa manda
24	26	24.8	12	VESP_VESXA	Q7M3C2 vespa xanth
25	26	24.8	13	BRK_PARID	P42717 parapolybia
26	26	24.8	13	SCX3_TITDI	P60261 clytus disc
27	26	24.8	14	BRK3_RANNI	Q71453 rana nigrom
28	26	24.8	15	Q9R5T1_9FLAO	Q9R5T1 flavobacter
29	26	24.8	17	TLO9_SPIOL	P82671 spinacia ol
30	26	24.8	17	VESP_VESMC	P57672 vesputia mac
31	26	24.8	18	Q16053_HUMAN	Q16053 homo sapien

32	25.5	24.3	18	2	Q763U4_USEUD	Q763U4 naravelia 1
33	25.5	24.3	18	2	Q763U5_CLEAVI	Q763U5 clematis vi
34	25.5	24.3	18	2	Q763W5_USEUD	Q763W5 clematis ja
35	25	23.8	10	1	TM0F_ABDAB	P19425 aedes aegypt
36	25	23.8	10	2	Q7M3T6_TRIGR	Q7M3T6 triripneutes
37	25	23.8	12	2	Q4W620_GCALI	Q4W620 norovirus n
38	25	23.8	12	2	Q84268_9PAPI	Q84268 human papil
39	25	23.8	13	1	PAB8_ASGSU	P43173 ascatis suu
40	25	23.8	13	2	Q16007_HUMAN	Q16007 homo sapien
41	25	23.8	18	2	Q92190_MOUSE	Q92190 mus musculu
42	25	23.8	19	1	TRP3_LERMA	P81735 leucophaea
43	25	23.8	20	1	PYRX_PSEFL	P56586 pseudomnas
44	25	23.8	20	2	Q9OV83_9MTRI	Q9OV83 ratus sp.
45	25	23.8	20	2	Q7LZK3_MEGGA	Q7LZK3 meleagris g
46	25	23.8	10	2	Q7M4B6_STRNU	Q7M4B6 strongyloce
47	25	23.8	10	2	Q7M4D4_PSEDP	Q7M4D4 pseudocente
48	25	23.8	11	2	P82436_TOBAC	P82436 nicotiana t
49	25	23.8	15	2	Q80X04_MESAV	Q80X04 mesocricetu
50	25	23.8	17	2	Q9HER1_PABER	Q9HER1 paracoccidi
51	25	23.8	17	2	Q9HEQ2_AJDEA	Q9HEQ2 ajellomyces
52	25	23.8	17	2	Q9HEQ3_AJDEA	Q9HEQ3 ajellomyces
53	25	23.8	17	2	Q49077_MYCCA	Q49077 mycoplasma
54	25	23.8	19	2	Q7M546_HALSA	Q7M546 halobacteri
55	25	23.8	19	2	Q7S06_9CIRC	Q7S06 porcine circ
56	25	23.8	19	2	Q9YTT3_9CIRC	Q9YTT3 bovine circ
57	25	23.8	20	2	Q9T2I8_NICSY	Q9T2I8 nicotiana s
58	25	23.8	20	2	Q9T2I9_NICSY	Q9T2I9 nicotiana s
59	25	23.8	12	2	Q5ISY4_9CALI	Q5ISY4 norovirus t
60	25	23.8	12	2	Q5ISY5_9CALI	Q5ISY5 norovirus t
61	25	23.8	16	2	Q506K8_9CALI	Q506K8 norovirus h
62	25	23.8	19	2	Q88290_9CALI	Q88290 small round
63	25	23.8	19	2	Q5IT04_9CALI	Q5IT04 norovirus s
64	25	23.8	8	1	RS7_MYCIT	P33564 mycobacteri
65	25	23.8	9	2	Q8MUT7_9PRIM	Q8MUT7 eulimur ful
66	25	23.8	9	2	Q8MUT8_9PRIM	Q8MUT8 eulimur ful
67	25	23.8	10	2	Q7M3T7_TRIGR	Q7M3T7 triripneutes
68	25	23.8	10	2	Q7M4B4_STRNU	Q7M4B4 strongyloce
69	25	23.8	10	2	Q7M4CO_HETMA	Q7M4CO heterocent
70	25	23.8	12	2	Q4W618_9CALI	Q4W618 norovirus n
71	25	23.8	13	2	Q60F86_9BRYO	Q60F86 sphagnum g1
72	25	23.8	13	2	Q60F89_TAKLE	Q60F89 takakia lep
73	25	23.8	13	2	P82866_RANPI	P82866 rana pipien
74	25	23.8	15	1	UC19_MAIZE	P80825 zea mays (m
75	25	23.8	15	1	Q561Y4_9FLAV	Q561Y4 click-borne
76	25	23.8	15	2	Q561Z6_9FLAV	Q561Z6 click-borne
77	25	23.8	16	2	Q9UCG5_HUMAN	Q9UCG5 homo sapien
78	25	23.8	17	1	BIOP1_PHYXY	P84521 phyllomedus
79	25	23.8	17	2	Q9UCLO_9HUMAN	Q9UCLO homo sapien
80	25	23.8	17	2	Q9UBJ5_HUMAN	Q9UBJ5 homo sapien
81	25	23.8	17	2	Q9BSJ3_MYCGA	Q9BSJ3 mycoplasma
82	25	23.8	18	2	Q9TWH0_9TRYP	Q9TWH0 trypanosoma
83	25	23.8	18	2	Q5ERY3_9BRYO	Q5ERY3 polytrichum
84	25	23.8	18	2	Q5ERY6_9BRYO	Q5ERY6 andreaea ru
85	25	23.8	18	2	Q6SKY0_CUSRE	Q6SKY0 cucurbita rel
86	25	23.8	18	2	Q9QV98_9MTRI	Q9QV98 mus sp. . v
87	25	23.8	19	1	F1BA_ANTAM	P14440 antilocapra
88	25	23.8	19	1	F1BA_BISBO	P14441 bisson bonas
89	25	23.8	19	1	F1BA_MONMU	P14457 mus musculu
90	25	23.8	19	2	Q9SRYS_DROMB	Q9SRYS dirosophila
91	25	23.8	19	2	Q9N613_TOXOC	Q9N613 toxoplasma
92	25	23.8	19	2	Q63058_LATCL	Q63058 latirraea cl
93	25	23.8	19	2	Q9RS08_PSEAE	Q9RS08 pseudomonas
94	25	23.8	20	1	Q9JK02_MOUSE	Q9JK02 mus musculu
95	25	23.8	20	2	PSAP_MAIZE	P13193 zea mays (m
96	25	23.8	20	2	Q8NED5_HUMAN	Q8NED5 homo sapien
97	25	23.8	20	2	Q7M264_TOLPR	Q7M264 lolium pere
98	25	23.8	20	2	Q9S8U1_TRIKI	Q9S8U1 trichosanthe
99	25	23.8	20	2	Q9S8Y0_PHLPR	Q9S8Y0 phleum prat
100	25	23.8	20	2	Q9R519_9MYCO	Q9R519 mycobacteri

## ALIGNMENTS

```

RESULT 1
Q7MAP9_HUMAN
ID Q7MAP9_HUMAN PRELIMINARY; PRT; 15 AA.
AC Q7MAP9;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DE Galbladder stone matrix protein 2, 41k (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCBI_TaxId=9606;
RN [1]
RP PROTEIN SEQUENCE.
RA Binette J.P., Binette M.B.;
RL Submitted (FEB-1996) to the PIR data bank.
DR PIR; F57789; F57789.
FT NON_TER 1 1
SQ SEQUENCE 15 AA; 1539 MW; D08774ED4B7A4786 CRC64;

Query Match
Best Local Similarity 30.5%; Score 32; DB 2; Length 15;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 8 PPGFTVGEFG 17
DB 5 PDGFTGSSG 14

RESULT 2
Q6N69_VITVI
ID Q6N69_VITVI PRELIMINARY; PRT; 17 AA.
AC Q6N69;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE 20S proteasome beta subunit (Fragment).
OS Vitis vinifera (Grape).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC Vitaceae; Vitis.
OX NCBI_TaxId=29760;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Leaf;
RA Carvalho M.B., Caeiro A.S., Price C.B., Teixeira A.R., Ferreira R.B.;
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY684130; AAU04834.1; -; mRNA.
DR GO; GO:0005829; C:cytosol; IEA.
KW Proteasome.
FT NON_TER 1 1
FT NON_TER 17 17
SQ SEQUENCE 17 AA; 1808 MW; C19F776A03A88D9F CRC64;

Query Match
Best Local Similarity 28.6%; Score 30; DB 2; Length 17;
Matches 7; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 2 PAKGMSPPGIVGB 15
DB 3 PAKGTTTAFIFKE 16

RESULT 3
Q8NFB4_HUMAN
ID Q8NFB4_HUMAN PRELIMINARY; PRT; 18 AA.
AC Q8NFB4;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)

```

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DE Mutant enamelIn (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCBI_TaxId=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22294456; PubMed=12407086;
RA Kida M., Ariga T., Shitakawa T., Oguchi H., Sakiyama Y.;
RT "Autosomal-dominant hypoplastic form of amelogenesis imperfecta caused
RT by an amelotin gene mutation at the exon-intron boundary.";
DR J. Dent. Res. 81:738-742(2002).
DR EMBL; AF530444; AAM97323.1; -; Genomic_DNA.
FT NON_TER 1 1
FT NON_TER 18 18
SQ SEQUENCE 18 AA; 1893 MW; 492D2B23BBB512 CRC64;

Query Match
Best Local Similarity 28.6%; Score 30; DB 2; Length 18;
Matches 7; Conservative 2; Mismatches 3; Indels 4; Gaps 1;

QY 6 MSPGPF---IVGEEG 17
DB 2 LPPGGRPPISNEEG 17

RESULT 4
Q7M2N0_BOVIN
ID Q7M2N0_BOVIN PRELIMINARY; PRT; 10 AA.
AC Q7M2N0;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Collagen alpha 1(VI) chain (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxId=9913;
RN [1]
RP PROTEIN SEQUENCE.
RX PubMed=6852033;
RA Jander R., Rautenberg U., Glanville R.W.;
RT "Further characterization of the three polypeptide chains of bovine
RT and human short-chain collagen (Intima collagen).";
RL Eur. J. Biochem. 133:39-46(1983).
DR PIR; S26506; S26506.
FT NON_TER 1 1
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 965 MW; CAA96668640DC776 CRC64;

Query Match
Best Local Similarity 26.7%; Score 28; DB 2; Length 10;
Matches 6; Conservative 1; Mismatches 0; Indels 2; Gaps 1;

QY 2 PAKGMSPPG 10
DB 4 PAKG--PPG 10

RESULT 5
Q7MLF8_MAIZE
ID Q7MLF8_MAIZE PRELIMINARY; PRT; 15 AA.
AC Q7MLF8;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Zein Zp22/5 protein.
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.

```

OX NCBI\_TaxID=4577;  
 RN [1]  
 RP PROTEIN SEQUENCE.  
 RX MEDLINE=95206245; PubMed=7898438; DOI=10.1007/BF00290716;  
 RA Chaudhuri S., Messing J.;  
 RT "RFLP mapping of the maize drr1 locus, which regulates methionine-rich  
 RT 10 kDa zein accumulation.";  
 RL Mol. Gen. Genet. 246:707-715 (1995).  
 DR PIR; 854712; 854712.  
 SQ SEQUENCE 15 AA; 1605 MW; 5DFB414D8D001609 CRC64;

Query Match 26.7%; Score 28; DB 2; Length 15;  
 Best Local Similarity 36.4%; Pred. No. 3.5e+03;  
 Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 2 PAKGSPPGRI 12  
 DB 4 PQGSLAPPALI 14

## RESULT 6

ID Q7SM54\_9DELA  
 AC Q7SM54;  
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
 DE Tax protein (Fragment).  
 OS Human T-lymphotropic virus 1.  
 OC Viruses; Retroviridae; Retroviridae; Deltaretrovirus.  
 OX NCBI\_TaxID=11908;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Gonzalez Perez M.F., Garcia Salz A.;  
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF529962; AAP87693.1; -; Genomic\_DNA.  
 FT NON TER 1  
 SQ SEQUENCE 16 AA; 1782 MW; 9CDDDFPR4146BA2F CRC64;

Query Match 26.7%; Score 28; DB 2; Length 16;  
 Best Local Similarity 66.7%; Pred. No. 3.7e+03;  
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 5 GMSPPG 10  
 DB 2 GLBPPG 7

## RESULT 7

ID Q7IHR5\_LACDL  
 AC Q7IHR5;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DE Hieridyl-tRNA synthetase (EC 6.1.1.21) (Fragment).  
 OS Lactobacillus delbrueckii (subsp. lactis).  
 OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;  
 OC Lactobacillus.  
 OX NCBI\_TaxID=29397;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Langenhelm J.F., Ulrich R.L.;  
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF496531; AA007223.1; -; Genomic DNA.  
 DR GO; GO:0004821; F:ligase activity; IEA.  
 DR GO; GO:0016874; F:ligase activity; IEA.  
 KW Aminoacyl-tRNA synthetase; Ligase.  
 FT NON TER 1  
 SQ SEQUENCE 20 AA; 2123 MW; 43ABC93211F8210C CRC64;

Query Match 26.7%; Score 28; DB 2; Length 20;  
 Best Local Similarity 50.0%; Pred. No. 4.7e+03;  
 Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 10 GPVIGEGVL 19  
 DB 11 GFGIGERLIM 20

## RESULT 8

ID Q79CF0\_RHILE  
 AC Q79CF0;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DE 4-hydroxybenzoate hydroxylase (EC 1.14.13.2) (Fragment).  
 GN Name=poba;  
 OS Rhizobium leguminosarum.  
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
 OC Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium.  
 OX NCBI\_TaxID=384;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=B155;  
 RA Wong C.M., Dilworth M.J., Glenn A.R.;  
 RT "4-Hydroxybenzoate hydroxylase (poba) is positively regulated by poba  
 RT in Rhizobium leguminosarum bv. viciae1.";  
 RL FEMS Microbiol. Lett. 0:0-0(1995).  
 DR EMBL; U40388; AAA83007.1; -; Genomic\_DNA.  
 DR HSSP; P20586; 1K01.  
 DR GO; GO:0018659; F:4-hydroxybenzoate 3-monooxygenase activity; IEA.  
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.  
 DR InterPro; IPR002938; MoxY\_PAD binding.  
 DR Pfam; PF01494; PAD\_binding\_3; 1.  
 KW Oxidoreductase.  
 FT NON TER 20  
 SQ SEQUENCE 20 AA; 2011 MW; 378D1B9CB7605522 CRC64;

Query Match 26.7%; Score 28; DB 2; Length 20;  
 Best Local Similarity 36.4%; Pred. No. 4.7e+03;  
 Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 5 GMSPPG 15  
 DB 9 GSGPSGLIGQ 19

## RESULT 9

ID Q7M281\_ORYSA  
 AC Q7M281;  
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)  
 DE 28k protein 4209 (Fragment).  
 OS Oryza sativa (Rice).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC Ehrhartoideae; Oryzaceae; Oryza.  
 OX NCBI\_TaxID=4530;  
 RN [1]  
 RP PROTEIN SEQUENCE.  
 RA Teugita A., Miyake N.;  
 RL Submitted (APR-1993) to the PIR data bank.  
 DR PIR; PS0210; PS0210.  
 DR Gramene; Q7M281; -;  
 FT NON TER 1  
 SQ SEQUENCE 16 AA; 1579 MW; DAC3ABBA68B47CAC CRC64;

Query Match 25.7%; Score 27; DB 2; Length 16;  
 Best Local Similarity 42.9%; Pred. No. 5.3e+03;

Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 9 PGFIVE 15  
DB 1 PGLVIGD 7

RESULT 10  
09T204 BRANA PRELIMINARY; PRT; 16 AA.

AC 09T204;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DE 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
DE Chaperonin-60 L33 fragment (Fragment).  
OS Brassica napus (Rape).  
OC Mitochondrion.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC euroside II; Brassicales; Brassicaceae; Brassica.  
OX NCBI\_Taxid=3708;  
RN [1]  
RP PROTEIN SEQUENCE.  
RX MEDLINE=94302168; PubMed=7913238; DOI=10.1104/pp.105.1.233;  
RA Cloney L.P., Bekkouli D.R., Feist G.L., Lane W.S., Hemmingsen S.M.;  
RT "Brassica napus plastid and mitochondrial chaperonin-60 proteins  
contain multiple distinct polypeptides."  
RL Plant Physiol. 105:233-241(1994).  
FT NON\_TER 1 16  
FT NON\_TER 1 16  
SQ SEQUENCE 16 AA; 1901 MW; CFAET799B7C938063 CRC64;

Query Match Score 27; DB 2; Length 16;

Best Local Similarity 42.9%; Pred. No. 5.3e+03; Indels 0; Gaps 0;

QY 3 AKGMSPPGFIVEB 16  
DB 3 ARGYISPYITDEK 16

RESULT 11  
09N195 BOVIN PRELIMINARY; PRT; 19 AA.

AC 09N195;  
DT 01-OCT-2000 (TREMBLrel. 15, Created)  
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
DE 01-OCT-2000 (TREMBLrel. 15, Last annotation update)  
DE Parvalbumin (Fragment).  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;  
OC Pecora; Bovidae; Bovinae; Bos.  
OX NCBI\_Taxid=9913;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=21599054; PubMed=11736808;  
RA Ariza F., Harrison B., Drinkwater R.D.;  
RT "The assignment by linkage mapping of four genes from human chromosome 22 to bovine chromosome 5 and 17."  
RL Anim. Genet. 32:371-374(2001).  
DR EMBL; AF217654; AAF26420.1; -; Genomic\_DNA.  
FT NON\_TER 1 19  
FT NON\_TER 1 19  
SQ SEQUENCE 19 AA; 2151 MW; DSEA9D89C3BE951 CRC64;

Query Match Score 27; DB 2; Length 19;

Best Local Similarity 71.4%; Pred. No. 6.4e+03; Indels 0; Gaps 0;

QY 4 KGMSPPG 10  
DB 5 KGFSPDG 11

RESULT 12  
BRKI\_RANNI STANDARD; PRT; 9 AA.

AC 07L254;  
DT 05-JUL-2004 (Rel. 44, Created)  
DT 05-JUL-2004 (Rel. 44, Last sequence update)  
DE 10-MAY-2005 (Rel. 47, Last annotation update)  
DE Bradykinin-like peptide I.  
OS Rana nigromaculata (Japanese pond frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana;  
OC Pelophylax.  
OX NCBI\_Taxid=8409;  
RN [1]  
RP PROTEIN SEQUENCE.  
RX TISSUE=skin;  
RX MEDLINE=68412013; PubMed=56767638;  
RA Nakajima T.;  
RT "Occurrence of a new active peptide on smooth muscle and bradykinin in the skin of Rana nigromaculata hallowell.";  
RL Chem. Pharm. Bull. 16:769-770(1968).  
CC -1- FUNCTION: Induces smooth muscle contraction.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- SIMILARITY: Belongs to the bradykinin family.  
CC -----  
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CC -----  
CC PIR; A61358; A61358.  
DR Bradykinin; Direct protein sequencing; Vasoactive; Vasodilator.  
KW SEQUENCE 9 AA; 1017 MW; 3687D771A9C86777 CRC64;

Query Match Score 26; DB 1; Length 9;

Best Local Similarity 100.0%; Pred. No. 2.2e+06; Indels 0; Gaps 0;

QY 8 PGF 11  
DB 2 PGF 5

RESULT 13  
KNL3 BOMVA STANDARD; PRT; 9 AA.

AC P83058;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 13-SEP-2005 (Rel. 48, Last annotation update)  
DE [Three]bradykinin.  
OS Bombina variegata (Yellow-bellied toad).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Archeobatrachia; Bombinatoridae; Bombina.  
OX NCBI\_Taxid=8348;  
RN [1]  
RP PROTEIN SEQUENCE, SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY.  
RX TISSUE=skin secretion;  
RX MEDLINE=22217713; PubMed=12230583;  
RA Chen T., Orr D.F., Bjournson A.J., McLean S., O'Rourke M., Hirst D.G., Rao P., Shaw C.;

RT "Novel bradykinins and their precursor cDNAs from European yellow-bellied toad (Bombina variegata) skin."  
RL Eur. J. Biochem. 269:4693-4700(2002).  
CC -1- FUNCTION: Produces in vitro relaxation of rat arterial smooth muscle and constriction of intestinal smooth muscle.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- TISSUE SPECIFICITY: Expressed by the skin glands.  
CC -1- SIMILARITY: Belongs to the bradykinin family.

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use as long as its content is in no way modified and this statement is not  
CC removed.

CC -----  
CC Amphibian defense peptide; Bradykinin; Direct protein sequencing;  
CC Vasoactive; Vasodilator.  
CC  
SQ SEQUENCE 9 AA, 1074 MW, 3393D771A9C86777 CRC64;

Query Match 24.8%; Score 26; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.2e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 PGPF 11  
DB 2 PGPF 5

RESULT 14  
KNU3\_CYPDO STANDARD; PRT; 9 AA.  
ID KNU3\_CYPDO  
AC P83659;  
DT 05-JUL-2004 (Rel. 44, Created)  
DT 05-JUL-2004 (Rel. 44, Last sequence update)  
DT 10-MAY-2005 (Rel. 47, Last annotation update)  
DE [Thr6]bradykinin.  
OS Cyphononyx dorsalis (spider wasp).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Pterygota;  
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;  
OC Pompilidae; Cyphononyx.  
OX NCBI\_TaxID=246266;  
RN [1]  
RP PROTEIN SEQUENCE, SUBCELLULAR LOCATION, TISSUE SPECIFICITY, AND MASS  
RP SPECTROMETRY.

RC MEDLINE=21203862; PubMed=11306139; DOI=10.1016/S0041-0101(00)00262-2;  
RX Kono K., Hisada M., Naoki H., Itagaki Y., Yasuhara T., Juliano M.A.,  
RA Juliano L., Palma M.S., Yamane T., Nakajima T.;  
RT "Isolation and sequence determination of peptides in the venom of the  
RT spider wasp (Cyphononyx dorsalis) guided by matrix-assisted laser  
RT desorption/ionization time of flight (MALDI-TOF) mass spectrometry.";  
RL Toxicon 39:1257-1260(2001).  
CC -1- FUNCTION: Produces in vitro relaxation of rat arterial smooth  
CC muscle and constriction of intestinal smooth muscle (By  
CC similarity).  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- TISSUE SPECIFICITY: Expressed by the venom gland.  
CC -1- MASS SPECTROMETRY: MW=1074.58; METHOD=MALDI; RANGE=1-9;  
CC NOT=Ref.1.  
CC -1- SIMILARITY: Belongs to the bradykinin family.

CC -----  
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use as long as its content is in no way modified and this statement is not  
CC removed.

CC GO: GO:0005615; Extracellular space; IDA.  
DR GO: GO:0045776; P-negative regulation of blood pressure; ISS.  
DR GO: GO:0045987; P-positive regulation of smooth muscle contra. . .; ISS.  
KW Bradykinin; Direct protein sequencing; Vasoactive; Vasodilator.  
SQ SEQUENCE 9 AA, 1074 MW, 3393D771A9C86777 CRC64;

Query Match 24.8%; Score 26; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.2e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 PGPF 11  
DB 2 PGPF 5

RESULT 15  
P84497\_TRASC PRELIMINARY; PRT; 9 AA.  
ID P84497;  
AC P84497;  
DT 10-MAY-2005 (TrEMBLrel. 30, Created)  
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)  
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)  
DE [Thr6]bradykinin.  
OS Trachemys scripta (Red-eared slider turtle) (Pseudemys scripta).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Testudines; Cryptodira; Testudinoidea; Emydidae; Trachemys.  
OX NCBI\_TaxID=34903;  
RN [1]  
RP PROTEIN SEQUENCE.  
RX PubMed=2298179;  
RA Conlon J.M., Hicks J.W., Smith D.D.;  
RT "Isolation and biological activity of a novel kinin  
RT ([Thr(6)]bradykinin) from the turtle, Pseudemys scripta.";  
RL Endocrinology 126:985-991(1990).  
KW Direct protein sequencing.  
SQ SEQUENCE 9 AA, 1074 MW, 3393D771A9C86777 CRC64;

Query Match 24.8%; Score 26; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.2e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 PGPF 11  
DB 2 PGPF 5

RESULT 16  
Q7LZ50\_CHICK PRELIMINARY; PRT; 9 AA.  
ID Q7LZ50;  
AC Q7LZ50;  
DT 01-MAR-2004 (TrEMBLrel. 26, Created)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Ornitho-kinin.  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
OC Gallus.  
OX NCBI\_TaxID=9031;  
RN [1]  
RP PROTEIN SEQUENCE.  
RX MEDLINE=90102072; PubMed=2603803;  
RA Kimura M., Sueyoshi T., Morita T., Tanaka K., Iwanaga S.;  
RT "Ornitho-kininogen and ornitho-kinin: Isolation, characterization and  
RT chemical structure.";  
RL Adv. Exp. Med. Biol. 247A:359-367(1989).  
DR PIR; B60246; B60246.  
SQ SEQUENCE 9 AA, 1040 MW, 339D3771A9C86777 CRC64;

Query Match 24.8%; Score 26; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.2e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 PGPF 11  
DB 2 PGPF 5

RESULT 17  
Q7LZJ8\_RANTR PRELIMINARY; PRT; 9 AA.  
ID Q7LZJ8;  
AC Q7LZJ8;  
DT 01-MAR-2004 (TrEMBLrel. 26, Created)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Bradykinin.  
OS Rana temporaria (European common frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Query Match 24.8%; Score 26; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.2e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana;
OC Rana.
OX NCBI_TaxID=8407;
RN [1]
RN PROTEIN SEQUENCE.
RA Anaastasi A., Erspamer V., Bertaccini G.;
RT "Occurrence of bradykinin in the skin of Rana temporaria.";
RL Comp. Biochem. Physiol. 14:43-52(1965).
DR PIR; A61363; A61363.
SQ SEQUENCE 9 AA; 1060 MW; 3393D775B9C86777 CRC64;

Query Match          24.8%; Score 26; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PPGF 11
   |||
   |||
DB 2 PPGF 5

RESULT 18
Q7L2I7_9NEOB          24.8%; Score 26; DB 2; Length 9;
Q7L2I7_9NEOB PRELIMINARY; PRT; 9 AA.
AC Q7L2I7;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hydroxyproline-3-bradykinin.
OS Helophryne purcellii (Cape ghost frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Helaophrynidae;
OC Helophryne.
OX NCBI_TaxID=31911;
RN [1]
RN PROTEIN SEQUENCE.
RA Nakajima T., Yasuhara T., Erspamer G.F., Viseer J.;
RT "Occurrence of Hyp(3)-bradykinin in methanol extracts of the skin of
RT the South African leptodactylid frog Helophryne purcellii.";
RL Experimentia 35:1133-1133(1979).
DR PIR; A43065; A43065.
SQ SEQUENCE 9 AA; 1060 MW; 3393D775B9C86777 CRC64;

Query Match          24.8%; Score 26; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PPGF 11
   |||
   |||
DB 2 PPGF 5

RESULT 19
BRKP_PHYRO          24.8%; Score 26; DB 2; Length 9;
BRKP_PHYRO STANDARD; PRT; 11 AA.
AC Q7L252;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Phyllokinin (Bradykinin1-Isolucyl-L-tyrosine O-sulfate).
OS Phyllomedusa rohdei (Rohde's leaf frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Hylidae;
OC Phyllomedusinae; Phyllomedusa.
OX NCBI_TaxID=8394;
RN [1]
RN PROTEIN SEQUENCE, AND SULFATION OF TYR-11.

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RX MEDLINE=67179312; PubMed=5970899;
RA Anaastasi A., Bertaccini G., Erspamer V.;
RT "Pharmacological data on phyllokinin (bradykinin1-Isolucyl-L-tyrosine O-
RT sulphate) and bradykinin1-Isolucyl-L-tyrosine.";
RL Br. J. Pharmacol. 27:479-485(1966).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the bradykinin family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use as long as its content is in no way modified and this statement is not
CC removed.
DR PIR; A61365; A61365.
KW Bradykinin; direct protein sequencing; Sulfation; Vasodilator;
FT MOD_RES 11
FT MOD_RES 11 Sulfotyrosine.
KW Vasodilator.
SQ SEQUENCE 11 AA; 1337 MW; 25051393D775B9C8 CRC64;

Query Match          24.8%; Score 26; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 5.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PPGF 11
   |||
   |||
DB 2 PPGF 5

RESULT 20
BRK_MEGFL          24.8%; Score 26; DB 1; Length 11;
BRK_MEGFL STANDARD; PRT; 11 AA.
AC P12797;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Megascollakinin ((Thr6)bradykinin-Lys-Ala) [Contains: Bradykinin-like
DE peptide ((Thr6)bradykinin)].
OS Megascollia flavifrons (Garden dagger wasp) (Solitary wasp).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
OC Scoliidae; Megascollia.
OX NCBI_TaxID=7437;
RN [1]
RN PROTEIN SEQUENCE.
RP TISSUE=Venom;
RX MEDLINE=87293024; PubMed=3617088; DOI=10.1016/0041-0101(87)90288-1;
RA Yasuhara T., Mantel P., Nakajima T., Plek T.;
RT "Two kinins isolated from an extract of the venom reservoirs of the
RT solitary wasp Megascollia flavifrons.";
RL Toxicon 25:527-535(1987).
RN [2]
RN PROTEIN SEQUENCE.
RP TISSUE=Venom;
RA Nakajima T., Plek T., Yasuhara T., Mantel P.;
RT "Two kinins isolated from the venom of Megascollia flavifrons.";
RL Toxicon 26:34-34(1988).
CC -1- FUNCTION: Both proteins have bradykinin-like, although lower
CC activities (e.g. smooth muscle contraction).
CC -1- SUBCELLULAR LOCATION: Secreted; venom reservoirs.
CC -1- SIMILARITY: Belongs to the bradykinin family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use as long as its content is in no way modified and this statement is not
CC removed.
DR PIR; A26744; A26744.
DR PIR; B26744; B26744.
DR GO; GO:0005615; C:extracellular space; IDA.
DR GO; GO:0045776; P:negative regulation of blood pressure; ISS.
DR GO; GO:0045987; P:positive regulation of smooth muscle contra. . .; TAS.

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KM Bradykinin; Direct protein sequencing; Vasoactive; Vasodilator.  
 FT PEPTIDE 1 11 Megascollakinin.  
 SEQUENCE 11 AA, 1274 MW, 33867333DD71A5C8 CRC64.

Query Match 24.8%; Score 26; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 5.1e+03;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PAGE 11  
 DB 2 PAGE 5

## RESULT 21

075811 HUMAN  
 ID 075811 HUMAN PRELIMINARY; PRT; 11 AA.

AC 075811  
 DT 01-NOV-1998 (TEMBLrel. 08, Created)  
 DT 01-NOV-1998 (TEMBLrel. 08, Last sequence update)  
 DT 01-NOV-1998 (TEMBLrel. 08, Last annotation update)  
 DE ErbB-3 R2 (Fragment).  
 GN Name=c-erbB-3;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;  
 OC Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Ovarian carcinoma;  
 RX MEDLINE=98345147; PubMed=9681822; DOI=10.1038/sj.onc.1201866;  
 RA Lee H., Matile N.J.;  
 RT "Isolation and characterization of four alternative c-erbB3 transcripts  
 RT expressed in ovarian carcinoma-derived cell lines and normal human  
 RT tissues.";  
 RL Oncogene 16:3243-3252(1998).  
 DR EMBL; U88358; AAC39858.1; mRNA.  
 FT NON TER 1  
 SQ SEQUENCE 11 AA, 1017 MW, 21B236366B72878 CRC64;

Query Match 24.8%; Score 26; DB 2; Length 11;  
 Best Local Similarity 40.0%; Pred. No. 5.1e+03;  
 Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 DPAKMSPPG 10  
 DB 1 EPCGGLCPKG 10

## RESULT 22

07M4P1 HUMAN  
 ID 07M4P1 HUMAN PRELIMINARY; PRT; 11 AA.

AC 07M4P1  
 DT 01-MAR-2004 (TEMBLrel. 26, Created)  
 DT 01-MAR-2004 (TEMBLrel. 26, Last sequence update)  
 DT 01-MAR-2004 (TEMBLrel. 26, Last annotation update)  
 DE 11e-8er-bradykinin (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;  
 OC Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP PROTEIN SEQUENCE.  
 RX MEDLINE=9116748; PubMed=2076202;  
 RA Wunderer G., Walter I., Eschenbacher B., Lang M., Kellermann J.,  
 RT "11e-8er-bradykinin is an aberrant permeability factor in various  
 RT human malignant effusions.";  
 RL Biol. Chem. Hoppe-Seyler 371:977-981(1990).  
 DR PIR; S13279; S13279. 1  
 FT NON TER 1

FT NON TER 11 11  
 SQ SEQUENCE 11 AA; 1260 MW; 33D55258B9C86777 CRC64;

Query Match 24.8%; Score 26; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 5.1e+03;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PAGE 11  
 DB 4 PAGE 7

## RESULT 23

VESP\_VESMA  
 ID VESP\_VESMA STANDARD; PRT; 12 AA.

AC 07M3T3;  
 DT 05-JUL-2004 (Rel. 44, Created)  
 DT 05-JUL-2004 (Rel. 44, Last sequence update)  
 DT 10-MAY-2005 (Rel. 47, Last annotation update)  
 DE Vespakinin M.  
 OS Vespa mandarinia (Hornet).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;  
 OC Vespidae; Vespinae; Vespa.  
 OX NCBI\_TaxID=7446;  
 RN [1]  
 RP PROTEIN SEQUENCE, AND HYDROXYLATION.  
 RC TISSUE=Venom;  
 RX MEDLINE=77114342; PubMed=1017116;  
 RA Kishimura H., Yasuhara T., Yoshida H., Nakajima T.;  
 RT "Vespakinin-M, a novel bradykinin analogue containing hydroxyproline,  
 RT in the venom of Vespa mandarinia Smth.";  
 RL Chem. Pharm. Bull. 24:2896-2897(1976).  
 CC -1- FUNCTION: Bradykinin are a potent but short-lived agent of  
 CC arteriolar dilation and increased capillary permeability (By  
 CC similarity).  
 CC -1- SUBCELLULAR LOCATION: Secreted; venom reservoir.  
 CC -1- SIMILARITY: Belongs to the bradykinin family.

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 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.

DR PIR; A61360; A61360.  
 KM Bradykinin; Direct protein sequencing; Hydroxylation; Vasoactive;  
 KW Vasodilator.  
 FT MOD\_RES 4  
 SQ SEQUENCE 12 AA; 1346 MW; 34F513C44C75B9C8 CRC64;

Query Match 24.8%; Score 26; DB 1; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 5.6e+03;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PAGE 11  
 DB 3 PAGE 6

## RESULT 24

VESP\_VESXA  
 ID VESP\_VESXA STANDARD; PRT; 12 AA.

AC 07M3T2;  
 DT 05-JUL-2004 (Rel. 44, Created)  
 DT 05-JUL-2004 (Rel. 44, Last sequence update)  
 DT 10-MAY-2005 (Rel. 47, Last annotation update)  
 DE Vespakinin X.  
 OS Vespa xanthoptera (Japanese hornet).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;  
 OC Vespidae; Vespinae; Vespa.  
 OX NCBI\_TaxID=7446;

```

RN [1]
RP PROTEIN SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=87187853; PubMed=264186;
RA Yasuhara T., Yoshida H., Nakajima T.;
RT "Chemical investigation of the hornet (Vespa xanthoptera Cameron) venom. The structure of a new bradykinin analogue vespakinin-X.";
RL Chem. Bull. 25:936-941(1977).
CC -1- FUNCTION: Bradykinin are a potent but short-lived agent of arteriolar dilation and increased capillary permeability (By similarity).
CC -1- SUBCELLULAR LOCATION: Secreted; venom reservoirs.
CC -1- SIMILARITY: Belongs to the bradykinin family.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.
CC -----
DR PIR; A61359; A61359.
KM Bradykinin; Direct protein sequencing; Vasoactive; Vasodilator.
SQ SEQUENCE 12 AA; 1344 MW; 2C9513C3D275B9C8 CRC64;

Query Match
Best Local Similarity 24.8%; Score 26; DB 1; Length 12;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PGF 11
DB 3 PGF 6

RESULT 25
BRK PARID STANDARD; PRT; 13 AA.
AC P42717;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Waspkinin.
OS Parapolybia indica.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea; OC Vespidae; Polistinae; Parapolybia.
OX NCBI_Taxid=31921;
RN [1]
RP PROTEIN SEQUENCE.
RC TISSUE=Venom;
RA Toki T., Yasuhara T., Nakajima T.;
RT "Isolation and sequential analysis of peptides on the venom sac of Parapolybia indica.";
RL Eisai Dobutsu 39:105-111(1988).
CC -1- FUNCTION: Induces smooth muscle contraction.
CC -1- SUBCELLULAR LOCATION: Secreted; venom reservoirs.
CC -1- SIMILARITY: Belongs to the bradykinin family.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.
CC -----
KM Bradykinin; Direct protein sequencing; Pyrrolidone carboxylic acid; KM Vasoactive; Vasodilator.
FT MOD_RES 1 Pyrrolidone carboxylic acid.
SQ SEQUENCE 13 AA; 1573 MW; 2673CB3D83ECC867 CRC64;

Query Match
Best Local Similarity 24.8%; Score 26; DB 1; Length 13;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PGF 11

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DB 5 PGF 8

RESULT 26
SCX2 TTIDI STANDARD; PRT; 13 AA.
AC P60261;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Toxin Td11-2 (Fragment).
OS Tityus discrepans (Venezuelan scorpion).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones; OC Butridae; Buthidae; Tityus.
OX NCBI_Taxid=57059;
RN [1]
RP PROTEIN SEQUENCE.
RC TISSUE=Venom;
RX PubMed=8783453; DOI=10.1016/0041-0101(95)00156-5;
RA D'Suze G., Corona F., Posanti L.D., Sevcik C.;
RT "High performance liquid chromatography purification and amino acid sequence of toxins from the muscarinic fraction of Tityus discrepans scorpion venom.";
RL Toxicon 34:591-598(1996).
CC -1- FUNCTION: Binds voltage-independently to sodium channels and shift the voltage of activation toward more negative potentials (By similarity). This toxin is active against mammals and crustaceans.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the venom gland.
CC -1- SIMILARITY: Belongs to the alpha/beta-scorpion toxin family. Beta-toxin subfamily.
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CC -----
KM Direct protein sequencing; Ionic channel inhibitor; Neurotoxin; KM Sodium channel inhibitor; Toxin.
FT NON_TER 13
SQ SEQUENCE 13 AA; 1444 MW; 256147777B34867 CRC64;

Query Match
Best Local Similarity 24.8%; Score 26; DB 1; Length 13;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 10 PGF 17
DB 3 GYLPGNEG 10

RESULT 27
BRK3 RANNI STANDARD; PRT; 14 AA.
AC 07LZ53;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Bradykinin-like peptide III.
OS Rana nigromaculata (Japanese pond frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana; OC Pelophylax.
OX NCBI_Taxid=8409;
RN [1]
RP PROTEIN SEQUENCE.
RC TISSUE=Skin;
RX MEDLINE=69117202; PubMed=5751736;
RA Nakajima T.;
RT "On the third active peptide on smooth muscle in the skin of Rana nigromaculata hallowell.";

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RL Chem. Pharm. Bull. 16:2088-2089(1968).
CC -1- FUNCTION: Induces smooth muscle contraction.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the bradykinin family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC PIR; A61362; A61362.
KW Bradykinin; Direct protein sequencing; Vasoactive; Vasodilator.
SQ SEQUENCE 14 AA; 1486 MW; 33344EB3978393D7 CRC64;

Query Match
Best Local Similarity 24.8%; Score 26; DB 1; Length 14;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PPGF 11
DB 2 PPGF 5

RESULT 28
O9R5T1_9FLAO PRELIMINARY; PRT; 15 AA.
AC O9R5T1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DB 3-HYDROXYPHENYLACETATE 6-hydroxylase, PAD-dependent monooxygenase
DE (Fragment).
OS Flavobacterium.
OC Bacteri; Bacteroidetes; Flavobacteria; Flavobacteriales;
OC Flavobacteriaceae.
OX NCBI_TaxID=237;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=92037613; PubMed=1935954;
RA Van Berkel W.J., Van Den Tweel W.J.;
RT "Purification and characterization of 3-hydroxyphenylacetate 6-
RT hydroxylase: a novel PAD-dependent monooxygenase from a Flavobacterium
RT species.";
RL Eur. J. Biochem. 201:585-592(1991).
FT NON_TER 1
FT NON_TER 15
SQ SEQUENCE 15 AA; 1416 MW; D673378E0221F9D9 CRC64;

Query Match
Best Local Similarity 24.8%; Score 26; DB 2; Length 15;
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 DPAKGMSP 9
DB 7 DPAKGMSP 15

RESULT 29
TL09_SPIOL STANDARD; PRT; 17 AA.
AC P82671;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DB Thylakoid lumenal 9 kDa protein (P9) (Fragment).
OS Spinacia oleracea (Spinach).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC Caryophyllales; Amaranthaceae; Spinacia.
OX NCBI_TaxID=3562;
RN [1]
RP PROTEIN SEQUENCE.

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RA Kieselbach T., Pettersson U., Byström M., Schroeder W.P.;
RL Submitted (MAY-2000) to Swiss-Prot.
CC -1- SUBCELLULAR LOCATION: Chloroplast; within the thylakoid lumen.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC Chloplast; Direct protein sequencing; Thylakoid.
KW Bradykinin; Direct protein sequencing; Glycoprotein; Vasoactive;
FT NON_TER 17
SQ SEQUENCE 17 AA; 1684 MW; A8B04C2AEBDBD8C1 CRC64;

Query Match
Best Local Similarity 24.8%; Score 26; DB 1; Length 17;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 10 GFIYBEGV 18
DB 1 GFIYBEGV 9

RESULT 30
VESP_VESMC STANDARD; PRT; 17 AA.
AC P57672;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DB Vespolakitin 1 [Contains: Vespolakitin 2]
OS Vespaula maculifrons (Bassett yellow jacket) (Vesp).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
OC Vespidae; Vespinae; Vespa.
OX NCBI_TaxID=7453;
RN [1]
RP PROTEIN SEQUENCE.
RX TISSUE=Venom;
RC MEDLINE=76114777; PubMed=1247511;
RA Yoshida H., Geller R.G., Pisano J.J.;
RT "Vespolakitin: a new carbohydrate-containing bradykinin derivatives.";
RL Biochemistry 15:61-64(1976).
RN [2]
RP SYNTHESIS.
RX MEDLINE=88057857; PubMed=3679673;
RA Rocchi R., Biondi L., Filippa F., Scolaro B.;
RT "Synthesis, conformation, and biological activity of the carbohydrate-
RT free vespolakitin 1.";
RL Int. J. Pept. Protein Res. 30:240-256(1987).
CC -1- FUNCTION: Induces smooth muscle contraction.
CC -1- SUBCELLULAR LOCATION: Secreted; venom reservoirs.
CC -1- SIMILARITY: Belongs to the bradykinin family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC PIR; A61339; A61339.
KW Bradykinin; Direct protein sequencing; Glycoprotein; Vasoactive;
KW Vasodilator.
FT PEPTIDE 1 17 Vespolakitin 1.
FT PEPTIDE 3 17 Vespolakitin 2.
FT CARBOHYD 3 3 O-linked (GalNAc...).
FT CARBOHYD 4 4 O-linked (GalNAc...).
SQ SEQUENCE 17 AA; 1960 MW; 58B2CBA864122323 CRC64;

Query Match
Best Local Similarity 24.8%; Score 26; DB 1; Length 17;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 8 PGPF 11  
 ||||  
 Db 10 PGPF 13

## RESULT 31

Q16053 HUMAN  
 ID Q16053\_HUMAN PRELIMINARY; PRT; 18 AA.  
 AC Q16053\_  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Type I procollagen alpha 1 chain (Fragment).  
 GN Name=COL1A1;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;  
 OC Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=93339042; PubMed=8339541;  
 RA Wirtz M.K., Rao V.H., Glanville R.W., Labhard M.E., Pretorius P.J.,  
 RA de Vries W.N., de Wet W., Hollister D.W.;  
 RT "A cysteine for glycine substitution at position 175 in an alpha 1 (I)  
 RT chain of type I collagen produces a clinically heterogeneous form of  
 RT osteogenesis imperfecta.";  
 RL Connect. Tissue Res. 29:1-11(1993).  
 DR EMBL; S64717; AAB27677.1; -; mRNA.  
 DR PIR; I60114; CGHUS.  
 KM Collagen.  
 FT NON TER  
 SQ SEQUENCE 18 AA; 1640 MW; E86475B62F05583A CRC64;

Query Match 24.8%; Score 26; DB 2; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 8.7e+03;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

## RESULT 32

Q763U4 USEUD  
 ID Q763U4\_USEUD PRELIMINARY; PRT; 18 AA.  
 AC Q763U4\_  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE RNA polymerase beta subunit (Fragment).  
 GN Name=rpob;  
 OS Naravellia laurifolia.  
 OC Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; Ranunculales;  
 OC Ranunculaceae; Naravellia.  
 OX NCBI\_TaxID=231673;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Mileda O., Kita K., Handa T., Yukawa T.;  
 RL Submitted (Aug-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB116905; BAC82230.1; -; Genomic\_DNA.  
 DR GO; GO:0009507; C:chloroplast; IEA.  
 KM Chloroplast.  
 FT NON TER  
 SQ SEQUENCE 18 AA; 1953 MW; 20325A4785C6AF52 CRC64;

Query Match 24.3%; Score 25.5; DB 2; Length 18;  
 Best Local Similarity 58.3%; Pred. No. 1e+04;  
 Matches 7; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

QY 1 DPAKGMP-PGF 11

Db 4 DNEGMSSTIPGF 15

## RESULT 33

Q763U5 CLEVI  
 ID Q763U5\_CLEVI PRELIMINARY; PRT; 18 AA.  
 AC Q763U5\_  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE RNA polymerase beta subunit (Fragment).  
 GN Name=rpob;  
 OS Clematis vitalba (Evergreen clematis) (Traveller's joy).  
 OC Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; Ranunculales;  
 OC Ranunculaceae; Clematis.  
 OX NCBI\_TaxID=37490;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Mileda O., Kita K., Handa T., Yukawa T.;  
 RL Submitted (Aug-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB116904; BAC82229.1; -; Genomic\_DNA.  
 DR GO; GO:0009507; C:chloroplast; IEA.  
 KM Chloroplast.  
 FT NON TER  
 SQ SEQUENCE 18 AA; 1953 MW; 20325A4785C6AF52 CRC64;

Query Match 24.3%; Score 25.5; DB 2; Length 18;  
 Best Local Similarity 58.3%; Pred. No. 1e+04;  
 Matches 7; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

QY 1 DPAKGMP-PGF 11  
 ||||  
 Db 4 DNEGMSSTIPGF 15

## RESULT 34

Q763W5 USEUD  
 ID Q763W5\_USEUD PRELIMINARY; PRT; 20 AA.  
 AC Q763W5\_  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE RNA polymerase beta subunit (Fragment).  
 GN Name=rpob;  
 OS Clematis japonica.  
 OC Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; Ranunculales;  
 OC Ranunculaceae; Clematis.  
 OX NCBI\_TaxID=231650;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Mileda O., Kita K., Handa T., Yukawa T.;  
 RL Submitted (Aug-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB116884; BAC82209.1; -; Genomic\_DNA.  
 DR GO; GO:0009507; C:chloroplast; IEA.  
 KM Chloroplast.  
 FT NON TER  
 SQ SEQUENCE 20 AA; 2229 MW; 8E32F0325A4785C6 CRC64;

Query Match 24.3%; Score 25.5; DB 2; Length 20;  
 Best Local Similarity 58.3%; Pred. No. 1.2e+04;  
 Matches 7; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

QY 1 DPAKGMP-PGF 11  
 ||||  
 Db 4 DNEGMSSTIPGF 15

RESULT 35

TMOF\_AEDAB  
ID TMOF\_AEDAB STANDARD; PRT; 10 AA.  
AC p19425;  
DT 01-NOV-1990 (Rel. 16, Created)  
DT 01-NOV-1990 (Rel. 16, Last sequence update)  
DT 10-MAY-2005 (Rel. 47, Last annotation update)  
DE Tryptin-modulating oostatic factor (TMOF) (OOSH).  
OS Aedes aegypti (Yellowfever mosquito).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Culicidae;  
OC Culinera; Culicini; Aedes; Stegomyia.  
OX NCBI\_TaxID=7159;  
RN  
RP PROTEIN SEQUENCE.  
RC STRAIN=Vero beach; TISSUE=Ovary;  
RX MEDLINE=90367888; PubMed=2394318;  
RA Borovsky D., Carlson D.A., Griffin P.R., Shabanowitz J., Hunt D.F.;  
RT "Mosquito oostatic factor: a novel decapeptide modulating trypsin-like  
enzyme biosynthesis in the midgut.";  
RL FASEB J. 4:3015-3020(1990).  
[2]  
RP PROTEIN SEQUENCE.  
RC STRAIN=Vero beach; TISSUE=Ovary;  
RX MEDLINE=90367888; PubMed=2394318;  
RA Borovsky D., Carlson D.A., Griffin P.R., Shabanowitz J., Hunt D.F.;  
RT "Mosquito oostatic factor: a novel decapeptide modulating trypsin-like  
enzyme biosynthesis in the midgut.";  
RL FASEB J. 4:3015-3020(1990).  
[2]  
RP PROTEIN SEQUENCE.  
RC STRAIN=Vero beach; TISSUE=Ovary;  
RX MEDLINE=93357794; PubMed=8535326; DOI=10.1016/0965-1748(93)90044-S;  
RA Borovsky D., Carlson D.A., Griffin P.R., Shabanowitz J., Hunt D.F.;  
RT "Mass spectrometry and characterization of Aedes aegypti trypsin  
modulating oostatic factor (TMOF) and its analogs.";  
RL Insect Biochem. Mol. Biol. 23:703-712(1993).  
CC -1- FUNCTION: Has an oostatic activity. Inhibits trypsin biosynthesis  
in the midgut which indirectly reduces the vitellogenin  
concentration in the hemolymph resulting in inhibition of oocyte  
development.  
CC -1- DEVELOPMENTAL STAGE: Synthesized and released from follicular  
epithelium 18-24 hours after a blood meal. Synthesis peaks at 36  
hours and stops at 56 hours.  
CC -----  
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removed.  
CC  
CC PIR; A36454; A36454.  
CC Direct protein sequencing; Hormone.  
CC COMPBIAS 3 10 Poly-Pro.  
CC VARIANT 1 2 YD -> DY (in TMOF(B)).  
CC FT SEQUENCE 10 AA; 1047 MW; 236D0A7777776DC7 CRC64;  
SQ  
Query Match 23.8%; Score 25; DB 1; Length 10;  
Best Local Similarity 55.6%; Pred. No. 6.6e+03;  
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 1 DPAKMSPP 9  
|||  
Db 2 DPAPPPPP 10  
RESULT 36  
QTM3T6 TRIGR PRELIMINARY; PRT; 10 AA.  
ID QTM3T6  
AC QTM3T6  
DT 01-MAR-2004 (TREMBLrel. 26, Created)  
DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)  
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
DE Sperm-activating peptide (Ser-3, Ile-4, Gly-5 SAP-1).  
OS Tripteneustes gracillia (Hawaiian sea urchin).  
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinzoa;  
OC Echinoidea; Euechinozoa; Echinacea; Temnopileuroidea; Toxopneustidae;  
OC Tripteneustes;  
OX NCBI\_TaxID=7673;  
RN  
RP PROTEIN SEQUENCE.  
RC  
RX Yoshino K.I., Kajitara H., Nomura K., Takao T., Shimonishi Y.,

RA Kurita M., Yamaguchi M., Suzuki N.;  
RT "A halogenated amino acid-containing sperm activating peptide and its  
related peptides isolated from the egg jelly of sea urchins,  
Tripteneustes gracillia, Pseudobolita maculata, Strongylocentrotus  
nudus, Echinometra mathaei and Heterocentrotus mammillatus.";  
RL Comp. Biochem. Physiol. 94:739-751(1989).  
RN [2]  
RP PROTEIN SEQUENCE.  
RC MEDLINE=91283461; PubMed=2059627;  
RX Yoshino K., Takao T., Sunara M., Kitai T., Hori H., Nomura K.,  
RA Yamaguchi M., Shimonishi Y., Suzuki N.;  
RT "Identification of a novel amino acid, o-bromo-L-phenylalanine, in  
egg-associated peptides that activate spermatzoa.";  
RL Biochemistry 30:6203-6209(1991).  
DR PIR; C60527; C60527.  
SQ SEQUENCE 10 AA; 807 MW; 91BB53787878045 CRC64;  
Query Match 23.8%; Score 25; DB 2; Length 10;  
Best Local Similarity 55.6%; Pred. No. 6.6e+03;  
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
QY 10 GFIVGEGV 18  
|||  
Db 1 GFIVGEGV 9  
RESULT 37  
Q04620 9CALI PRELIMINARY; PRT; 12 AA.  
ID Q04620  
AC Q04620  
DT 13-SEP-2005 (TREMBLrel. 31, Created)  
DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)  
DT 13-SEP-2005 (TREMBLrel. 31, Last annotation update)  
DE RNA dependent RNA polymerase (Fragment).  
GN Name=ORF1;  
OS Norovirus NV/Yuri/1/95/JP.  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Caliciviridae;  
OC Norovirus.  
OX NCBI\_TaxID=329818;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=Yuri;  
RX MEDLINE=98351364; PubMed=9688078;  
RA Saito H., Saito S., Kamada K., Harata S., Sato H., Morita M.,  
RA Miyajima Y.;  
RT "Application of RT-PCR designed from the sequence of the local SRSV  
strain to the screening in viral gastroenteritis outbreaks.";  
RL Microbiol. Immunol. 42:439-446(1998).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=Yuri;  
RA Saito H.;  
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB214364; BMD98806.1; -; Genomic\_RNA.  
FT NON TER 1 1  
SQ SEQUENCE 12 AA; 1228 MW; 25568821D71452C8 CRC64;  
Query Match 23.8%; Score 25; DB 2; Length 12;  
Best Local Similarity 46.2%; Pred. No. 8e+03;  
Matches 6; Conservative 3; Mismatches 2; Indels 2; Gaps 1;  
QY 6 MSPPGIVGEGV 18  
::|::|::|  
Db 1 LAPEG--VVEDGV 11  
RESULT 38  
Q084268 9PAPI PRELIMINARY; PRT; 12 AA.  
ID Q084268  
AC Q084268  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)

DE B1 ORF (Fragment).  
OS Human papillomavirus.  
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
OC unclassified Papillomaviridae.  
NC NCB1\_TaxID=10566;  
RN (1)  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=89095007; PubMed=2536104;  
RA Choo K.-B., Cheung W.-F., Liew L.-N., Lee H.-H., Han S.-H.;  
RT "Presence of Genated Human Papillomavirus Type 16 Episomes in a  
DL Cervical Carcinoma Cell Line";  
RL EMBL; M24215; AAA46945.1; -; Genomic\_DNA.  
FT NON TER 12 12  
SQ SEQUENCE 12 AA; 1178 MW; 993F1P424D51A861 CRC64;  
  
Query Match 23.8%; Score 25; DB 2; Length 12;  
Best Local Similarity 50.0%; Pred. No. 8e+03;  
Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;  
  
Qy 6 MSPPGVGEEG 17  
Db 1 MADPTGNGEEG 12  
|:|:|:|:|  
|:|:|:|:|  
  
RESULT 39  
FARB\_ASCSU STANDARD; PRT; 13 AA.  
ID FARB\_ASCSU  
AC P43173;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE FMRFamide-like neuropeptide Af11.  
OS Ascaris suum (Pig roundworm) (Ascaris lumbricoides)  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Ascarididae; Ascaridoidea;  
OC Ascarididae; Ascaris.  
OX NCB1\_TaxID=6253;  
RN (1)  
RP PROTEIN SEQUENCE.  
RX MEDLINE=95580362; PubMed=7651904; DOI=10.1016/0196-9781(94)00211-N;  
RA Cowden C., Stretton A.O.W.;  
RT "Eight novel FMRFamide-like neuropeptides isolated from the nematode  
RL Ascaris suum";  
RL Peptides 16:491-500(1995).  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- SIMILARITY: Belongs to the FARB (FMRFamide related peptide)  
CC family.  
CC -----  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use as long as its content is in no way modified and this statement is not  
CC removed.  
CC -----  
CC Amlatation; Direct protein sequencing; Neuropeptide.  
KW MOD RES 13 Phenylalanine amide.  
FT SEQUENCE 13 AA; 1495 MW; 9CABG50D686B05 CRC64;  
SQ SEQUENCE 13 AA; 1495 MW; 9CABG50D686B05 CRC64;  
  
Query Match 23.8%; Score 25; DB 1; Length 13;  
Best Local Similarity 50.0%; Pred. No. 8.7e+03;  
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
  
Qy 5 GMSPPGFI 12  
Db 4 GISBPNFL 11  
|:|:|:|:|  
|:|:|:|:|  
  
RESULT 40  
O16007\_HUMAN PRELIMINARY; PRT; 13 AA.  
ID O16007\_HUMAN  
AC O16007;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)

DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)  
DE Lysosomal acid beta-galactosidase (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euteria; Euarchontoglires; Primates; Carnivora; Homiidae;  
OC Homo.  
OX NCB1\_TaxID=9606;  
RN (1)  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=91369478; PubMed=1909871;  
RA Morreau H., Bonten B., Zhou X.Y., D'Azzo A.;  
RT "Organization of the gene encoding human Lysosomal beta-  
DL galactosidase.";  
RL DNA Cell Biol. 10:495-504(1991).  
DR EMBL; S59584; AAB19814.1; -; Genomic\_DNA.  
FT NON TER 13 13  
SQ SEQUENCE 13 AA; 1482 MW; D70DABE928194412 CRC64;  
  
Query Match 23.8%; Score 25; DB 2; Length 13;  
Best Local Similarity 80.0%; Pred. No. 8.7e+03;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 9 PGFTV 13  
Db 2 PGFTV 6  
|:|:|:|:|  
|:|:|:|:|  
  
RESULT 41  
O92190\_MOUSE PRELIMINARY; PRT; 18 AA.  
ID O92190\_MOUSE  
AC O92190;  
DT 01-MAY-1999 (TREMBLrel. 10, Created)  
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)  
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
DE Mus musculus Ptn-P.  
GN Name=Ptnp;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euteria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Murinae; Mus.  
OX NCB1\_TaxID=10090;  
RN (1)  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=9909213; PubMed=9790898; DOI=10.1006/hbrc.1998.9405;  
RA Schroeder B., Groschup M., Hunsmann G., Bodemer W.;  
RT "A differentially expressed prion gene mRNA is found in prion-infected  
RT mouse brains and in NZA cells but not in uninfected mice.";  
RL Biochem. Biophys. Res. Commun. 251:6-6(1998).  
DR EMBL; Y17510; CAA76774.1; -; Genomic\_DNA.  
DR MGI; MGI:97769; Ptnp.  
DR GO; GO:0005783; C:cytoplasmic reticulum; IDA.  
DR GO; GO:0005794; C:Golgi apparatus; IDA.  
DR GO; GO:0045121; C:lipid raft; IDA.  
DR GO; GO:0005507; F:copper ion binding; IDA.  
DR GO; GO:0006878; F:copper ion homeostasis; TAS.  
DR GO; GO:0006139; P:nucleus; nucleosome, nucleotide and nucl. . .; TAS.  
DR GO; GO:0006979; P:response to oxidative stress; IDA.  
SQ SEQUENCE 18 AA; 1973 MW; F35D48870B0E6B3 CRC64;  
  
Query Match 23.8%; Score 25; DB 2; Length 18;  
Best Local Similarity 58.3%; Pred. No. 1.2e+04;  
Matches 7; Conservative 2; Mismatches 1; Indels 2; Gaps 1;  
  
Qy 11 FIVGE-EGVIS 20  
Db 3 FIVAEEROGVLT 14  
|:|:|:|:|:|:|  
|:|:|:|:|:|:|  
  
RESULT 42  
TRP3\_LEUMA STANDARD; PRT; 19 AA.  
ID TRP3\_LEUMA  
AC P81735;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)

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DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DB Tachykinin-related peptide 3 (LentRP 3).
OC Leucophaea maderae (Maderia cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC Blaberidae; Leucophaea.
OC NCBI_TaxID=6989;
RN [1]
RP PROTEIN SEQUENCE.
RC TISSUE=Midgut; PubMed=8897641;
RX MEDLINE=97053012;
RA Muren J.E., Naessel D.R.;
RT "Isolation of five tachykinin-related peptides from the midgut of the
RT cockroach Leucophaea maderae: existence of N-terminally extended
RT isoforms."
RL Regul. Pept. 65:185-196(1996).
CC -1- FUNCTION: Myoactive peptide. Increases the amplitude and frequency
CC of spontaneous contractions and tonus of hindgut muscle.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Midgut.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
KW Amlidation; Direct protein sequencing; Neuropeptide; Tachykinin.
FT MOD RES 19 19 Arginine amide.
SQ SEQUENCE 19 AA; 1930 MW; 99B5471A011625B5 CRC64;

Query Match 23.8%; Score 25; DB 1; Length 19;
Best Local Similarity 36.4%; Pred. NO. 1.3e+04;
Matches 4; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 2 PAKMSPPGPI 12
Db 6 PGGKAPSGFL 16

RESULT 43
PYRX PSRFL STANDARD; PRT; 20 AA.
AC P56586;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Dihydroorotase-like protein (Aspartate carboxyltransferase 45 kDa
DE Non-catalytic chain) (Fragment).
GN Name=pyrC;
OS Pseudomonas fluorescens.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OC NCBI_TaxID=294;
RN [1]
RP PROTEIN SEQUENCE.
RC STRAIN=ATCC 13525;
RX MEDLINE=94052183; PubMed=8234318;
RA Bergh S.T., Evans D.R.;
RT "Subunit structure of a class A aspartate transcarboxylase from
RT Pseudomonas fluorescens."
RL Proc. Natl. Acad. Sci. U.S.A. 90:9818-9822(1993).
CC -1- FUNCTION: Non-functional DHOase.
CC -1- SUBUNIT: Heterododecamer of 6 active pyrB subunits and 6 non-
CC catalytic pyrC subunits.
CC -1- SIMILARITY: Belongs to the DHOase family. PyrC subfamily.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use as long as its content is in no way modified and this statement is not

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CC removed.
CC -----
DR HAMAP; MF_00220; acylcyl; 1.
KW Direct protein sequencing; Pyrimidine biosynthesis.
FT NON TER 20
SQ SEQUENCE 20 AA; 2063 MW; 735D157A430778B1 CRC64;

Query Match 23.8%; Score 25; DB 1; Length 20;
Best Local Similarity 66.7%; Pred. NO. 1.4e+04;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DPAKGM 6
Db 12 DPASGL 17

RESULT 44
Q9QV83 9MURI
ID Q9QV83_9MURI PRELIMINARY; PRT; 20 AA.
AC Q9QV83;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE Temperature-labile cholesterol ester hydrolase (Fragment).
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Rattus.
OC NCBI_TaxID=10118;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=93216794; PubMed=8463327;
RA Wee S., Grogan W.M.;
RT "Testicular temperature-labile cholesterol ester hydrolase.
RT Relationship to isoenzymes from other tissues, correlation with
RT spermatogenesis, and inhibition by physiological concentrations of
RT divalent cations."
RL J. Biol. Chem. 268:8158-8163(1993).
SQ SEQUENCE 20 AA; 2080 MW; BR9D076DE6DD8AFC CRC64;

Query Match 23.8%; Score 25; DB 2; Length 20;
Best Local Similarity 50.0%; Pred. NO. 1.4e+04;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 6 MSPPGFVGE 15
Db 6 VSPPAVVL 15

RESULT 45
Q7LZH3_MELGA
ID Q7LZH3_MELGA PRELIMINARY; PRT; 20 AA.
AC Q7LZH3;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Myosin light chain kinase, smooth muscle (Fragment).
OS Meleagris gallopavo (Common turkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Meleagris.
OC NCBI_TaxID=9103;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=89214114; PubMed=2708351;
RA Ikebe M., Marita S., Reardon S.;
RT "Location of the inhibitory region of smooth muscle myosin light chain
RT kinase."
RL J. Biol. Chem. 264:6967-6971(1989).
DR PIR; A33878; A33878.
FT NON TER 1 1
SQ SEQUENCE 20 AA; 2147 MW; B1EFPD5269872B93 CRC64;

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Query Match 23.8%; Score 25; DB 2; Length 20;  
 Best Local Similarity 50.0%; Pred. No. 1.4e+04;  
 Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 2 PAKGMSPP 9  
 ||:|  
 DB 8 PPKAATPP 15

## RESULT 46

Q7M4B6\_STRNU  
 ID Q7M4B6\_STRNU PRELIMINARY; PRT; 10 AA.

AC Q7M4B6;  
 DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)  
 DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)  
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
 DE Sperm-activating peptide (A1a-3, Gly-5 SAP-1).  
 OS Strongylocentrotus nudus (Sea urchin).  
 OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;  
 OC Echinoidae; Euechinoidae; Echinacea; Echinacea; Strongylocentrotidae;  
 OC Strongylocentrotus.  
 OK NCBI\_TaxID=7666;  
 RN [1]  
 RP PROTEIN SEQUENCE.  
 RA Yoshino K.I., Kajitara H., Nomura K., Takao T., Shimonishi Y.,  
 RA Kurita M., Yamaguchi M., Suzuki N.;  
 RT "A halogenated amino acid-containing sperm activating peptide and its  
 RT related peptides isolated from the egg jelly of sea urchins,  
 RT tripneustes gratilla, pseudoboleia maculata, strongylocentrotus  
 RT nudus, echinometra mathaei and heterocentrotus mammillatus.";  
 RL Comp. Biochem. Physiol. 94:739-751(1989).  
 DR PIR; B60588; B60588.  
 SQ SEQUENCE 10 AA; 791 MW; CBBB537878772D CRC64;

Query Match 22.9%; Score 24; DB 2; Length 10;  
 Best Local Similarity 55.6%; Pred. No. 9.4e+03;  
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 10 GFVGEGBV 18  
 ||:|  
 DB 1 GFALGGGV 9

RESULT 47  
 Q7M4D4\_PSEDP  
 ID Q7M4D4\_PSEDP PRELIMINARY; PRT; 10 AA.

AC Q7M4D4;  
 DT 01-MAR-2004 (TREMBLrel. 26, Created)  
 DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)  
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
 DE Sperm-activating peptide (A1a-3, Gly-5 speract).  
 OS Pseudocentrotus depressus (sea urchin).  
 OC Eukaryota; Metazoa; Echinoidae; Echinacea; Echinoidae; Echinidae;  
 OC Echinoidae; Euechinoidae; Echinacea; Echinacea; Strongylocentrotidae;  
 OC Pseudocentrotus.  
 OK NCBI\_TaxID=7678;  
 RN [1]  
 RP PROTEIN SEQUENCE.  
 RA Suzuki N., Kajitara H., Nomura K., Garbers D.L., Yoshino K., Kurita M.,  
 RA Tanaka H., Yamaguchi M.;  
 RT "Some more speract derivatives associated with eggs of sea urchins,  
 RT pseudocentrotus depressus, strongylocentrotus purpuratus,  
 RT hemicentrotus pulcherrimus and Anthocidaris crassispina.";  
 RL Comp. Biochem. Physiol. 89:687-693(1988).  
 RN [2]

RP PROTEIN SEQUENCE.  
 RA Suzuki N., Kajitara H., Nomura K., Garbers D.L., Yoshino K., Kurita M.,  
 RA Tanaka H., Yamaguchi M.;  
 RT "Some more speract derivatives associated with eggs of sea urchins,  
 RT pseudocentrotus depressus, strongylocentrotus purpuratus,  
 RT hemicentrotus pulcherrimus and Anthocidaris crassispina.";  
 RL Comp. Biochem. Physiol. B, Comp. Biochem. 89:687-693(1988).

DR PIR; E60788; E60788.  
 SQ SEQUENCE 10 AA; 791 MW; CBBB537878772D CRC64;

Query Match 22.9%; Score 24; DB 2; Length 10;  
 Best Local Similarity 55.6%; Pred. No. 9.4e+03;  
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 10 GFVGEGBV 18  
 ||:|  
 DB 1 GFALGGGV 9

## RESULT 48

P82436\_TOBAC  
 ID P82436\_TOBAC PRELIMINARY; PRT; 11 AA.

AC P82436;  
 DT 01-JUN-2000 (TREMBLrel. 14, Created)  
 DT 01-JUN-2000 (TREMBLrel. 14, Last sequence update)  
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)  
 DE 65 kDa cell wall protein (Fragment).  
 OS Nicotiana tabacum (Common tobacco).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;  
 OC Lamiales; Solanales; Solanaceae; Nicotiana.  
 OK NCBI\_TaxID=4097;  
 RN [1]  
 RP PROTEIN SEQUENCE.  
 RC STRAIN=cv. PETIT HAVANA.  
 RA Blee K.A., Bonham V.A., Mitchell G.P., Robertson D., Slabas A.R.,  
 RA Wolaszek P., Bolwell G.P.;  
 RT "Proteomic study of secondary cell wall proteins from transformed  
 RT tobacco culture.";  
 RL Planta 200:0-0(2000).  
 CC -1- SUBCELLULAR LOCATION: CELL WALL.  
 CC -1- TISSUE SPECIFICITY: XYLEM.  
 DR GO; GO:0005618; C:cell wall; IEA.  
 KW Cell wall.  
 FT NON TER 11 11  
 SQ SEQUENCE 11 AA; 1068 MW; 34FD25CCB325B867 CRC64;

Query Match 22.9%; Score 24; DB 2; Length 11;  
 Best Local Similarity 80.0%; Pred. No. 1e+04;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 6 MSPPG 10  
 ||||  
 DB 1 MPPEG 5

## RESULT 49

O80X04\_MESAU  
 ID O80X04\_MESAU PRELIMINARY; PRT; 15 AA.

AC O80X04;  
 DT 01-JUN-2003 (TREMBLrel. 24, Created)  
 DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)  
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)  
 DE C-Ki-ras (Fragment).  
 OS Name=C-Ki-ras;  
 OS Mesocricetus auratus (Golden hamster).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Cricetinae; Mesocricetus.  
 OK NCBI\_TaxID=10036;  
 RN [1]

RP NUCLEOTIDE SEQUENCE.  
 RA MEDLINE=95246257; PubMed=7728976;  
 RA Takehashi T., Moyer M.P., Cano M., Wang Q.J., Mountjoy C.P.,  
 RA Sanger W., Adrian T.B., Sugitara H., Katoh H., Pour P.M.;  
 RT "Differences in molecular biological, biological and growth  
 RT characteristics between the immortal and malignant hamster pancreatic  
 RT cells.";  
 RL Carcinogenesis 16:931-939(1995).  
 DR EMBL; S77069; AAP31994.1; -; Genomic\_DNA.

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FT  NON TER      15      15
SQ  SEQUENCE     15 AA, 1538 MW, C4B2EC93858939EB CRC64;

Query Match
Best Local Similarity 22.9%; Score 24; DB 2; Length 15;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY  12 IVGEGV 18
    |||
DB  8 VVGADGV 14

RESULT 50
Q9HEQ1_PARB_R PRELIMINARY; PRT; 17 AA.
ID  Q9HEQ1_PARB_R PRELIMINARY; PRT; 17 AA.
AC  Q9HEQ1;
DT  01-MAR-2001 (TrEMBLrel. 16, Created)
DT  01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DE  01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DN  Alpha-tubulin (Fragment).
GN  Name=TUB1;
OS  Paracoccidiodae brasiliensis.
OC  Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC  Onygenales; microsporitic Onygenales; Paracoccidiodae.
OX  NCBI_TaxId=121759;
RN  [1]
RP  NUCLEOTIDE SEQUENCE.
RC  STRAIN=PB18;
RA  Kasuga T., White T.J., Taylor J.W.;
RT  "The molecular clock in fungi in the class Plecomycetes.";
RL  Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR  GO; GO:000874; C:microtubule; IEA.
DR  GO; GO:0005198; F:structural molecule activity; IEA.
DR  GO; GO:0007018; P:microtubule-based movement; IEA.
DR  InterPro; IPR002452; Alpha_tubulin.
DR  PANTHER; PTHR11588:SF1; Alpha_tubulin; 1.
FT  NON TER      17      17
SQ  SEQUENCE     17 AA, 2039 MW, B8E787547655F90A CRC64;

Query Match
Best Local Similarity 22.9%; Score 24; DB 2; Length 17;
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY  5 GMSPPGFI 12
    |||
DB  10 GIQPDGYL 17

RESULT 51
Q9HEQ2_AJED_R PRELIMINARY; PRT; 17 AA.
ID  Q9HEQ2_AJED_R PRELIMINARY; PRT; 17 AA.
AC  Q9HEQ2;
DT  01-MAR-2001 (TrEMBLrel. 16, Created)
DT  01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DE  01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DN  Alpha-tubulin (Fragment).
GN  Name=TUB1;
OS  Ajellomyces dermatitidis (Blastomyces dermatitidis).
OC  Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC  Onygenales; Ajellomycetaceae; Ajellomyces.
OX  NCBI_TaxId=5039;
RN  [1]
RP  NUCLEOTIDE SEQUENCE.
RC  STRAIN=ATCC60915;
RA  Kasuga T., White T.J., Taylor J.W.;
RT  "The molecular clock in fungi in the class Plecomycetes.";
RL  Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR  EMBL; AY013313; MAG40954.1; -; Genomic_DNA.
DR  GO; GO:000874; C:microtubule; IEA.
DR  GO; GO:0005198; F:structural molecule activity; IEA.
DR  GO; GO:0007018; P:microtubule-based movement; IEA.

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DR  InterPro; IPR002452; Alpha_tubulin.
DR  PANTHER; PTHR11588:SF1; Alpha_tubulin; 1.
FT  NON TER      17      17
SQ  SEQUENCE     17 AA, 2039 MW, B8E787547655F90A CRC64;

Query Match
Best Local Similarity 22.9%; Score 24; DB 2; Length 17;
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY  5 GMSPPGFI 12
    |||
DB  10 GIQPDGYL 17

RESULT 52
Q9HEQ3_AJEC_A PRELIMINARY; PRT; 17 AA.
ID  Q9HEQ3_AJEC_A PRELIMINARY; PRT; 17 AA.
AC  Q9HEQ3;
DT  01-MAR-2001 (TrEMBLrel. 16, Created)
DT  01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DE  01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DN  Alpha-tubulin (Fragment).
GN  Name=TUB1;
OS  Ajellomyces capsulata (Histoplasma capsulatum).
OC  Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC  Onygenales; Ajellomycetaceae; Ajellomyces.
OX  NCBI_TaxId=5037;
RN  [1]
RP  NUCLEOTIDE SEQUENCE.
RC  STRAIN=ATCC26032;
RA  Kasuga T., White T.J., Taylor J.W.;
RT  "The molecular clock in fungi in the class Plecomycetes.";
RL  Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR  EMBL; AY013312; MAG40953.1; -; Genomic_DNA.
DR  GO; GO:000874; C:microtubule; IEA.
DR  GO; GO:0005198; F:structural molecule activity; IEA.
DR  GO; GO:0007018; P:microtubule-based movement; IEA.
DR  InterPro; IPR002452; Alpha_tubulin.
DR  PANTHER; PTHR11588:SF1; Alpha_tubulin; 1.
FT  NON TER      17      17
SQ  SEQUENCE     17 AA, 2039 MW, B8E787547655F90A CRC64;

Query Match
Best Local Similarity 22.9%; Score 24; DB 2; Length 17;
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY  5 GMSPPGFI 12
    |||
DB  10 GIQPDGYL 17

RESULT 53
Q49077_MYCC_A PRELIMINARY; PRT; 17 AA.
ID  Q49077_MYCC_A PRELIMINARY; PRT; 17 AA.
AC  Q49077;
DT  01-NOV-1996 (TrEMBLrel. 01, Created)
DT  01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE  01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DN  DNA-directed RNA polymerase (beta) (Fragment).
OS  Mycoplasma capricolum.
OC  Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX  NCBI_TaxId=2095;
RN  [1]
RP  NUCLEOTIDE SEQUENCE.
RC  STRAIN=ATCC 27343;
RA  Bork P., Ouzounis C., Casari G., Schneider R., Sander C., Dolan M.,
RT  Gilbert W., Gillelev P.M.;
RT  "Exploring the Mycoplasma capricolum genome: a minimal cell reveals
its physiology.";
RL  Mol. Microbiol. 16:955-967(1995).

```

DR EMBL; Z33297; CAA63830.1; -; Genomic\_DNA.  
 DR PIR; S77834; S77834.  
 DR GO; GO:0003899; F:DNA-directed RNA polymerase activity; IRA.  
 KW DNA-directed RNA polymerase.  
 FT NON TER 17 17  
 SQ SEQUENCE 17 AA; 1930 MW; B353351EF997B46 CRC64;

Query Match 22.9%; Score 24; DB 2; Length 17;  
 Best Local Similarity 45.5%; Pred. No. 1.7e+04;  
 Matches 5; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 6 MSPGFVGE 16  
 Db 1 MGAPSIIVNE 11

RESULT 54  
 Q7M546 HALSA PRELIMINARY; PRT; 19 AA.  
 AC Q7M546;  
 DT 01-MAR-2004 (TREMBLrel. 26, Created)  
 DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)  
 DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)  
 DE Ribosomal protein S2 (Fragment).  
 OS Halobacterium salinarum (Halobacterium halobium).  
 OC Archaea; Euryarchaeota; Halobacteria; Halobacteriales;  
 OC Halobacteriaceae; Halobacterium.  
 OK NCBI\_TaxID=2242;  
 RN [1]  
 RP PROTEIN SEQUENCE.  
 RA Yaguchi M., Visentin L.P., Zuker M., Matheson A.T., Roy C.,  
 RA Strom A.R.;  
 RT "Amino-terminal sequences of ribosomal proteins from the 30S subunit  
 of archaeobacterium Halobacterium cutriburum.";  
 RL Submitted (DEC-1990) to the PIR data bank.  
 DR PIR; S1611; S1611.  
 FT NON TER 1 19  
 FT NON TER 19 19  
 SQ SEQUENCE 19 AA; 2062 MW; 3F35304BB4B4B0D CRC64;

Query Match 22.9%; Score 24; DB 2; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+04;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 SPPG 10  
 Db 15 SPPG 18

RESULT 55  
 Q7S06\_9CIRC PRELIMINARY; PRT; 19 AA.  
 ID Q7S06\_9CIRC PRELIMINARY; PRT; 19 AA.  
 AC Q7S06;  
 DT 05-JUL-2004 (TREMBLrel. 27, Created)  
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)  
 DE ORF-7.  
 OS Porcine circovirus type 2-C.  
 OC Viruses; ssDNA viruses; Circoviridae; Circovirus.  
 OK NCBI\_TaxID=85543;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=20142849; PubMed=10680656;  
 RA Hamel A.L., Lin L., Sachvie C., Grudecki E., Nayar G.P.S.;  
 RT "PCR detection and characterization of type-2 porcine circovirus.";  
 RL Can. J. Vet. Res. 64:44-52(2000).  
 DR EMBL; AF109398; AAD03067.1; -; Genomic DNA.  
 SQ SEQUENCE 19 AA; 1893 MW; 384FB58B920BC23 CRC64;

Query Match 22.9%; Score 24; DB 2; Length 19;  
 Best Local Similarity 37.5%; Pred. No. 1.9e+04;  
 Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PAKGMSPP 9  
 Db 7 PSSAVTPP 14

RESULT 56  
 Q9Y713\_9CIRC PRELIMINARY; PRT; 19 AA.  
 ID Q9Y713\_9CIRC PRELIMINARY; PRT; 19 AA.  
 AC Q9Y713;  
 DT 01-MAY-1999 (TREMBLrel. 10, Created)  
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
 DE ORF-7.  
 OS Bovine circovirus.  
 OC Viruses; ssDNA viruses; Circoviridae; Circovirus.  
 OK NCBI\_TaxID=85542;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Hamel A.L., Nayar G.P.S.;  
 RL Submitted (FEB-1999) to the EMBL/Genbank/DBJ databases.  
 DR EMBL; AF109397; AAD11934.1; -; Genomic DNA.  
 SQ SEQUENCE 19 AA; 1893 MW; 384FB58B920BC23 CRC64;

Query Match 22.9%; Score 24; DB 2; Length 19;  
 Best Local Similarity 37.5%; Pred. No. 1.9e+04;  
 Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PAKGMSPP 9  
 Db 7 PSSAVTPP 14

RESULT 57  
 Q9T218\_NICSY PRELIMINARY; PRT; 20 AA.  
 ID Q9T218\_NICSY PRELIMINARY; PRT; 20 AA.  
 AC Q9T218;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)  
 DE 14.1 kDa photosystem I PSAB protein (Fragment).  
 OS Nicotiana glauca (Wood tobacco).  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;  
 OC lamids; Solanales; Solanaceae; Nicotiana.  
 OK NCBI\_TaxID=4096;  
 RN [1]  
 RP PROTEIN SEQUENCE.  
 RX MEDLINE=94105345; PubMed=8278548; DOI=10.1104/pp.102.4.1259;  
 RA Obokata J., Mikami K., Hayashida N., Nakamura M., Sugitara M.;  
 RT "Molecular heterogeneity of photosystem I. psab, psabf, psah, and  
 psal are all present in isoforms in Nicotiana spp.";  
 RL Plant Physiol. 102:1259-1267(1993).  
 SQ SEQUENCE 20 AA; 1822 MW; E458944B2F5E5D94 CRC64;

Query Match 22.9%; Score 24; DB 2; Length 20;  
 Best Local Similarity 57.1%; Pred. No. 2e+04;  
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 AKGMSPP 9  
 Db 14 AEGRAP 20

RESULT 58  
 Q9T219\_NICSY PRELIMINARY; PRT; 20 AA.  
 ID Q9T219\_NICSY PRELIMINARY; PRT; 20 AA.  
 AC Q9T219;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-JUN-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)  
 DE 14 kDa photosystem I PSAB protein (Fragment).  
 OS Nicotiana glauca (Wood tobacco).



OG Chloroplast.  
 OC Burkholderia; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;  
 OC Lamiales; Solanales; Solanaceae; Nicotiana.  
 OK NCBI\_TaxID=4096;  
 RN (1)  
 RP PROTEIN SEQUENCE.  
 RX MEDLINE=94105345; PubMed=8278548; DOI=10.1104/pp.102.4.1259;  
 RA Obokata J., Mikami K., Hayashida N., Nakamura M., Sugitara M.,  
 RT "Molecular heterogeneity of photosystem I. psad, psab, psaf, psah, and  
 psal are all present in isoforms in Nicotiana spp."  
 RL Plant Physiol. 102:1259-1267(1993).  
 SQ SEQUENCE 20 AA; 1822 MW; A8945894392825D CRC64;

Query Match 22.9%; Score 24; DB 2; Length 20;  
 Best Local Similarity 57.1%; Pred. No. 2e+04;  
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 3 AKGMSPP 9  
 DB 13 ABCEAPP 19

RESULT 59  
 Q51S14\_9CALI PRELIMINARY; PRT; 12 AA.  
 ID Q51S14\_9CALI PRELIMINARY;  
 AC Q51S14\_9CALI PRELIMINARY;  
 DT 10-MAY-2005 (TrEMBLrel. 30, Created)  
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)  
 DE RNA polymerase (Fragment).  
 OS Norovirus Tak-69/Thailand.  
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Caliciviridae;  
 OC Norovirus.  
 OK NCBI\_TaxID=300739;  
 RN (1)  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=Tak-69/Thailand;  
 RX PubMed=15623956;  
 RA Gunatpong R., Hanman G.S., Oka T., Ogawa S., Kageyama T.,  
 RA Pongsuwanana Y., Katayama K.,  
 RT "Norovirus and sapovirus infections in Thailand."  
 RL Jpn. J. Infect. Dis. 57:276-278(2004).  
 DR EMBL; AY646878; AAV69611.1; -; Genomic\_DNA.  
 FT NON\_TER 1  
 SQ SEQUENCE 12 AA; 1276 MW; C3988821D71452C9 CRC64;

Query Match 22.4%; Score 23.5; DB 2; Length 12;  
 Best Local Similarity 60.0%; Pred. No. 1.4e+04;  
 Matches 6; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

OY 9 PGFVGESEV 18  
 DB 3 PSF-VNEDGV 11

RESULT 60  
 Q51S15\_9CALI PRELIMINARY; PRT; 12 AA.  
 ID Q51S15\_9CALI PRELIMINARY;  
 AC Q51S15\_9CALI PRELIMINARY;  
 DT 10-MAY-2005 (TrEMBLrel. 30, Created)  
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)  
 DE RNA polymerase (Fragment).  
 OS Norovirus Tak-62/Thailand.  
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Caliciviridae;  
 OC Norovirus.  
 OK NCBI\_TaxID=300738;  
 RN (1)  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=Tak-62/Thailand;  
 RX PubMed=15623956;  
 RA Gunatpong R., Hanman G.S., Oka T., Ogawa S., Kageyama T.,

RA Pongsuwanana Y., Katayama K.,  
 RT "Norovirus and sapovirus infections in Thailand."  
 RL Jpn. J. Infect. Dis. 57:276-278(2004).  
 DR EMBL; AY646877; AAV69609.1; -; Genomic\_DNA.  
 FT NON\_TER 1  
 SQ SEQUENCE 12 AA; 1276 MW; C3988821D71452C9 CRC64;

Query Match 22.4%; Score 23.5; DB 2; Length 12;  
 Best Local Similarity 60.0%; Pred. No. 1.4e+04;  
 Matches 6; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

OY 9 PGFVGESEV 18  
 DB 3 PSF-VNEDGV 11

RESULT 61  
 Q506K8\_9CALI PRELIMINARY; PRT; 16 AA.  
 ID Q506K8\_9CALI PRELIMINARY;  
 AC Q506K8\_9CALI PRELIMINARY;  
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
 DE RNA-dependent RNA polymerase (Fragment).  
 OS Norovirus Hu/Berlin/11/03/Germany.  
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Caliciviridae;  
 OC Norovirus.  
 OK NCBI\_TaxID=324082;  
 RN (1)  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=Hu/Berlin/11/03/Germany;  
 RA Petznick S., Hoehne M., Schreier E.,  
 RT "Characterization of a recombinant norovirus in Germany."  
 RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY994531; AAY25352.1; -; Genomic\_RNA.  
 KM RNA-directed RNA polymerase.  
 FT NON\_TER 1  
 SQ SEQUENCE 16 AA; 1719 MW; 0FC888218BA59CCA CRC64;

Query Match 22.4%; Score 23.5; DB 2; Length 16;  
 Best Local Similarity 60.0%; Pred. No. 1.9e+04;  
 Matches 6; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

OY 9 PGFVGESEV 18  
 DB 7 PSF-VNEDGV 15

RESULT 62  
 Q88290\_9CALI PRELIMINARY; PRT; 18 AA.  
 ID Q88290\_9CALI PRELIMINARY;  
 AC Q88290\_9CALI PRELIMINARY;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE RNA polymerase (Fragment).  
 OS Small round structured virus.  
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Caliciviridae;  
 OC Norovirus.  
 OK NCBI\_TaxID=37141;  
 RN (1)  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=Auckland;  
 RA Regal W.J., Green D.H., Lewis G.D.,  
 RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; U46039; AAB00436.1; -; Genomic\_RNA.  
 FT NON\_TER 1  
 SQ SEQUENCE 18 AA; 2034 MW; 7FCC53718BA59CCA CRC64;

Query Match 22.4%; Score 23.5; DB 2; Length 18;  
 Best Local Similarity 60.0%; Pred. No. 2.1e+04;  
 Matches 6; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

```

QY 9 PGFIVEEGV 18
   |||:|
Db 9 PSF-VNEDGV 17

RESULT 63
Q5IT04_9CALI PRELIMINARY; PRT; 19 AA.
ID Q5IT04_9CALI
AC Q5IT04;
DT 10-MAY-2005 (TREMBLrel. 30, Last sequence update)
DB 10-MAY-2005 (TREMBLrel. 30, Last annotation update)
DE RNA polymerase (Fragment).
OS Norovirus Sakaao-14/Thailand.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Caliciviridae;
   Norovirus.
OC NCB1_TaxID=300729;
RN (1)
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Sakaao-14/Thailand;
RX PubMed=15623956;
RA Gunatrong R., Hansman G.S., Oka T., Ogawa S., Kageyama T.,
   Pongsuwanana Y., Katsayama K.;
RT "Norovirus and sapovirus infections in Thailand.";
RL Jpn. J. Infect. Dis. 57:276-278(2004).
DR EMBL; AF646868; AAV69591.1; -; Genomic_DNA.
FT NON_TER 1
SQ SEQUENCE 19 AA; 2121 MW; 7FCC3A771BA59CCA CRC64;

Query Match 22.4%; Score 23.5; DB 2; Length 19;
Best Local Similarity 60.0%; Pred. No. 2.2e+04;
Matches 6; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

QY 9 PGFIVEEGV 18
   |||:|
Db 10 PSF-VNEDGV 18

RESULT 64
RS7_MYCIT STANDARD; PRT; 8 AA.
ID RS7_MYCIT
AC P33564;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE 30S ribosomal protein S7 (Fragment).
GN Name=rpS7;
OS Mycobacterium intracellulare.
OC Bacteria; Actinobacteria; Actinomycetales;
   Corynebacteriaceae; Mycobacteriaceae; Mycobacterium;
OC Mycobacterium avium complex (MAC).
OX NCB1_TaxID=1767;
RN (1)
RP NUCLEOTIDE SEQUENCE (GENOMIC DNA).
RX MEDLINE=93197130; PubMed=8451173;
RA Nair J., Rouse D.A., Morris S.L.;
RT "Nucleotide sequence analysis of the ribosomal S12 gene of
   Mycobacterium intracellulare.";
RL Nucleic Acids Res. 21:1039-1039(1993).
CC -1- FUNCTION: One of the primary rRNA binding proteins, it binds
   directly to 16S rRNA where it nucleates assembly of the head
   domain of the 30S subunit. Is located at the subunit interface
   close to the decoding center, probably blocks exit of the E-site
   tRNA (by similarity).
CC -1- SUBUNIT: Part of the 30S ribosomal subunit. Contacts proteins S9
   and S11 (by similarity).
CC -1- SIMILARITY: Belongs to the ribosomal protein S7P family.
-----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
   between the Swiss Institute of Bioinformatics and the EMBL outstation-
   CC the European Bioinformatics Institute. There are no restrictions on its
   CC use as long as its content is in no way modified and this statement is not
   CC removed.

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CC -----
DR EMBL; L08171; AAA5376.1; -; Genomic_DNA.
DR PIR; S35538; S35538.
DR HAMAP; MF_00480; -; 1.
DR InterPro; IPR000235; Ribosomal_S7.
DR PROSITE; PS00052; RIBOSOMAL_S7; PARTIAL.
KW Ribonucleoprotein; Ribosomal protein; RNA-binding; rRNA-binding;
   tRNA-binding.
FT INIT MET 0 0 By similarity.
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 850 MW; 63276DC768732417 CRC64;

Query Match 21.9%; Score 23; DB 1; Length 8;
Best Local Similarity 57.1%; Pred. No. 2.2e+06;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 PAKGNSP 8
   |||:|
Db 1 PRKGPAP 7

RESULT 65
Q8MJT7_9PRIM PRELIMINARY; PRT; 9 AA.
ID Q8MJT7_9PRIM
AC Q8MJT7;
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Hemopexin (Fragment).
OS Eulemur fulvus (brown lemur).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
   Mammalia; Eutheria; Euarchontoglires; Primates; Strepsirrhini;
   OC Lemnuriidae; Eulemur.
OX NCB1_TaxID=13515;
RN (1)
RP NUCLEOTIDE SEQUENCE.
RA Wyner Y.M., Johnson S.E., Stumpf R., Desalle R.;
RL Submitted (APR-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF258049; AAM43870.1; -; Genomic_DNA.
FT NON_TER 1
FT NON_TER 1
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 1110 MW; 738CC9C720587B1B CRC64;

Query Match 21.9%; Score 23; DB 2; Length 9;
Best Local Similarity 80.0%; Pred. No. 2.2e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 15 EGVVL 19
   |||:|
Db 2 EGVIL 6

RESULT 66
Q8MJT8_9PRIM PRELIMINARY; PRT; 9 AA.
ID Q8MJT8_9PRIM
AC Q8MJT8;
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Hemopexin (Fragment).
OS Eulemur fulvus albocollaris.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
   Mammalia; Eutheria; Euarchontoglires; Primates; Strepsirrhini;
   OC Lemnuriidae; Eulemur.
OX NCB1_TaxID=122224;
RN (1)
RP NUCLEOTIDE SEQUENCE.
RA Wyner Y.M., Johnson S.E., Stumpf R., Desalle R.;
RL Submitted (APR-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF258028; AAM43849.1; -; Genomic_DNA.
FT NON_TER 1
FT NON_TER 1
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 1110 MW; 738CC9C720587B1B CRC64;

```

Query Match 21.9%; Score 23; DB 2; Length 9;  
 Best Local Similarity 80.0%; Pred. No. 2.2e+06;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 15 EBGVL 19  
 |||:  
 Db 2 EBGIL 6

## RESULT 67

Q7M3T7 TRIGR

ID Q7M3T7 TRIGR PRELIMINARY; PRT; 10 AA.

AC Q7M3T7;

DT 01-MAR-2004 (TrEMBLrel. 26, Created)

DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)

DE Sperm-activating peptide (Ser-3, Gly-5 SAP-I).

OS Tripteneutes gracillia (Hawaiian sea urchin).

OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;

OC Echinozoa; Euechinozoa; Echinacea; Temnopneustidae;

OC Tripteneutes;

OC NCBI\_TaxID=7673;

OX NCBI\_TaxID=7673;

RN PROTEIN SEQUENCE.

RA Yoshino K.I., Kajitara H., Nomura K., Takao T., Shimonishi Y.,

RA Kurita M., Yamaguchi M., Suzuki N.;

RT "A halogenated amino acid-containing sperm activating peptide and its

RT related peptides isolated from the egg jelly of sea urchin,

RT Tripteneutes gracillia, Pseudobolella maculata, Strongylocentrotus

RT nudus, Echinometra mathaei and Heterocentrotus mammillatus.";

RL Comp. Biochem. Physiol. 94:739-751(1989).

RL PIR; B60527; E60527.

SQ SEQUENCE 10 AA; 807 MW; 91BBS378787735 CRC64;

Query Match 21.9%; Score 23; DB 2; Length 10;  
 Best Local Similarity 55.6%; Pred. No. 1.3e+04;  
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 10 GPFVBEGV 18  
 ||:|  
 Db 1 GPFSLGGGV 9

## RESULT 68

Q7M4B4 STRNU

ID Q7M4B4 STRNU PRELIMINARY; PRT; 10 AA.

AC Q7M4B4;

DT 01-MAR-2004 (TrEMBLrel. 26, Created)

DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)

DE Sperm-activating peptide (Ser-3, Gly-5 SAP-I).

OS Strongylocentrotus nudus (Sea urchin).

OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;

OC Echinozoa; Euechinozoa; Echinacea; Echinozoa; Strongylocentrotidae;

OC Strongylocentrotus;

OC NCBI\_TaxID=7666;

OX NCBI\_TaxID=7666;

RN PROTEIN SEQUENCE.

RA Yoshino K.I., Kajitara H., Nomura K., Takao T., Shimonishi Y.,

RA Kurita M., Yamaguchi M., Suzuki N.;

RT "A halogenated amino acid-containing sperm activating peptide and its

RT related peptides isolated from the egg jelly of sea urchins,

RT Tripteneutes gracillia, Pseudobolella maculata, Strongylocentrotus

RL Comp. Biochem. Physiol. 94:739-751(1989).

DR PIR; C60588; C60588. 807 MW; 91BBS378787735 CRC64;

SQ SEQUENCE 10 AA; 807 MW; 91BBS378787735 CRC64;

Query Match 21.9%; Score 23; DB 2; Length 10;  
 Best Local Similarity 55.6%; Pred. No. 1.3e+04;  
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 10 GPFVBEGV 18  
 ||:|  
 Db 1 GPFSLGGGV 9

## RESULT 69

Q7M4C0 HETMA

ID Q7M4C0 HETMA PRELIMINARY; PRT; 10 AA.

AC Q7M4C0;

DT 01-MAR-2004 (TrEMBLrel. 26, Created)

DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)

DE Sperm-activating peptide (Glu-3, Met-4, Gly-5, Thr-7 SAP-I).

OS Heterocentrotus mammillatus (Slate-pencil urchin).

OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;

OC Echinozoa; Euechinozoa; Echinacea; Echinozoa; Echinometridae;

OC Heterocentrotus;

OC NCBI\_TaxID=31180;

OX NCBI\_TaxID=31180;

RN PROTEIN SEQUENCE.

RA Yoshino K.I., Kajitara H., Nomura K., Takao T., Shimonishi Y.,

RA Kurita M., Yamaguchi M., Suzuki N.;

RT "A halogenated amino acid-containing sperm activating peptide and its

RT related peptides isolated from the egg jelly of sea urchins,

RT Tripteneutes gracillia, Pseudobolella maculata, Strongylocentrotus

RT nudus, Echinometra mathaei and Heterocentrotus mammillatus.";

RL Comp. Biochem. Physiol. 94:739-751(1989).

RL PIR; I60588; I60588.

SQ SEQUENCE 10 AA; 911 MW; 7FBS361A87879B CRC64;

Query Match 21.9%; Score 23; DB 2; Length 10;  
 Best Local Similarity 55.6%; Pred. No. 1.3e+04;  
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 10 GPFVBEGV 18  
 ||:|  
 Db 1 GPFSLGGGV 9

## RESULT 70

Q4W618 9CALI

ID Q4W618 9CALI PRELIMINARY; PRT; 12 AA.

AC Q4W618;

DT 13-SEP-2005 (TrEMBLrel. 31, Created)

DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)

DE RNA dependent RNA polymerase (Fragment).

OS Name=ORF1;

OS Norovirus NV/Futatsui/11/05/JP.

OC Viruses; ssRNA positive-strand viruses, no DNA stage; Caliciviridae;

OC Norovirus.

OC NCBI\_TaxID=329819;

OX NCBI\_TaxID=329819;

RN NUCLEOTIDE SEQUENCE.

RA STRAIN=Futatsui;

RA Saito H.;

RT "Outbreak of norovirus with water supply service line in the small

RT village.";

RT Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.

DR EMBL; AB214365; BAD98808.1; -; Genomic\_RNA.

PT NON TER 1 1

SQ SEQUENCE 12 AA; 1242 MW; 41988821D71452C7 CRC64;

Query Match 21.9%; Score 23; DB 2; Length 12;  
 Best Local Similarity 57.1%; Pred. No. 1.6e+04;

Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 QY 12 IYGEV 18  
 : ||:  
 Db 5 LVNEDGV 11

RESULT 71  
 Q60F86\_9BRYO PRELIMINARY; PRT; 13 AA.  
 ID Q60F86\_9BRYO PRELIMINARY; PRT; 13 AA.  
 AC Q60F86\_9BRYO PRELIMINARY; PRT; 13 AA.  
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
 DE 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
 GN Ribosomal protein S11 (Fragment).  
 OS Name=rp11;  
 OG Sphagnum glaucophyllum.  
 OC Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;  
 OC Sphagnopsida; Sphagnales; Sphagnaceae; Sphagnum.  
 OX NCBI\_TaxID=128204;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Sugita M., Sugita C., Arikawa T., Higuchi M.,  
 RT "Molecular evidence of an rpoA gene in the basal moss chloroplast  
 RT genomes: rpoA is a useful molecular marker for phylogenetic analysis  
 RT of mosses.";  
 RL Hikobia 0:0-0(2004).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Sugita M., Sugita C., Arikawa T., Higuchi M.,  
 RT "Molecular evidence of an rpoA gene in the basal moss chloroplast  
 RT genomes: rpoA is a useful molecular marker for phylogenetic analysis  
 RT of mosses.";  
 RL Hikobia 14:171-175(2004).  
 DR EMBL; AB193122; BAD60946.1; -; Genomic\_DNA.  
 DR GO; GO:0009507; C:chloroplast; IEA.  
 DR GO; GO:0005622; C:intracellular; IEA.  
 DR GO; GO:0005840; C:ribosome; IEA.  
 DR GO; GO:0003735; F:structural constituent of ribosome; IEA.  
 DR GO; GO:0006412; P:protein biosynthesis; IEA.  
 DR InterPro; IPR001971; Ribosomal\_S11.  
 DR Pfam; PF00411; Ribosomal\_S11; 1.  
 KW Chloroplast; Ribosomal protein.  
 FT NON TER 1  
 SQ SEQUENCE 13 AA; 1545 MW; 7A0CD3AE1E377774 CRC64;  
 Query Match 21.9%; Score 23; DB 2; Length 13;  
 Best Local Similarity 50.0%; Pred. No. 1.8e+04;  
 Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 QY 2 PAKGMSPP 9  
 : ||:  
 Db 1 PHNGCRPP 8

RT "Molecular evidence of an rpoA gene in the basal moss chloroplast  
 RT genomes: rpoA is a useful molecular marker for phylogenetic analysis  
 RT of mosses.";  
 RL Hikobia 0:0-0(2004).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Sugita M., Sugita C., Arikawa T., Higuchi M.,  
 RT "Molecular evidence of an rpoA gene in the basal moss chloroplast  
 RT genomes: rpoA is a useful molecular marker for phylogenetic analysis  
 RT of mosses.";  
 RL Hikobia 14:171-175(2004).  
 DR EMBL; AB193121; BAD60943.1; -; Genomic\_DNA.  
 DR GO; GO:0009507; C:chloroplast; IEA.  
 DR GO; GO:0005622; C:intracellular; IEA.  
 DR GO; GO:0005840; C:ribosome; IEA.  
 DR GO; GO:0003735; F:structural constituent of ribosome; IEA.  
 DR GO; GO:0006412; P:protein biosynthesis; IEA.  
 DR InterPro; IPR001971; Ribosomal\_S11.  
 DR Pfam; PF00411; Ribosomal\_S11; 1.  
 KW Chloroplast; Ribosomal protein.  
 FT NON TER 1  
 SQ SEQUENCE 13 AA; 1545 MW; 7A0CD3AE1E377774 CRC64;  
 Query Match 21.9%; Score 23; DB 2; Length 13;  
 Best Local Similarity 50.0%; Pred. No. 1.8e+04;  
 Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 QY 2 PAKGMSPP 9  
 : ||:  
 Db 1 PHNGCRPP 8

RESULT 73  
 P82866\_RANPI PRELIMINARY; PRT; 13 AA.  
 ID P82866\_RANPI PRELIMINARY; PRT; 13 AA.  
 AC P82866;  
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE RNA-binding protein (Fragment).  
 OS Rana pipiens (Northern leopard frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Rana.  
 OX NCBI\_TaxID=8404;  
 RN [1]  
 RP PROTEIN SEQUENCE.  
 RC TISSUE=embryonic epithelium;  
 RA Banerjee H.N., Blackmon R.H., Moses A., Harmon G.L., Peterson B.L.,  
 RA Khan A.;  
 RT "Isolation, identification and characterization of a novel 5'UTR  
 RT binding protein for VCAW-1.";  
 RL Submitted (NOV-2000) to Swiss-Prot.  
 CC -1- FUNCTION: Binds to the VCAW-1 5'UTR region.  
 CC -1- SIMILARITY: Belongs to the fecuin family.  
 DR PIR; A59387; A59387.  
 DR GO; GO:0003723; P:RNA binding; IEA.  
 DR InterPro; IPR001363; Prot inh fecuin.  
 DR PROSITE; PS01254; FETUIN\_1; PARTIAL.  
 DR PROSITE; PS01255; FETUIN\_2; PARTIAL.  
 KW RNA-binding.  
 FT NON TER 13  
 SQ SEQUENCE 13 AA; 1370 MW; C683612A61757DC2 CRC64;  
 Query Match 21.9%; Score 23; DB 2; Length 13;  
 Best Local Similarity 44.4%; Pred. No. 1.8e+04;  
 Matches 4; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
 QY 1 DPAKGMSP 9  
 : ||:  
 Db 4 DPAKGMSP 12

RESULT 74

UC19\_MA1ZB  
ID UC19\_MA1ZB STANDARD; PRT; 15 AA.  
AC P80625;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Unknown protein from 2D-PAGE of etiolated coleoptile (Spot 406) (Fragment).  
OS Zea mays (Maize).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
OC PACCAD clade; Panicoidae; Andropogoneae; Zea.  
OX NCBI\_TaxID=4577;  
RN [1]  
RP PROTEIN SEQUENCE.  
RC TISUB=COLEOPTILE;  
RA Pourcel F., Riccardi F., Morin C., Damerval C., Huet J.-C.,  
RT Pournet J.-C., Zivy M., de Vienne D.;  
RT "The maize two dimensional gel protein database: towards an integrated genome analysis program."  
RT Theor. Appl. Genet. 93:997-1005(1996).  
CC -1- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown protein is: 5.6, its MW is: 18.4 kDa.  
CC -----  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.  
CC -----  
CC Maize-2DPAGE; P80625; COLEOPTILE.  
DR Gramene; P80625; -;  
DR MaizeDB; 123951; -;  
KW Direct protein sequencing.  
FT NON\_TER 1 1  
FT NON\_TER 15 15  
SQ SEQUENCE 15 AA; 1672 MW; 1CF69DADA6737F9D CRC64;  
  
Query Match 21.9%; Score 23; DB 1; Length 15;  
Best Local Similarity 80.0%; Pred. No. 2.1e+04;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
OY 5 GMSPP 9  
DB 9 GCSPP 13  
  
RESULT 75  
0561Y4\_9FLAV PRELIMINARY; PRT; 15 AA.  
ID 0561Y4\_9FLAV PRELIMINARY; PRT; 15 AA.  
AC 0561Y4;  
DT 10-MAY-2005 (TrEMBLrel. 30, Created)  
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)  
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)  
DE C protein (Fragment).  
OS Tick-borne encephalitis virus.  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Flavivirus; tick-borne encephalitis virus group.  
OC NCBI\_TaxID=11084;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=BR85;  
RA Casati S., Gern L., Piffaretti J.-C.;  
RT "Diversity of the tick-borne Encephalitis Virus population infecting RT Ixodes ricinus ticks in a risk region of central Switzerland (Canton Bern)."  
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY45366; AAK57481.1; -, Genomic\_RNA.  
FT NON\_TER 15 15  
SQ SEQUENCE 15 AA; 1523 MW; 735110858796B95D CRC64;  
  
Query Match 21.9%; Score 23; DB 2; Length 15;  
Best Local Similarity 66.7%; Pred. No. 2.1e+04;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
OY 5 GMSPP 9  
DB 9 GCSPP 13  
  
RESULT 76  
0561Z6\_9FLAV PRELIMINARY; PRT; 15 AA.  
ID 0561Z6\_9FLAV PRELIMINARY; PRT; 15 AA.  
AC 0561Z6;  
DT 10-MAY-2005 (TrEMBLrel. 30, Created)  
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)  
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)  
DE C protein (Fragment).  
OS Tick-borne encephalitis virus.  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Flavivirus; tick-borne encephalitis virus group.  
OC NCBI\_TaxID=11084;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=BR241;  
RA Casati S., Gern L., Piffaretti J.-C.;  
RT "Diversity of the tick-borne Encephalitis Virus population infecting RT Ixodes ricinus ticks in a risk region of central Switzerland (Canton Bern)."  
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY45350; AAK57469.1; -, Genomic\_RNA.  
FT NON\_TER 15 15  
SQ SEQUENCE 15 AA; 1523 MW; 735110858796B95D CRC64;  
  
Query Match 21.9%; Score 23; DB 2; Length 15;  
Best Local Similarity 66.7%; Pred. No. 2.1e+04;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
  
OY 4 KGSPP 9  
DB 10 KGSAPP 15  
  
RESULT 77  
09UCG5\_HUMAN PRELIMINARY; PRT; 16 AA.  
ID 09UCG5\_HUMAN PRELIMINARY; PRT; 16 AA.  
AC 09UCG5;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
DE T-suppressor LYMPHOKINE.  
OS Homo sapiens (human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.  
OC NCBI\_TaxID=9606;  
RN [1]  
RP PROTEIN SEQUENCE.  
RC MEDLINE=9321626; PubMed=7682534;  
RA Quan C.P., Watanabe S., Vuillier F., Pires R., Matsuo T.,  
RA Stanislawski M., Pillot J., Bouvet J.P.;  
RT "Purification and partial amino acid sequence of suppressive RT lymphokine from a CD8+ CD57+ human T hybridoma."  
RL Immunology 78:205-209(1993).  
SQ SEQUENCE 16 AA; 1587 MW; 4565578EBB6F9C29 CRC64;  
  
Query Match 21.9%; Score 23; DB 2; Length 16;  
Best Local Similarity 80.0%; Pred. No. 2.2e+04;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
OY 13 VGBEG 17  
DB 5 VGBEG 9  
  
RESULT 78

BIOP1\_PHYNY STANDARD; PRT; 17 AA.  
 ID BIOP1\_PHYNY  
 AC P84521;  
 DT 10-MAY-2005 (Rel. 47, Created)  
 DT 10-MAY-2005 (Rel. 47, Last sequence update)  
 DE Bioactive peptide 1.  
 OS Phyllomedusa hypochondrialis (Orange-legged leaf frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Hylidae;  
 OC Phyllomedusinae; Phyllomedusa.  
 NCBI\_TaxID=317381;  
 RN [1]  
 RP PROTEIN SEQUENCE, MASS SPECTROMETRY, AND PYRROLIDONE CARBOXYLIC ACID.  
 RC TISSUE=Venom;  
 RA Thompson A.H.;  
 RT "Bioactive peptides derived from the venom of the South American tree  
 frog, Phyllomedusa hypochondrialis.";  
 RL Submitted (APR-2005) to Swiss-Prot.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: Venom.  
 CC -1- MASS SPECTROMETRY: MW=1732.86; MW\_ERR=0.1; METHOD=Electrospray;  
 CC RANGES=1-17; NOTE=Ref.1.  
 CC -----  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC -----  
 CC Direct protein sequencing; Pyroglutamate carboxylic acid.  
 KW MOD\_RES 1 1  
 FT UNSURE 11 11 L or I.  
 FT 14 14 L or I.  
 SQ SEQUENCE 17 AA; 1750 MW; 23AC9C40FB8BF1F7 CRC64;  
 Query Match 21.9%; Score 23; DB 1; Length 17;  
 Best Local Similarity 50.0%; Pred. No. 2.4e+04;  
 Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
 QY 2 PAKGMSPP 11  
 DB 7 PYGGLSPLR 16  
 RESULT 79  
 Q9UCU9\_HUMAN PRELIMINARY; PRT; 17 AA.  
 ID Q9UCU9;  
 AC Q9UCU9;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Proteoglycan 80 kDa polypeptide (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;  
 OC Homo.  
 NCBI\_TaxID=9606;  
 RN [1]  
 RP PROTEIN SEQUENCE.  
 RX MEDLINE=93054750; PubMed=1429726;  
 RA Perides G., Rahemulla F., Lane W.S., Asher R.A., Bignami A.;  
 RT "Isolation of a large aggregating proteoglycan from human brain.";  
 RL J. Biol. Chem. 267:23883-23887(1992).  
 SQ SEQUENCE 17 AA; 1771 MW; 1BDAB561B2F71614 CRC64;  
 Query Match 21.9%; Score 23; DB 2; Length 17;  
 Best Local Similarity 80.0%; Pred. No. 2.4e+04;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 5 GMSPP 9  
 DB 1 1 1 1 1

DB 7 GKSP 11  
 RESULT 80  
 Q9UEJ5\_HUMAN PRELIMINARY; PRT; 17 AA.  
 ID Q9UEJ5;  
 AC Q9UEJ5;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE PLAU protein (Fragment).  
 GN Name=PLAU;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;  
 OC Homo.  
 NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=86050639; PubMed=3933505;  
 RA Nagamine Y., Pearson D., Gratian M.;  
 RT "Exon-intron boundary sliding in the generation of two mRNAs coding  
 RT for porcine urokinase-like plasminogen activator.";  
 RL Biochem. Biophys. Res. Commun. 132:563-569(1985).  
 DR EMBL; K03027; AAA61257.1; -; Genomic\_DNA.  
 FT NON\_TER 1 1  
 FT NON\_TER 17 17  
 SQ SEQUENCE 17 AA; 1801 MW; 9989927BA849E253 CRC64;  
 Query Match 21.9%; Score 23; DB 2; Length 17;  
 Best Local Similarity 55.6%; Pred. No. 2.4e+04;  
 Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 DPAKMSPP 9  
 DB 9 DKKPSP 17  
 RESULT 81  
 Q9RSJ3\_MYCGA PRELIMINARY; PRT; 17 AA.  
 ID Q9RSJ3;  
 AC Q9RSJ3;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)  
 DE Major hemagglutinin (Fragment).  
 OS Mycoplasma gallisepticum.  
 OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.  
 NCBI\_TaxID=2096;  
 RN [1]  
 RP PROTEIN SEQUENCE.  
 RX MEDLINE=9263591; PubMed=1379991;  
 RA Marham P.F., Glew W.D., Brandon M.R., Walker I.D., Whitehead K.G.;  
 RT "Characterization of a major hemagglutinin protein from Mycoplasma  
 RT gallisepticum.";  
 RL Infect. Immun. 60:3885-3891(1992).  
 SQ SEQUENCE 17 AA; 1692 MW; 466461BD34163413 CRC64;  
 Query Match 21.9%; Score 23; DB 2; Length 17;  
 Best Local Similarity 50.0%; Pred. No. 2.4e+04;  
 Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
 QY 2 PAKGMSPP 9  
 DB 8 PAPNP 15  
 RESULT 82  
 Q9TWH0\_9TRYP PRELIMINARY; PRT; 18 AA.  
 ID Q9TWH0;  
 AC Q9TWH0;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-JUN-2000 (Tremblrel. 14, Last annotation update)  
 DE Histone 1.3 (Fragment).  
 OS Trypanosoma brucei.  
 OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.  
 ON NCBI\_TaxID=5691;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=95375686; PubMed=7647705; DOI=10.1016/0248-4900(96)89928-X;  
 RA Buril M., Schlimme W., Betschart B., Lindner H., Kampfer U.,  
 RA Schaller U., Hecker H.,  
 RT "Partial amino acid sequence and functional aspects of histone H1  
 RT proteins in Trypanosoma brucei brucei".  
 RL Biol. Cell 83:23-31(1995).  
 SQ SEQUENCE 18 AA; 1635 MW; B45007F885B6784D CRC64;

Query Match 21.9%; Score 23; DB 2; Length 18;  
 Best Local Similarity 57.1%; Pred. No. 2.5e+04;  
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 AKGMSPP 9  
 DB 12 AKSAPP 18

RESULT 83  
 OSEFY3\_9BRYO PRELIMINARY; PRT; 18 AA.  
 ID OSEFY3;  
 AC OSEFY3;  
 DT 10-MAY-2005 (Tremblrel. 30, Created)  
 DT 10-MAY-2005 (Tremblrel. 30, Last sequence update)  
 DE 10-MAY-2005 (Tremblrel. 30, Last annotation update)  
 DE Ribosomal protein S11 (Fragment).  
 GN Name=rp11;  
 OS Polytichum pallidisetum.  
 OC Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;  
 OC Polytichopsida; Polytichales; Polytichaceae; Polytichum.  
 ON NCBI\_TaxID=46548;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Goffinet B., Wickett N.J., Shaw J.A., Cox C.J.,  
 RT "Phylogenetic significance of the rpoa loss in the chloroplast genome  
 RT of mosses".  
 RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY886747; AM81784.1; -; Genomic\_DNA.  
 DR GO; GO:0009507; C:chloroplast; IEA.  
 DR GO; GO:0003735; P:structural constituent of ribosome; IEA.  
 DR InterPro; IPR001971; Ribosomal S11.  
 DR Prodom; PD001010; Ribosomal S11; 1.  
 KW Chloroplast; Ribosomal protein.  
 FT NON\_TER 1  
 FT SEQUENCE 18 AA; 2030 MW; 130F2F81E680B24 CRC64;

Query Match 21.9%; Score 23; DB 2; Length 18;  
 Best Local Similarity 50.0%; Pred. No. 2.5e+04;  
 Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 PAKGMSPP 9  
 DB 6 PHNGCRPP 13

RESULT 84  
 OSEFY6\_9BRYO PRELIMINARY; PRT; 18 AA.  
 ID OSEFY6;  
 AC OSEFY6;  
 DT 10-MAY-2005 (Tremblrel. 30, Created)  
 DT 10-MAY-2005 (Tremblrel. 30, Last sequence update)  
 DT 10-MAY-2005 (Tremblrel. 30, Last annotation update)  
 DE Ribosomal protein S11 (Fragment).  
 GN Name=rp11;  
 OS Andrena rufescens.  
 OC Chloroplast.

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;  
 OC Andreaeopsida; Andreales; Andreaeaceae; Andraea.  
 ON NCBI\_TaxID=13797;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Goffinet B., Wickett N.J., Shaw J.A., Cox C.J.,  
 RT "Phylogenetic significance of the rpoa loss in the chloroplast genome  
 RT of mosses".  
 RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY886745; AM81779.1; -; Genomic\_DNA.  
 DR GO; GO:0009507; C:chloroplast; IEA.  
 DR GO; GO:0003735; P:structural constituent of ribosome; IEA.  
 DR InterPro; IPR001971; Ribosomal S11.  
 DR Prodom; PD001010; Ribosomal S11; 1.  
 KW Chloroplast; Ribosomal protein.  
 FT NON\_TER 1  
 FT SEQUENCE 18 AA; 2088 MW; 130D426E1E680B24 CRC64;

Query Match 21.9%; Score 23; DB 2; Length 18;  
 Best Local Similarity 50.0%; Pred. No. 2.5e+04;  
 Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 PAKGMSPP 9  
 DB 6 PHNGCRPP 13

RESULT 85  
 O8SKY0\_CUSRB PRELIMINARY; PRT; 18 AA.  
 ID O8SKY0;  
 AC O8SKY0;  
 DT 01-JUN-2002 (Tremblrel. 21, Created)  
 DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)  
 DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)  
 DE Ribosomal protein S11 (Fragment).  
 GN Name=rp11;  
 OS Cuscuta reflexa (southern Asian dodder).  
 OC Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
 OC Asteridae; lamiales; Solanales; Convolvulaceae; Cuscutae; Cuscuta.  
 ON NCBI\_TaxID=4129;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Berg S.,  
 RT "Sequence analysis and coding potential of the holoparasitic flowering  
 RT plant genus Cuscuta".  
 RL Thesis (2002), Department of Institute of Botany,  
 RL Christian-Albrechts-University, Kiel, Germany.  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Krause K., Berg S., Krupinska K.,  
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
 CC -1- Similarity: Belongs to the EMBL/GenBank protein S11P family.  
 DR EMBL; AY433611; CND28796.1; -; Genomic\_DNA.  
 DR GO; GO:0005840; C:ribosome; IEA.  
 DR GO; GO:0003735; P:structural constituent of ribosome; IEA.  
 DR GO; GO:006412; P:protein biosynthesis; IEA.  
 DR InterPro; IPR001971; Ribosomal S11.  
 DR Pfam; PF00411; Ribosomal\_S11; 1.  
 DR Prodom; PD001010; Ribosomal S11; 1.  
 KW Ribonucleoprotein; Ribosomal protein.  
 FT NON\_TER 1  
 FT SEQUENCE 18 AA; 2088 MW; 130D427BF8680B24 CRC64;

Query Match 21.9%; Score 23; DB 2; Length 18;  
 Best Local Similarity 50.0%; Pred. No. 2.5e+04;  
 Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 PAKGMSPP 9  
 DB 6 PHNGCRPP 13

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RESULT 86
OQOV98_9MURI PRELIMINARY; PRT; 18 AA.
ID OQOV98_9MURI
AC OQOV98;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE Vitronectin (Fragment).
OS Mus sp..
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_Taxid=10095;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=93155525; PubMed=7679136; DOI=10.1111/1523-1747.ep12462792;
RA Dahlback K., Wolf H.C., Dahlback B.;
RT "Vitronectin in mouse skin: immunohistochemical demonstration of its
association with cutaneous amyloid."
RL J. Invest. Dermatol. 100:166-170 (1993).
SQ SEQUENCE 18 AA, 1961 MW, 99ECB76571B6EC94 CRC64;

Query Match 21.9%; Score 23; DB 2; Length 18;
Best Local Similarity 26.7%; Pred. No. 2.5e+04;
Matches 4; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

OY 1 DPAGKSPRGPIVGE 15
: ||| :
Db 4 ESKKGRXQTGFMAK 18

RESULT 87
FIBA_ANTAM
ID FIBA_ANTAM STANDARD; PRT; 19 AA.
AC P14440;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 01-FEB-2005 (Rel. 46, Last annotation update)
DE Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
GN Name=FGA;
OS Antilocapra americana (Pronghorn).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Antilocapridae; Antilocapra.
OX NCBI_Taxid=9891;
RN [1]
RP PROTEIN SEQUENCE.
RA Moses G.A., Doolittle R.F.;
RT "Amino acid sequence studies on aridodactyl fibrinopeptides."
RL Arch. Biochem. Biophys. 122:674-684 (1967).
CC -1- FUNCTION: Fibrinogen has a double function: yielding monomers that
polymerize into fibrin and acting as a cofactor in platelet
aggregation.
CC -1- SUBUNIT: Heterohexamer; disulfide linked. Contains 2 sets of 3
nondidentical chains (alpha, beta and gamma). The 2 heterotrimers
are in head to head conformation with the N-termini in a small
central domain (by similarity).
CC -1- DOMAIN: A long coiled coil structure formed by 3 polypeptide
chains connects the central module to the C-terminal domains
(distal nodules). The long C-terminal ends of the alpha chains
fold back, contributing a fourth strand to the coiled coil
structure.
CC -1- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin,
which cleaves fibrinopeptides A and B from alpha and beta chains,
and thus exposes the N-terminal polymerization sites responsible
for the formation of the soft clot.
-----
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use as long as its content is in no way modified and this statement is not
removed.

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CC -----
CC Blood coagulation; Coiled coil; Direct protein sequencing; Plasma.
CC PEPTIDE 1 19 Fibrinopeptide A.
CC FT NON_TER 19
CC SQ SEQUENCE 19 AA; 1758 MW; 8BBA0873C861F375 CRC64;

Query Match 21.9%; Score 23; DB 1; Length 19;
Best Local Similarity 55.6%; Pred. No. 2.7e+04;
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 DPAGKSP 9
: ||| :
Db 5 DPVGGRSLP 13

RESULT 88
FIBA_BISBO
ID FIBA_BISBO STANDARD; PRT; 19 AA.
AC P14441;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 01-FEB-2005 (Rel. 46, Last annotation update)
DE Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
GN Name=FGA;
OS Bison bonasus (European bison).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bison.
OX NCBI_Taxid=9902;
RN [1]
RP PROTEIN SEQUENCE.
RA Blomback B., Grondahl N.J.;
RT "Studies on fibrinopeptides from mamale."
RL Acta Chem. Scand. 19:1789-1791 (1965).
CC -1- FUNCTION: Fibrinogen has a double function: yielding monomers that
polymerize into fibrin and acting as a cofactor in platelet
aggregation.
CC -1- SUBUNIT: Heterohexamer; disulfide linked. Contains 2 sets of 3
nondidentical chains (alpha, beta and gamma). The 2 heterotrimers
are in head to head conformation with the N-termini in a small
central domain (by similarity).
CC -1- DOMAIN: A long coiled coil structure formed by 3 polypeptide
chains connects the central module to the C-terminal domains
(distal nodules). The long C-terminal ends of the alpha chains
fold back, contributing a fourth strand to the coiled coil
structure.
CC -1- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin,
which cleaves fibrinopeptides A and B from alpha and beta chains,
and thus exposes the N-terminal polymerization sites responsible
for the formation of the soft clot.
-----
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removed.
CC Blood coagulation; Coiled coil; Direct protein sequencing; Plasma.
CC PEPTIDE 1 19 Fibrinopeptide A.
CC FT NON_TER 19
CC SQ SEQUENCE 19 AA; 1836 MW; 9BA55A0F47B59C5 CRC64;

Query Match 21.9%; Score 23; DB 1; Length 19;
Best Local Similarity 80.0%; Pred. No. 2.7e+04;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 DPAGK 5
: ||| :
Db 5 DPAGK 9

RESULT 89
FIBA_MUNMU

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ID  F1BA_MUNMU  STANDARD;  PRT;  19 AA.
AC  P1457;
DT  01-JAN-1990 (Rel. 13, Created)
DT  01-JAN-1990 (Rel. 13, Last sequence update)
DE  01-FEB-2005 (Rel. 46, Last annotation update)
DE  Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
GN  Name=FGA;
OS  Muntiacus muntjak (Muntjak).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC  Pecora; Cervidae; Muntiacinae; Muntiacus.
OX  NCBI_TaxID=9888;
RN  [1]
RP  PROTEIN SEQUENCE.
RA  Mross G.A., Doolittle R.F.;
RT  "Amino acid sequence studies on artiodactyl fibrinopeptides.";
RL  Arch. Biochem. Biophys. 122:674-684(1967).
CC  -1- FUNCTION: Fibrinogen has a double function: yielding monomers that
CC  polymerize into fibrin and acting as a cofactor in platelet
CC  aggregation.
CC  -1- SUBUNIT: Heterohexamer; disulfide linked. Contains 2 sets of 3
CC  nonidentical chains (alpha, beta and gamma). The 2 heterotrimers
CC  are in head to head conformation with the N-termini in a small
CC  central domain (By similarity).
CC  -1- DOMAIN: A long coiled coil structure formed by 3 polypeptide
CC  chains connects the central node to the C-terminal domains
CC  (distal nodules). The long C-terminal ends of the alpha chains
CC  fold back, contributing a fourth strand to the coiled coil
CC  structure.
CC  -1- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin,
CC  which cleaves fibrinopeptides A and B from alpha and beta chains,
CC  and thus exposes the N-terminal polymerization sites responsible
CC  for the formation of the soft clot.
CC  -----
CC  This Swiss-Prot entry is copyright. It is produced through a collaboration
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CC  the European Bioinformatics Institute. There are no restrictions on its
CC  use as long as its content is in no way modified and this statement is not
CC  removed.
CC  -----
KW  Blood coagulation; Coiled coil; Direct protein sequencing; Plasma.
FT  PEPTIDE 1 19 Fibrinopeptide A.
FT  NON_TER 19 19
SQ  SEQUENCE 19 AA; 1822 MW; 9BA1862873B45B5 CRC64;

Query Match 21.9%; Score 23; DB 1; Length 19;
Best Local Similarity 80.0%; Pred. No. 2.7e+04;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DPAKG 5
DB 5 DPASG 9

RESULT 90
095RY5_DROME PRELIMINARY; PRT; 19 AA.
ID 095RY5;
AC 095RY5;
DT 01-DEC-2001 (TEMBLrel. 19, Created)
DT 01-DEC-2001 (TEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TEMBLrel. 26, Last annotation update)
DE H107889P.
GN Name=gem1 ORFName=CG30011;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA STRAIN=Berkely;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Farfan D., Friese E., George R.,

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RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
RA Munco J., Pacleb J., Paragae V., Park S., Phouanavong S., Wan K.,
RA Yu C., Lewis S.B., Rubin G.M., Ceiniker S.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY061040; AAL28588.1; -; mRNA.
DR FLYBase; FBgn0050011; CG30011.
DR FLYBase; FBgn0050011; Gen.
SQ SEQUENCE 19 AA; 2105 MW; 07A74ED38EA1A7F3 CRC64;

Query Match 21.9%; Score 23; DB 2; Length 19;
Best Local Similarity 50.0%; Pred. No. 2.7e+04;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 5 GMSPPGPI 12
DB 6 GFSKPRPV 13

RESULT 91
09N613_TOXGO PRELIMINARY; PRT; 19 AA.
ID 09N613;
AC 09N613;
DT 01-OCT-2000 (TEMBLrel. 15, Created)
DT 01-OCT-2000 (TEMBLrel. 15, Last sequence update)
DT 01-FEB-2005 (TEMBLrel. 29, Last annotation update)
DE Beta-tubulin (Fragment).
GN Name=TUB2;
OS Toxoplasma gondii.
OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Sarcocystidae;
OC Toxoplasma.
OX NCBI_TaxID=5811;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21011398; PubMed=11128519;
RA Lehmann T., Blackston C.R., Parmley S.F., Remington J.S., Dubey J.P.;
RT "Strain typing of Toxoplasma gondii: comparison of antigen-coding and
RT housekeeping genes.";
RL J. Parasitol. 86:960-971(2000).
DR EMBL; AF249703; AAF79161.1; -; Genomic DNA.
DR EMBL; AF249702; AAF79160.1; -; Genomic DNA.
DR EMBL; AF249701; AAF79159.1; -; Genomic DNA.
FT NON_TER 1 1
FT NON_TER 19 19
SQ SEQUENCE 19 AA; 1995 MW; 5BDD964EDB7CED73 CRC64;

Query Match 21.9%; Score 23; DB 2; Length 19;
Best Local Similarity 36.4%; Pred. No. 2.7e+04;
Matches 4; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 5 GMSPPGPIVGB 15
DB 8 GIDPTGYCGD 18

RESULT 92
063058_LATCL PRELIMINARY; PRT; 19 AA.
ID 063058;
AC 063058;
DT 01-AUG-1998 (TEMBLrel. 07, Created)
DT 01-AUG-1998 (TEMBLrel. 07, Last sequence update)
DT 01-JUN-2003 (TEMBLrel. 24, Last annotation update)
DE Ribosomal protein S11 (Fragment).
GN Name=rps11;
OS Lathraea clandestina (Purple toothwort).
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC asterids; Lamiales; Lamiaceae; Orobanchaceae;
OC Orobanchaceae incertae sedis; Lathraea.
OX NCBI_TaxID=41911;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Luson N., Delavault P., Thalonarn P.,

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RT "The rbcL gene from *Lathraea* (holoparasitic) is not transcribed by a  
 RT plasmid-encoded RNA polymerase."  
 RT Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: Belongs to the ribosomal protein S11P family.  
 DR EMBL: AF039983; AAC16521.1; -; Genomic\_DNA.  
 DR GO: GO:0005907; C:chloroplast; IEA.  
 DR GO: GO:0005840; C:ribosome; IEA.  
 DR GO: GO:0003735; F:structural constituent of ribosome; IEA.  
 DR GO: GO:0006412; F:protein biosynthesis; IEA.  
 DR InterPro: IPR01971; Ribosomal\_S11.  
 DR Pfam: PF00411; Ribosomal\_S11; I.  
 DR ProDom: PD001010; Ribosomal\_S11; 1.  
 KW Chloroplast; Ribonucleoprotein; Ribosomal protein.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 19 AA; 2245 MW; 130D2AB3FE680B24 CRC64;  
 Query Match 21.9%; Score 23; DB 2; Length 19;  
 Best Local Similarity 50.0%; Pred. No. 2.7e+04;  
 Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 QY 2 PAKGMSPP 9  
 Db 7 PANGCRPP 14  
 RESULT 93  
 Q9R5C8\_PSEAE PRELIMINARY; PRT; 19 AA.  
 AC Q9R5C8;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)  
 DE Quinoprotein ethanol dehydrogenase (Fragment).  
 OS Pseudomonas aeruginosa.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
 OC Pseudomonadaceae; Pseudomonas.  
 OX NCBI\_TaxId=287;  
 RN [1]  
 RP PROTEIN SEQUENCE.  
 RX MEDLINE=93176105; PubMed=8382472;  
 RA Schover J.M., Frank J., van Wietlink J.E., Duine J.A.;  
 RT "Quaternary structure of quinoprotein ethanol dehydrogenase from  
 RT Pseudomonas aeruginosa and its reoxidation with a novel cytochrome c  
 RT from this organism."  
 RL Biochem. J. 290:123-127(1993).  
 DR PIR: S29766; S29766  
 SQ SEQUENCE 19 AA; 1896 MW; F58A0AB5EA077835 CRC64;  
 Query Match 21.9%; Score 23; DB 2; Length 19;  
 Best Local Similarity 57.1%; Pred. No. 2.7e+04;  
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 QY 4 KGMSPPG 10  
 Db 12 KGLEPPG 18  
 RESULT 94  
 Q9JK02\_MOUSE PRELIMINARY; PRT; 19 AA.  
 AC Q9JK02;  
 DT 01-OCT-2000 (TREMBLrel. 15, Created)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
 DE Fructose-1,6-bisphosphatase (EC 3.1.3.11) (Fragment).  
 GN Name=FBP2; Synonym=FBPase 2;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Murinae; Mus.  
 OX NCBI\_TaxId=10090;  
 RN [1]  
 SQ NUCLEOTIDE SEQUENCE.

RC TISSUE=Skeletal muscle;  
 RX MEDLINE=20237676; PubMed=10773464; DOI=10.1016/S0378-1119(00)00079-2;  
 RA Tilmann H., Stein S., Liehr T., Bschirich K.;  
 RT "Structure and chromosomal localization of the human and mouse muscle  
 RT fructose-1,6-bisphosphatase genes."  
 RL Gene 247:241-253(2000).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Skeletal muscle;  
 RA Stein S.;  
 RT "Mouse liver fructose-1,6-bisphosphatase: Gene structure,  
 RT transcriptional start point, chromosomal localization, cDNA cloning,  
 RT characterization of the recombinant protein, and analysis of tissue-  
 RT specific expression."  
 RL Arch. Biochem. Biophys. 0:0-0(0).  
 DR EMBL: AJ243027; CAB90674.1; -; Genomic\_DNA.  
 DR HSP; P06366; INTY.  
 DR MG1; MG1:95491; FBP2.  
 DR GO: GO:0042132; F:fructose-bisphosphatase activity; IEA.  
 DR GO: GO:0016787; F:hydrolase activity; IEA.  
 DR GO: GO:0042578; F:phosphoric ester hydrolase activity; IEA.  
 DR GO: GO:0005975; P:carbohydrate metabolism; IEA.  
 DR InterPro: IPR00146; In\_FB\_phphtase.  
 DR Pfam: PF00316; FBPase; I.  
 DR ProDom: PD001491; In\_FB\_phphtase; 1.  
 KW Carbohydrate metabolism; Hydrolase.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 19 AA; 2084 MW; AD2C153F5A375C18 CRC64;  
 Query Match 21.9%; Score 23; DB 2; Length 19;  
 Best Local Similarity 55.6%; Pred. No. 2.7e+04;  
 Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 QY 2 PAKGMSPP 10  
 Db 10 PANGKSPNG 18  
 RESULT 95  
 PSAF\_MAIZE STANDARD; PRT; 20 AA.  
 ID PSAF\_MAIZE  
 AC P13193;  
 DT 01-JAN-1990 (Rel. 13, Created)  
 DT 01-JAN-1990 (Rel. 13, Last sequence update)  
 DT 05-JUN-2004 (Rel. 44, Last annotation update)  
 DE Photosystem I reaction centre subunit III (Light-harvesting complex I  
 DE 17 kDa protein) (PSI-F) (Fragment).  
 GN Name=PSAF;  
 OS Zea mays (Maize).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC PACCAD clade; Panicoideae; Andropogoneae; Zea.  
 OX NCBI\_TaxId=4577;  
 RN [1]  
 RP PROTEIN SEQUENCE.  
 RC STRAIN=cv. N273;  
 RX MEDLINE=90033290; PubMed=2680596; DOI=10.1016/0014-5793(89)81737-5;  
 RA Anandan S., Vainstein A., Thorner J.P.;  
 RT "Correlation of some published amino acid sequences for photosystem I  
 RT polypeptides to a 17 kDa LHCI pigment-protein and to subunits III and  
 RT IV of the core complex."  
 RL FEBS Lett. 256:150-154(1989).  
 CC -1- FUNCTION: Probably participates in efficiency of electron transfer  
 CC from plastocyanin to P700 (or cytochrome c553 in algae and  
 CC cyanobacteria). This plastocyanin-docking protein contributes to  
 CC the specific association of plastocyanin to PSI.  
 CC -1- SUBCELLULAR LOCATION: Associated with luminal side of the  
 CC thylakoid membrane.  
 CC -1- SIMILARITY: Belongs to the psaf family.  
 CC -----  
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 CC removed.

DR PIR, S06150, S06150.  
 DR Gramene, P11193, -.  
 KW Chloplast, Direct protein sequencing; Membrane; Photosynthesis;  
 KW Photosystem I; Thylakoid.  
 FT NON\_TER 20  
 SQ SEQUENCE 20 AA; 2112 MW; F0499F98F6188997 CRC64;

Query Match  
 Best Local Similarity 60.0%; Score 23; DB 1; Length 20;  
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 GMSPP 9  
 DB 4 GLRTP 8

## RESULT 96

ID Q8NBD5\_HUMAN PRELIMINARY; PRT; 20 AA.  
 AC Q8NBD5;  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE Hypothetical protein (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;  
 OC Homo.  
 NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Testis;  
 RA Strausberg R.;  
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL, BC031977; AAH31977.1; -, mRNA.  
 KW Hypothetical protein.  
 FT NON\_TER 1  
 SQ SEQUENCE 20 AA; 2235 MW; D4992395E26B6C CRC64;

Query Match  
 Best Local Similarity 57.1%; Score 23; DB 2; Length 20;  
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 10 GFVGE 16  
 DB 14 GWALGE 20

## RESULT 97

ID Q7M264\_LOLPR PRELIMINARY; PRT; 20 AA.  
 AC Q7M264;  
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE 50K allergen (Fragment).  
 OS Lolium perenne (Perennial ryegrass).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;  
 OC Poaceae; Lolium.  
 NCBI\_TaxID=4522;  
 RN [1]  
 RP PROTEIN SEQUENCE.  
 RA MEDLINE=94092339; PubMed=7505588;  
 RA Petersen A., Schramm G., Becker W.M., Schlaak M.;  
 RT "Comparison of four grass pollen species concerning their allergens of  
 RT grass group V by 2D immunoblotting and microsequencing.";  
 RL Biol. Chem. Hoppe-Seyler 374:855-861(1993).

DR PIR, S38288, S38288.  
 FT NON\_TER 1  
 SQ SEQUENCE 20 AA; 1742 MW; 15C8174B4B4D9D8C CRC64;

Query Match  
 Best Local Similarity 57.1%; Score 23; DB 2; Length 20;  
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 PAKGMP 8  
 DB 13 PAAGATP 19

## RESULT 98

ID Q9S8J1\_TRIKI PRELIMINARY; PRT; 20 AA.  
 AC Q9S8J1;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE Intracellular basic DEFENSE-related protein class III chitinase  
 DE homolog (Fragment).  
 OS Trichosanthes kirilowii (Mongolian snake-gourd).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC Eusteroideae; Cucurbitales; Cucurbitaceae; Trichosanthes.  
 NCBI\_TaxID=3677;  
 RN [1]  
 RP PROTEIN SEQUENCE.  
 RX MEDLINE=95125116; PubMed=7824645; DOI=10.1104/pp.106.3.1195;  
 RA Savary B.J., Flores R.E.;  
 RT "Biosynthesis of defense-related proteins in transformed root cultures  
 RT of Trichosanthes kirilowii Maxim. var japonicum (Kittam.).";  
 RL Plant Physiol. 106:1195-1204(1994).  
 SQ SEQUENCE 20 AA; 2025 MW; 3B45284BBA44BB62 CRC64;

Query Match  
 Best Local Similarity 71.4%; Score 23; DB 2; Length 20;  
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 14 GREGVLS 20  
 DB 12 GNEGSLUS 18

## RESULT 99

ID Q9S8Y0\_PHLPR PRELIMINARY; PRT; 20 AA.  
 AC Q9S8Y0;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)  
 DE Allergen PHL p V (Fragment).  
 OS Phleum pratense (Common timothy).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;  
 OC Aveneae; Phleum.  
 NCBI\_TaxID=15957;  
 RN [1]  
 RP PROTEIN SEQUENCE.  
 RX MEDLINE=92353723; PubMed=1643437;  
 RA Petersen A., Becker W.M., Schlaak M.;  
 RT "Characterization of isoforms of the major allergen Phl p V by two-  
 RT dimensional immunoblotting and microsequencing.";  
 RL Int. Arch. Allergy Immunol. 98:105-109(1992).

Query Match  
 Best Local Similarity 57.1%; Score 23; DB 2; Length 20;  
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 PAKGMP 8



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 20, 2006, 18:54:14 ; Search time 45.3462 Seconds  
(without alignments)  
116.273 Million cell updates/sec

Title: US-09-662-293-5

Perfect score: 67  
Sequence: 1 DEKNSPECTLGP 12

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 244163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 880474

Minimum DB seq length: 0  
Maximum DB seq length: 20

Post-processing: Minimum Match 0%  
Listing first 100 summaries

Database :

1: A\_Geneseq\_21:\*  
2: geneseq19808:\*  
3: geneseq19908:\*  
4: geneseq20008:\*  
5: geneseq20018:\*  
6: geneseq20028:\*  
7: geneseq20038:\*  
8: geneseq20048:\*  
9: geneseq20058:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	67	100.0	12	3	AAV52514 House dms
2	67	100.0	12	5	AAU96318 Der HMW-m
3	64	50.7	20	2	AAV26547 Erythro
4	33	49.3	18	5	ABG66059 IGE Fcpep
5	32	47.8	13	7	ADCA2730 Peptide w
6	32	47.8	13	9	ADZ37865 Human kin
7	32	47.8	19	2	AAV26489 Erythro
8	31	46.3	20	6	ABP83269 G protein
9	30	44.8	18	5	ABV15265 IGF relat
10	30	44.8	19	2	AAV01776 Active fr
11	30	44.8	19	7	ADD29130 MTN-13/I
12	30	44.8	19	7	ADK40569 KDR & VRG
13	30	44.8	19	8	ADR40787 Cyclic KD
14	30	44.8	20	2	AAV26357 Erythro
15	30	44.8	20	2	AAV13684 Erythro
16	30	44.8	20	2	AAW26998 Monomer s
17	30	44.8	20	4	AAU05347 R1 and R2
18	29	43.3	10	4	AAAG8114 Seccharom
19	29	43.3	10	4	AAAG8115 Seccharom
20	29	43.3	10	8	ADT40845 NSARS vitr
21	29	43.3	10	8	ADSB0262 SARS vitr
22	29	43.3	10	8	ADT38375 hSARS vitr
23	29	43.3	15	5	ABW77729 N-termina
24	29	43.3	17	9	ADU91959 BRO-R ago

25	29	43.3	17	9	ADU91965 EPO-R ago
26	29	43.3	17	9	ADU92009 EPO-R ago
27	29	43.3	19	2	AAV26490 Erythro
28	29	43.3	19	8	ADBS3404 CMET-HGF
29	29	43.3	20	2	AAV13694 Erythro
30	29	43.3	20	2	AAV13720 Erythro
31	29	43.3	20	2	AAV13685 Erythro
32	29	43.3	20	2	AAV26375 Erythro
33	29	43.3	20	2	AAV26374 Erythro
34	29	43.3	20	2	AAW27034 Monomer s
35	29	43.3	20	2	AAW27008 Monomer s
36	29	43.3	20	4	AAU05356 R1 and R2
37	29	43.3	20	4	AAU05348 R1 and R2
38	29	43.3	20	4	AAU05381 R1 and R2
39	29	43.3	9	5	ABW83243 Human ETV
40	28	41.8	9	5	ABW83232 Wild-type
41	28	41.8	9	7	ADCS9364 GST bindl
42	28	41.8	9	8	ADG20335 Antigenic
43	28	41.8	9	9	ADK08674 HLA class
44	28	41.8	10	2	AAW98996 I domain
45	28	41.8	13	6	ABR91275 P. papata
46	28	41.8	14	5	ABJ00601 B lymphoc
47	28	41.8	14	5	ABG33462 B lymphoc
48	28	41.8	14	5	ADB48057 Novel hum
49	28	41.8	14	8	ADJ55612 Novel hum
50	28	41.8	15	2	AAW98993 638 Inter
51	28	41.8	15	2	AAW3075 B. t. PS63
52	28	41.8	15	2	AAW13880 N-termina
53	28	41.8	15	2	AAW73115 B. t. tox1
54	28	41.8	15	3	AAV13902 Internal
55	28	41.8	15	5	AAV10365 Bacillus
56	28	41.8	15	6	ABR30097 Human can
57	28	41.8	15	6	ABR30031 Human can
58	28	41.8	15	6	ABR30127 Human can
59	28	41.8	15	6	ABR30078 Human can
60	28	41.8	15	6	ABR329975 Human can
61	28	41.8	15	6	ABR30106 Human can
62	28	41.8	15	6	ABR30059 Human can
63	28	41.8	15	6	ABR91283 P. papata
64	28	41.8	15	6	ABR91282 P. papata
65	28	41.8	15	6	ADK08687 HLA class
66	28	41.8	16	2	AAW81961 Rat ENDO-
67	28	41.8	16	2	ABR91286 P. papata
68	28	41.8	17	6	ABR91288 P. papata
69	28	41.8	17	9	ADU92006 EPO-R ago
70	28	41.8	18	2	AAV26517 Erythro
71	28	41.8	18	2	AAW67525 IGF-1/IGF
72	28	41.8	18	2	AAW67523 IGF-1/IGF
73	28	41.8	18	2	ABR38888 Peptide #
74	28	41.8	18	4	AAW2107 Human bon
75	28	41.8	18	4	AAW2107 Human bon
76	28	41.8	18	4	AAW2107 Human bon
77	28	41.8	18	4	AAW2107 Human bon
78	28	41.8	18	4	AAW2107 Human bon
79	28	41.8	18	4	AAW2107 Human bon
80	28	41.8	18	4	AAW2107 Human bon
81	28	41.8	18	4	AAW2107 Human bon
82	28	41.8	18	4	AAW2107 Human bon
83	28	41.8	18	4	AAW2107 Human bon
84	28	41.8	18	4	AAW2107 Human bon
85	28	41.8	18	4	AAW2107 Human bon
86	28	41.8	18	4	AAW2107 Human bon
87	28	41.8	18	4	AAW2107 Human bon
88	28	41.8	18	4	AAW2107 Human bon
89	28	41.8	18	4	AAW2107 Human bon
90	28	41.8	18	4	AAW2107 Human bon
91	28	41.8	18	4	AAW2107 Human bon
92	28	41.8	18	4	AAW2107 Human bon
93	28	41.8	18	4	AAW2107 Human bon
94	28	41.8	18	4	AAW2107 Human bon
95	28	41.8	18	4	AAW2107 Human bon
96	28	41.8	18	4	AAW2107 Human bon
97	28	41.8	18	4	AAW2107 Human bon



XX Erythropoietin; EPO; receptor; EPO deficiency; renal failure; AIDS;  
 KW dialysis; anaemia; autoimmune disease; chronic inflammatory disease;  
 KW malignancy; beta-thalassemia; cystic fibrosis; prematurity; blood loss;  
 KW spinal cord injury; aging; neoplastic disease; erythropoiesis; EPO-R.  
 XX Synthetic.  
 OS  
 PN WO640749-A1.  
 PD 19-DEC-1996.  
 XX  
 PF 07-JUN-1996; 96WO-US009910.  
 XX  
 PR 07-JUN-1995; 95US-00484631.  
 PR 07-JUN-1995; 95US-00484635.  
 XX  
 PA (JOHN ) JOHNSON & JOHNSON CORP.  
 PA (AFY-) AFYMAX TECHNOLOGIES NV.  
 XX  
 PI W-1ghton NC, Dower WJ, Chang RS, Kaehny AK, Jolliffe LK;  
 PI Johnson D, Mulcahy L;  
 XX  
 DR WPI, 1997-052225/05.  
 XX  
 PT Erythropoietin receptor binding peptide - useful for treating disorders  
 PT characterised by deficiency of EPO, or low or defective red blood cell  
 PT population.  
 XX  
 PS Disclosure; Page 26, 95pp; English.  
 XX  
 CC The invention describes a peptide of 10-40 amino acid residues which  
 CC binds to erythropoietin (EPO) receptor and which includes the amino acid  
 CC sequence Cys-Xaa1-Xaa2-Gly-Pro-Xaa3-Trp-Xaa4-Cys, where Xaa1 = Arg,  
 CC His, Leu or Trp, Xaa2 = Met, Phe or Ile, Xaa3 = 1 of the 20 genetically  
 CC coded L-amino acids, and Xaa4 = Asp, Glu, Ile, Leu or Val. Optionally,  
 CC the peptide may be cyclised or dimerised. The peptide can be used to  
 CC treat a patient having a disorder characterised by a deficiency of EPO or  
 CC a low or defective red blood cell population. It can be used to treat end  
 CC stage renal failure or dialysis; anaemia associated with AIDS; autoimmune  
 CC disease, chronic inflammatory diseases or malignancy; beta-thalassemia;  
 CC cystic fibrosis; early anaemia of prematurity; spinal cord injury; acute  
 CC blood loss; aging; and neoplastic disease states accompanied by abnormal  
 CC erythropoiesis. The peptide can also be used as reagents for detecting  
 CC EPO receptors on living cells, in biological fluids, in tissue  
 CC homogenates, etc. Sequences AY6352-548 are representative peptides  
 CC falling within the above peptide motif and isolated during the affinity  
 CC selection process  
 CC  
 CC Sequence 20 AA;  
 SO  
 Query Match 50.7%; Score 34; DB 2; Length 20;  
 Best Local Similarity 50.0%; Pred. No. 95;  
 Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
 Oy 3 KNSPECTLGP 12  
 Db 2 KNNYRCQFGR 11  
 DB  
 RESULT 4  
 ABG66059  
 ID ABG66059 standard; peptide; 18 AA.  
 XX  
 AC ABG66059;  
 XX  
 DT 29-AUG-2002 (first entry)  
 XX  
 DB IGB Receptor RI binding peptide from phage displayed g8 library #9.  
 XX  
 KW IGB receptor; immunoglobulin; ReceptorRI; antagonist; phage display;  
 KW protein co-ordinate data; IGB-mediated disease; allergic rhinitis;  
 KW asthma; allergic asthma; atopic dermatitis; urticaria-angioedema;

KW parasitic infection; IGB myeloma; immune-related disorder;  
 KW inflammatory disorder; diabetes mellitus; reperfusion injury; stroke;  
 KW IGB-mediated gastrointestinal inflammatory disease; burn;  
 KW immune rejection of graft; myocardial infarction; atherosclerosis;  
 KW acute lung injury; haemorrhagic shock; septic shock;  
 KW acute tubular necrosis; endometriosis; degenerative joint disease;  
 KW pancreatitis.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200226781-A2.  
 PD 04-APR-2002.  
 XX  
 PF 26-SEP-2001; 2001WO-US030289.  
 XX  
 PR 26-SEP-2000; 2000US-0235353P.  
 PR 23-MAR-2001; 2001US-0278540P.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Lowman HB, Reynolds ME, Nakamura GR, Starovannik MA;  
 PI WPI, 2002-444016/47.  
 XX  
 DR  
 XX  
 PT A peptide useful for treating a IGB-mediated disease or disorder in a  
 PT host e.g. allergic rhinitis, asthma, which competes with immunoglobulin B  
 PT for binding to high affinity IGB receptor in an in vitro assay.  
 XX  
 PS Example 1; Page 79, 328pp; English.  
 XX  
 CC The invention relates to a peptide which competes with immunoglobulin  
 CC (Ig) B 134 comprising a sequence (S1), for binding the high affinity IGB  
 CC receptor (RepsilonRI) in an in vitro assay and having a formula given in  
 CC the specification. Also included are a fusion protein comprising the  
 CC peptide, a pharmaceutical composition (C) comprising the peptide,  
 CC designing a compound that mimics the three-dimensional surface structure  
 CC of the peptide, a compound with a solvent accessible surface that mimics  
 CC the solvent accessible surface defined by the side chains of residues (R)  
 CC Pro4, Phe6, Pro16, Cys3, Cys7, Cys15 and Cys19 of IGB134, a peptide with  
 CC structural coordinates as given in the specification, selecting a peptide  
 CC mimetic which binds to RepsilonRI and blocks binding of IGB and a  
 CC peptide mimetic which mimics the coordinates of IGB134 residues (R). (C)  
 CC is useful for inhibiting the binding of IGB to high affinity IGB receptor  
 CC (RepsilonRI). Peptides of the formula given in the specification are  
 CC useful for inhibiting the binding of an IGB to high affinity IGB  
 CC receptor. The peptide is useful for selecting a molecule which blocks the  
 CC interaction of IGB with high affinity IGB receptor. The peptide is also  
 CC useful for inhibiting the activation of high affinity IGB receptor. The  
 CC peptide is useful for treating an IGB-mediated disease or disorder in a  
 CC host. (C) is useful in research, diagnostic, therapeutic and prophylactic  
 CC methods. The peptide is also useful for inhibiting IGB-mediated or  
 CC associated processes such as IGB-dependent activation and degranulation  
 CC of mast cells and basophils, as well as consequent release of  
 CC inflammatory mediators such as histamine. (C) is useful for treating  
 CC allergic rhinitis, asthma (e.g. allergic asthma), atopic dermatitis,  
 CC urticaria-angioedema, parasitic infection, IGB myeloma, immune-related  
 CC disorders, inflammatory disorders, diabetes mellitus, IGB-mediated  
 CC gastrointestinal inflammatory disease, immune rejection of grafts,  
 CC reperfusion injury, stroke, myocardial infarction, atherosclerosis, acute  
 CC lung injury, haemorrhagic shock, burn, septic shock, acute tubular  
 CC necrosis, endometriosis, degenerative joint disease and pancreatitis. The  
 CC present sequence is a peptide of the invention expressed from a phage  
 CC display library  
 CC  
 CC Sequence 18 AA;  
 SO  
 Query Match 49.3%; Score 33; DB 5; Length 18;  
 Best Local Similarity 55.6%; Pred. No. 1.3e+02;  
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
 Oy 4 NSPECTLGP 12  
 Db 1  
 DB

Db 1 NYECCWGP 9

RESULT 5  
ADC42730  
ID ADC42730 standard; peptide; 13 AA.

XX  
XX  
AC ADC42730;  
XX  
XX  
DT 18-DEC-2003 (first entry)  
XX  
DE Peptide with potential MHC classII binding activity #45.  
XX  
KW human factor IX; FIX; human.  
XX  
OS Homo sapiens.  
XX  
XX WO2003020764-A2.  
XX  
XX 13-MAR-2003.  
XX  
XX  
XX 30-AUG-2002; 2002WO-EP009717.  
XX  
XX 04-SEP-2001; 2001EP-00121154.  
XX  
XX (MERB ) MERCK PATENT GMBH.  
XX  
XX Carr FU, Carter G;  
XX  
XX WPI; 2003-300864/29.  
XX  
XX  
XX Novel modified human factor IX molecule for therapeutic use, is  
XX substantially non-immunogenic or less immunogenic than any non-modified  
XX molecule having the same biological activity when used in vivo.  
XX  
XX Disclosure; SEQ ID NO 16; 49pp; English.  
XX  
XX  
XX The invention relates to a modified molecule having the biological  
XX activity of human factor IX (FIX) and being substantially non-immunogenic  
XX or less immunogenic than any non-modified molecule having the same  
XX biological activity when used in vivo. The present sequence represents a  
XX peptide from FIX with potential MHC class II binding activity.  
XX  
XX Sequence 13 AA;

Query Match 47.8%; Score 32; DB 7; Length 13;  
Best Local Similarity 62.5%; Pred. No. 1.4e+02;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 DEKNSPEC 8  
|:|:|:|:  
1 DDINSPEC 8

Db 1 DDINSPEC 8

RESULT 6  
ADZ37865  
ID ADZ37865 standard; peptide; 13 AA.

XX  
XX  
AC ADZ37865;  
XX  
XX  
XX 30-JUN-2005 (first entry)  
XX  
DE Human kinase substrate peptide SEQ ID 795.  
XX  
XX  
XX Kinase; substrate; drug delivery; cancer; restenosis; osteoporosis;  
XX Rheumatoid arthritis; asthma; psoriasis; inflammatory bowel disease;  
XX systemic lupus erythematosus; multiple sclerosis; transplant rejection;  
XX neoplasm; cytostatic; vasotropic; cardiovascular disease; osteopathic;  
XX degeneration; endocrine disease; musculoskeletal disease;  
XX antiinflammatory; inflammation; autoimmune disease; immunosuppressive;  
XX immune disorder; antiarthritic; antirheumatic; antiasthmatic;  
XX respiratory disease; antipsoriatic; dermatological disease;  
KW gastrointestinal-gen.; gastrointestinal disease; neuroprotective;

KW neurological disease; dermatological; dermatological disease.  
XX  
XX Homo sapiens.  
OS  
XX WO2005035003-A2.  
XX  
XX 21-APR-2005.  
XX  
XX 22-SEP-2004; 2004WO-US031148.  
XX  
XX 22-SEP-2003; 2003US-0505325P.  
XX  
XX 04-MAY-2004; 2004US-0568340P.  
XX  
XX 22-JUN-2004; 2004US-0581835P.  
XX  
XX (DIHR-) DIHEDRON CORP.  
XX  
XX Ballatore C, Gaetellino AJ, Desharnais J, Guo Z, Li Q, Newman MJ,  
XX Sun C;  
XX WPI; 2005-315493/32.  
XX  
XX  
XX New conjugate used for treating aberrant cellular activation, migration,  
XX proliferation or survival condition such as cancer, comprises drug and  
XX substrate for protein or lipid kinase linked to protein, optionally by  
XX non-releasable linker.  
XX  
XX Disclosure; SEQ ID NO 795; 407pp; English.

XX The invention relates to a conjugate (I) comprising a drug and a  
XX substrate for a protein kinase or a lipid kinase non-releasably linked to  
XX it, optionally by a non-releasable linker. Also included are preparing  
XX pacitaxel C10 carbamate of formula (8a) (which comprises reacting a  
XX pacitaxel compound of formula (5a) with a carbodiimide compound and  
XX reacting the obtained compound of formula (6a) with an amine of formula  
XX X, all formulae given in the specification), a pharmaceutical composition  
XX (PCI) comprising (I) and a carrier, an article (comprising packaging  
XX material, (I) or its derivatives, for treatment/prevention/amelioration  
XX of one or more symptoms (associated with aberrant cellular activation,  
XX migration, proliferation or survival (ACMPs) and a label that indicates  
XX that (I) is used for treatment, prevention or amelioration of one or more  
XX symptoms associated with ACMPs), and a peptide comprising an kinase  
XX substrate peptide. The conjugate has improved cytotoxic selectivity index  
XX as compared to an unconjugated drug. The conjugate is useful for treating  
XX conditions caused by ACMPs characterized by undesirable or aberrant  
XX activation, migration, proliferation or survival of tumor cells,  
XX endothelial cells, B cells, T cells, macrophages, neutrophils,  
XX eosinophils, basophils, monocytes, platelets, fibroblasts, other  
XX connective tissue cells, osteoblasts, osteoclasts and progenitors of  
XX these cell types. The ACMPs condition is a cancer, coronary restenosis,  
XX osteoporosis, chronic inflammation or autoimmune disease. The  
XX autoimmune disease is rheumatoid arthritis, asthma, psoriasis,  
XX inflammatory bowel disease, systemic lupus erythematosus, systemic  
XX dermatomyositis, inflammatory ophthalmic diseases, autoimmune hematologic  
XX disorders, multiple sclerosis, vasculitis, idiopathic nephrotic syndrome,  
XX transplant rejection or graft versus host disease. The cancer is non-  
XX small cell lung cancer, head squamous cancer, neck squamous cancer,  
XX colorectal cancer, prostate cancer, breast cancer, acute lymphocytic  
XX leukemia, adult acute myeloid leukemia, adult non-Hodgkin's lymphoma,  
XX brain tumor, cervical cancer, childhood cancer, childhood sarcoma,  
XX chronic lymphocytic leukemia, chronic myeloid leukemia, esophagial  
XX cancer, hairy cell leukemia, kidney cancer, liver cancer, multiple  
XX myeloma, neuroblastoma, oral cancer, pancreatic cancer, primary central  
XX nervous system lymphoma, skin cancer or small-cell lung cancer. The  
XX cancer is brain stem glioma, cerebellar astrocytoma, cerebral  
XX astrocytoma, ependymoma, Ewing's sarcoma, germ cell tumor, Hodgkin's  
XX disease, acute myelogenous leukemia, acute lymphoblastic leukemia, liver  
XX cancer, medulloblastoma, neuroblastoma, non-Hodgkin's lymphoma,  
XX osteosarcoma, malignant fibrous histiocytoma of bone, retinoblastoma,  
XX rhabdomyosarcoma, soft tissue sarcoma, supratentorial primitive  
XX neuroectodermal and pineal tumors, visual pathway and hypothalamic  
XX glioma, Wilms' tumor or other childhood kidney tumor. The cancer is  
XX originated from or has metastasized to the bone, brain, breast, digestive  
XX and gastrointestinal system, endocrine system, blood, lung, respiratory



CC system, thorax, musculoskeletal system, or skin. The cancer is selected  
CC from breast cancer, lung cancer, prostate cancer, ovarian cancer,  
CC esophageal cancer, bladder cancer, hepatoma, neuroblastoma, lymphoma,  
CC testicular cancer, renal cancer, leukemia, colorectal cancer and head and  
CC neck cancer. The conjugate is useful for identifying kinase substrates  
CC capable of selectively accumulating in a target system. The conjugate is  
CC useful for identifying conjugates capable of exhibiting selective  
CC toxicity against a target system. The conjugate is useful for enhancing  
CC drug efficiency. The present sequence is kinase substrate peptide useful  
CC in the conjugate of the invention.

XX SQ Sequence 13 AA;

Query Match 47.8%; Score 32; DB 9; Length 13;  
Best Local Similarity 62.5%; Pred. No. 1.4e+02;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 DENKSPFC 8  
| : | : | : |  
Db 4 DDINSYEC 11

RESULT 7  
AAV26489  
ID AAV26489 standard; peptide; 19 AA.  
AC AAV26489;  
XX  
XX 06-SBP-1999 (first entry)  
DT  
XX  
XX Erythropoietin receptor (EPO-R) binding peptide.  
DE  
XX  
XX Erythropoietin receptor (EPO-R) binding peptide.  
KW  
XX Erythropoietin; EPO; receptor; EPO deficiency; renal failure; AIDS;  
KW dialysis; anaemia; autoimmune disease; chronic inflammatory disease;  
KW malignancy; beta-thalassemia; cystic fibrosis; prematurity; blood loss;  
KW spinal cord injury; aging; neoplastic disease; erythropoiesis; EPO-R.  
XX  
XX Synthetic.  
OS  
XX  
XX WO9640749-A1.  
PN  
XX  
XX 19-DEC-1996.  
PD  
XX  
XX 07-JUN-1996; 96WO-US009810.  
PF  
XX  
XX 07-JUN-1995; 95US-00484631.  
PR  
XX 07-JUN-1995; 95US-00484635.  
XX  
XX (JOHN J. JOHNSON & JOHNSON CORP.  
XX (AFRY-) AFRYMAX TECHNOLOGIES NV.  
XX  
XX Wrighton NC, Dower WJ, Chang RS, Kaahya AK, Joliffe LK;  
XX Johnson D, Mulcahy L;  
XX  
XX WPI; 1997-052225/05.  
DR  
XX  
XX Erythropoietin receptor binding peptide - useful for treating disorders  
PT characterized by deficiency of EPO, or low or defective red blood cell  
PT population.  
XX  
XX  
XX Disclosure; Page 23; 95pp; English.

CC The invention describes a peptide of 10-40 amino acid residues which  
CC binds to erythropoietin (EPO) receptor and which includes the amino acid  
CC sequence Cys-Xaa1-Xaa2-Gly-Pro-Xaa3-Thr-Tyr-Xaa4-Cys, where Xaa1 = Arg,  
CC His, Leu or Tyr, Xaa2 = Met, Phe or Ile, Xaa3 = 1 of the 20 genetically  
CC coded L-amino acids, and Xaa4 = Asp, Glu, Ile, Leu or Val. Optionally,  
CC the peptide may be cyclized or dimerized. The peptide can be used to  
CC treat a patient having a disorder characterized by a deficiency of EPO or  
CC a low or defective red blood cell population. It can be used to treat and  
CC stage renal failure or dialysis; anaemia associated with AIDS, autoimmune  
CC disease, chronic inflammatory diseases or malignancy; beta-thalassemia;  
CC cystic fibrosis; early anaemia of prematurity; spinal cord injury; acute

CC blood loss; aging; and neoplastic disease states accompanied by abnormal  
CC erythropoiesis. The peptides can also be used as reagents for detecting  
CC EPO receptors on living cells, in biological fluids, in tissue  
CC homogenates, etc. Sequences AAV2632-548 are representative peptides  
CC falling within the above peptide motif and isolated during the affinity  
CC selection process  
XX

XX SQ Sequence 19 AA;

Query Match 47.8%; Score 32; DB 2; Length 19;  
Best Local Similarity 40.0%; Pred. No. 2e+02;  
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 KNSFCLGP 12  
| : | : | : |  
Db 2 KTKYKCYMGP 11

RESULT 8  
ABP83269  
ID ABP83269 standard; peptide; 20 AA.  
XX  
XX  
XX ABP83269;  
XX  
XX  
XX 04-MAR-2003 (first entry)  
DT  
XX  
XX  
XX G protein-coupled receptor (GPCR) antigenic peptide SEQ ID NO:1942.  
DE  
XX  
XX  
XX G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;  
KW G protein-coupled receptor modulator; antibody; immune-related disease;  
KW growth-related disease; cell regeneration-related disease; AIDS; cancer;  
KW immunological-related cell proliferative disease; autoimmune disease;  
KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;  
KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;  
KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;  
KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;  
KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;  
KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;  
KW ulcer.  
XX  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO200261087-A2.  
PN  
XX  
XX 08-AUG-2002.  
PD  
XX  
XX 19-DEC-2001; 2001WO-US050107.  
PF  
XX  
XX 19-DEC-2000; 2000US-0257144P.  
PR  
XX  
XX (LIFE-) LIFESPAN BIOSCIENCES INC.  
XX  
XX (LIFE-) LIFESPAN BIOSCIENCES INC.  
XX  
XX Burner GC, Roush CL, Brown JP;  
XX  
XX  
XX WPI; 2003-046718/04.  
DR  
XX  
XX New isolated antigenic peptides e.g., for G protein-coupled receptors  
PT (GPCR), useful for diagnosing and designing drugs for treating conditions  
PT in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or  
PT autoimmune diseases.  
XX  
XX  
XX Claim 1; Fig 2; 523pp; English.

CC The present invention describes antigenic peptides (1) comprising: (a)  
CC any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino  
CC acids. Also described: (1) an assay for the detection of a particular G  
CC protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;  
CC and (2) an isolated antibody having high specificity and high affinity or  
CC avidity for a particular GPCR. (1) can be used as GPCR modulators and in  
CC gene therapy. The antigenic peptides for GPCRs are useful in detecting an  
CC antibody against a particular GPCR, and in the production of specific  
CC antibodies. The peptides and antibodies are also useful for detecting the  
CC presence or absence of corresponding GPCRs. The antigenic peptides for

CC GPCRs and antibodies are useful for diagnosing and designing drugs for  
CC treating immune-related diseases, growth-related diseases, cell  
CC regeneration-related disease, immunological-related cell proliferative  
CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,  
CC atherosclerosis, bacterial, fungal, protozoan or viral infections,  
CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute  
CC inflammation, allergies, Crohn's disease, diabetes, graft versus host  
CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,  
CC anxiety, depression, schizophrenia, dementia, mental retardation, memory  
CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,  
CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or  
CC any other disorder in which GPCRs are involved. The antibodies may be  
CC used in immunoassays and immunodiagnosis. AB242523 to AB242869 encode  
CC GPCR proteins given in ABP81675 to ABP82018, which are used in the  
CC exemplification of the present invention  
XX  
SQ Sequence 20 AA;

Query Match 46.3%; Score 31; DB 6; Length 20;  
Best Local Similarity 62.5%; Pred. No. 3.2e+02;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 DEKMFEC 8  
||||:|  
DB 13 DEKNTKC 20

RESULT 9  
ABJ15265  
ID ABJ15265 standard; peptide; 18 AA.  
XX  
AC ABJ15265;  
XX  
DT 16-JUN-2003 (first entry)  
XX  
DE IGF related native phage peptide SEQ ID No 41.  
XX  
KW Cytostatic; antidiabetic; osteopathic; vasotropic; tranquilizer; IGF-1;  
KW vulnary; antiasmatic; ophthalmological; antagoise; ischemic injury;  
KW insulin-like growth hormone 1; IGF; cancer; diabetic; nephropathy;  
KW diabetic retinopathy; acromegaly; macular degeneration; trauma; asthma;  
KW restenosis.  
XX  
OS Unidentified.  
XX  
PN WO200272780-A2.  
XX  
PD 19-SEP-2002.  
XX  
PF 13-MAR-2002; 2002WO-US007606.  
XX  
PR 14-MAR-2001; 2001US-0275904P.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Deshayes K, Lowman HB, Schaffer ML, Sidhu SS;  
XX  
DR WPI; 2002-732826/79.  
XX  
PT New peptides antagonizing insulin-like growth factor (IGF), useful for  
PT treating disorder such as cancer, diabetic complication exacerbated by  
PT IGF-1, acromegaly, age-related macular degeneration, ischemic injury,  
PT trauma, asthma.  
XX  
PS Example 1; Page 42; 86pp; English.  
XX  
CC The invention relates to novel peptides that can antagonise the  
CC interaction of insulin-like growth hormone 1 (IGF-1). The peptides are  
CC useful for treating disorders such as cancer, diabetic complication  
CC exacerbated by IGF-1, e.g. diabetic retinopathy or nephropathy,  
CC acromegaly, age-related macular degeneration, ischemic injury or trauma.  
CC Other disorders that can be treated by the peptide include restenosis or  
CC asthma. This sequence represents a peptide relating to the IGF antagonist

CC peptides of the invention  
XX  
SQ Sequence 18 AA;

Query Match 44.8%; Score 30; DB 5; Length 18;  
Best Local Similarity 33.3%; Pred. No. 4.4e+02;  
Matches 3; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 4 NSFECILP 12  
:::|::|  
DB 1 DAMDCVGP 9

RESULT 10  
AAJ01776  
ID AAJ01776 standard; peptide; 19 AA.  
XX  
AC AAJ01776;  
XX  
DT 28-JUN-1999 (first entry)  
XX  
DE Active fragment of Brushtail possum ZP-2 protein.  
XX  
KW zona pellucida protein; ZP-2; vaccine; female marsupial; contraceptive;  
KW conception; Brushtail possum; koala; kangaroo; wallaroo; wallaby;  
KW Pademelon.  
XX  
OS Trichosurus vulpecula.  
XX  
PN AU9878554-A.  
XX  
PD 11-FEB-1999.  
XX  
PP 29-JUL-1998; 98AU-00078554.  
XX  
PR 31-JUL-1997; 97AU-00008354.  
XX  
PR 12-FEB-1998; 98AU-00001800.  
XX  
PA (MARS-) MARSUPIAL CRC LTD.  
XX  
PI Mate K, McCartney C, Duckworth J, Bradley M;  
XX  
DR WPI; 1999-229776/20.  
XX  
PT New marsupial zona pellucida (ZP2 and ZP3) polypeptides for use in  
PT contraceptive vaccines.  
XX  
PS Claim 23; Page 40; 43pp; English.  
XX  
CC AAJ01775-81 represent active fragments of the Brushtail possum zona  
CC pellucida protein-2 (ZP-2). The ZP-2 polypeptides or polynucleotides  
CC encoding them are administered as vaccines to female marsupials to raise  
CC an immune response against ZP-2 proteins and prevent conception. The  
CC population of koalas is growing which can cause death of food trees, and  
CC the Brushtail possum is New Zealand's number one vertebrate pest and can  
CC adversely affect the environment, animal health and the economy. Use of  
CC the new polypeptides as contraceptives can help control the population  
CC numbers of these and the Eastern grey and Western grey kangaroos, the Red  
CC kangaroo, the common wallaroo, Bennett's (or red necked) wallaby, the  
CC Tamar wallaby, the Whiptail wallaby, the Swamp wallaby, the Agile  
CC Wallaby and the Pademelon  
XX  
SQ Sequence 19 AA;

Query Match 44.8%; Score 30; DB 2; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4.7e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CILGP 12  
|||||  
DB 11 CILGP 15

RESULT 11  
 ADD29120 standard; peptide; 19 AA.  
 XX  
 AC ADD29120;  
 XX  
 DT 15-JAN-2004 (first entry)  
 XX  
 DE MTN-13/I KDR binding peptide SEQ ID NO:55.  
 DE  
 KM display vector library; binding peptide; modular phage display library;  
 KM recombinatorial phage display library.  
 KM  
 OS Synthetic.  
 OS  
 PN WO2003074678-A2.  
 PN  
 PD 12-SEP-2003.  
 PD  
 XX  
 PF 03-MAR-2003; 2003WO-US006582.  
 PF  
 XX  
 PR 01-MAR-2002; 2002US-0361121P.  
 PR  
 XX  
 PA (DYAX-) DYAX CORP.  
 PA  
 PI Ladner RC;  
 PI  
 DR WPI, 2003-779023/73.  
 DR  
 XX  
 PT New modular recombinatorial display libraries comprising a plurality of  
 PT DNA molecules, useful for isolating binding polypeptides for a target  
 PT molecule.  
 PT  
 XX  
 PS Example 2, SEQ ID NO 55; 53bp, English.  
 PS  
 XX  
 CC The present invention describes a library of display vectors comprising a  
 CC plurality of DNA molecules that comprise a general structure: R1-2-R2,  
 CC where R1 and R2 are independently variable regions; and Z is a constant  
 CC region that includes a cleavage site for a restriction endonuclease. Also  
 CC described: (1) obtaining a binding peptide, comprising: (a) selecting for  
 CC phage in the above library, where a displayed peptide binds to a target  
 CC of interest; (b) obtaining RF DNA for the selected phage; (c) cleaving  
 CC the library RF DNA at the first and second restriction sites; (d) mixing  
 CC the selected RF DNA fragments and the library RF DNA fragments; (e)  
 CC ligating the mixed fragments; (f) introducing the ligated fragments into  
 CC cells, such that phage displaying a new library are produced; and (g)  
 CC selecting and sequencing binding phage from the new library, and so  
 CC obtaining the binding peptide; (2) producing a modular phage display  
 CC library; and (3) producing a recombinatorial phage display library. The  
 CC methods are useful for obtaining a binding peptide, producing a modular  
 CC phage display library, and producing a recombinatorial phage display  
 CC library. The library of display vectors is useful in isolating binding  
 CC polypeptides for a target molecule. The present sequence is used in the  
 CC exemplification of the present invention.  
 CC  
 XX  
 SO Sequence 19 AA;  
 SO  
 Query Match 44.8%; Score 30; DB 7; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 4.7e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 NSPEC 8  
 QY |||||  
 DB 12 NSPEC 16  
 DB  
 RESULT 12  
 ADK40569 standard; peptide; 19 AA.  
 ID ADK40569  
 AC ADK40569;  
 XX  
 XX  
 DT 06-MAY-2004 (first entry)

XX  
 DE KDR & VEGF/KDR complex binding peptide of an MTN13 peptide library ID220.  
 DE  
 XX  
 KM endothelial cell; vascular endothelial growth factor; VEGF;  
 KM receptor tyrosine kinase; VEGF-2; kinase domain region; KDR;  
 KM foetal liver kinase-1; flk-1; VEGF/KDR complex; angiogenesis;  
 KM neoplastic tumour; radiotherapeutic; malaria; HIV; SIV infection;  
 KM simian haemorrhagic fever virus;  
 KM enterohaemorrhagic Escherichia coli infection; protozoacidal; anti-HIV;  
 KM virucidal; antibacterial; cytostatic.  
 KM  
 OS Synthetic.  
 OS  
 PN WO2003074005-A2.  
 PN  
 PD 12-SEP-2003.  
 PD  
 XX  
 PF 03-MAR-2003; 2003WO-US006731.  
 PF  
 XX  
 PR 01-MAR-2002; 2002US-0360851P.  
 PR 15-JAN-2003; 2003US-0440411P.  
 PR  
 XX  
 PA (DYAX-) DYAX CORP.  
 PA (BRAC ) BRACCO INT BV.  
 PA  
 PI Sato AK, Sexton DJ, Ladner RC, Dransfield DT, Swenson RE;  
 PI Marinelli ER, Ramalingam K, Nunn AD, Von Wronski MA, Shrivastava A;  
 PI Pochon S, Bussat P, Arbogast C, Pillal R, Fan H, Linder KE, Song B,  
 PI Nanjappa P;  
 PI  
 DR WPI, 2003-779009/73.  
 DR  
 XX  
 PT New polypeptide that binds to vascular endothelial growth factor receptor  
 PT -2, useful for diagnosis and treatment of e.g. tumors, and its conjugates  
 PT with therapeutic or imaging agents.  
 PT  
 XX  
 PS Claim 79; SEQ ID NO 220; 350bp, English.  
 PS  
 XX  
 CC This invention relates to novel peptides useful for detecting and  
 CC targeting primary receptors on endothelial cells that bind vascular  
 CC endothelial growth factor (VEGF). Specifically, it refers to detecting  
 CC the receptor tyrosine kinase identified as VEGF-2, which is also known as  
 CC kinase domain region (KDR) and foetal liver kinase-1 (flk-1). The present  
 CC invention describes the involvement of the VEGF/KDR complex as important  
 CC in angiogenesis, and that VEGF/KDR complex binding or KDR binding  
 CC polypeptides can be used for imaging neoplastic tumours. Furthermore,  
 CC these compositions are useful for targeting radiotherapeutics to specific  
 CC sites for treating diseases associated with KDR activation, which include  
 CC malaria, HIV, SIV infection, simian haemorrhagic fever virus and  
 CC enterohaemorrhagic Escherichia coli infection. Accordingly, these  
 CC compositions exhibit various activities including protozoacidal, anti-  
 CC HIV, virucidal, antibacterial and cytostatic. This peptide sequence is a  
 CC high affinity binding peptide of KDR and the VEGF/KDR complex, part of  
 CC the MTN13 peptide library of the invention.  
 CC  
 XX  
 SO Sequence 19 AA;  
 SO  
 Query Match 44.8%; Score 30; DB 7; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 4.7e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 NSPEC 8  
 QY |||||  
 DB 12 NSPEC 16  
 DB  
 RESULT 13  
 ADK40787 standard; peptide; 19 AA.  
 ID ADK40787  
 AC ADK40787;  
 XX  
 XX  
 DT 21-OCT-2004 (first entry)

XX Cyclic KDR/ VEGF binding peptide of the secondary MTN13 library Seq 220.  
 XX  
 DE kinase domain region; KDR: vascular endothelial growth factor; VEGF;  
 KM VEGF receptor 2; VEGFR2; foetal liver kinase 1, fllk-1; angiogenesis;  
 KM neoplastic tumour; malaria; HIV infection; SIV infection;  
 KM simian haemorrhagic fever virus infection;  
 KM enterohaemorrhagic Escherichia coli infection; cytotoxic;  
 KM antiangiogenic; antimalarial; anti-HIV; virucidal; antibacterial;  
 KM MTN13 library; cyclic.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Disulfide-bond 4. 16  
 XX  
 PN WO2004065621-A1.  
 XX  
 PD 05-AUG-2004.  
 XX  
 PF 11-SEP-2003; 2003WO-US028787.  
 XX  
 PR 15-JAN-2003; 2003US-0440411P.  
 PR 03-MAR-2003; 2003US-00382082.  
 PR 03-MAR-2003; 2003WO-US006731.  
 XX  
 PA (DYAX-) DYAX CORP.  
 PA (BRAC) BRACCO INT BV.  
 XX  
 PI Sato AK, Sexton DJ, Dransfield DT, Ladhner RC, Arbogast C,  
 PI Busse P, Fan H, Kurana S, Linder KE, Marinelli ER, Nanjappan P,  
 PI Nunn A, Pallal R, Pochon S, Ramalingam K, Shrivastava A, Song B,  
 PI Swenson RE, Von Wronski MA;  
 XX  
 DR MPI, 2004-580734/56.  
 XX  
 PT Novel isolated polypeptide having ability to bind to kinase domain region  
 PT or vascular endothelial growth factor/kinase domain region complex,  
 PT useful in inhibiting vascular endothelial growth factor activation of  
 PT kinase domain region.  
 XX  
 PS Claim 11; SEQ ID NO 220; 470bp; English.  
 XX  
 CC This invention relates to novel isolated peptides that can bind to a  
 CC kinase domain region (KDR) or vascular endothelial growth factor  
 CC (VEGF)/KDR complex. Specifically, it refers to polypeptides, peptide  
 CC dimers and multimeric complexes that bind with high affinity to KDR (also  
 CC known as the VEGF receptor 2 (VEGFR2) and foetal liver kinase 1 (fllk-1))  
 CC or the VEGF/KDR complex, and as such due to the involvement of VEGF and  
 CC KDR in angiogenesis these binding peptides can be used for imaging  
 CC important sites of angiogenesis, as well as in targeting therapeutics to  
 CC such sites. The present invention describes these peptides as useful for  
 CC promoting or inhibiting angiogenesis and pathogenic conditions associated  
 CC therewith such as neoplastic tumours. Furthermore, these binding peptides  
 CC are useful for treating malaria, HIV infection, SIV infection, simian  
 CC haemorrhagic fever virus infection and enterohaemorrhagic Escherichia  
 CC coli infection. Accordingly, they exhibit cytotoxic, antiangiogenic,  
 CC antimalarial, anti-HIV, virucidal and antibacterial activities. In  
 CC particular, they inhibit VEGF activation of its receptor (i.e. KDR), and  
 CC enable efficient detection, imaging and localisation of activated  
 CC endothelial cells exhibiting upregulated KDR expression. This peptide  
 CC sequence is a high affinity KDR and VEGF/KDR cyclic binding peptide  
 CC belonging to the secondary MTN13 library of the invention.  
 CC  
 XX  
 SQ Sequence 19 AA;  
 XX

RESULT 14  
 AAY26357  
 ID AAY26357 standard; peptide, 20 AA.  
 XX  
 AC AAY26357;  
 XX  
 DT 06-SEP-1999 (first entry)  
 XX  
 DE Erythropoietin receptor (EPO-R) binding peptide.  
 XX  
 KM Erythropoietin; EPO; receptor; EPO deficiency; renal failure; AIDS;  
 KM dialysis; anaemia; autoimmune disease; chronic inflammatory disease;  
 KM malignancy; beta-thalassemia; cystic fibrosis; prematurity; blood loss;  
 KM spinal cord injury; aging; neoplastic disease; erythropoiesis; EPO-R.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9640749-A1.  
 XX  
 PD 19-DEC-1996.  
 XX  
 PF 07-JUN-1996; 96WO-US009810.  
 XX  
 PR 07-JUN-1995; 95US-00484631.  
 PR 07-JUN-1995; 95US-00484635.  
 XX  
 PA (JOHJ) JOHNSON & JOHNSON CORP.  
 PA (AFRY-) AFRYMAX TECHNOLOGIES NV.  
 XX  
 PI Wrighton NC, Dower WJ, Chang RS, Kashyap AK, Jolliffe LK;  
 PI Johnson D, Mulcahy L;  
 XX  
 DR MPI, 1997-052225/05.  
 XX  
 PT Erythropoietin receptor binding peptide - useful for treating disorders  
 PT characterised by deficiency of EPO, or low or defective red blood cell  
 PT population.  
 XX  
 PS Disclosure; Page 16; 95pp; English.  
 XX  
 CC The invention describes a peptide of 10-40 amino acid residues which  
 CC binds to erythropoietin (EPO) receptor and which includes the amino acid  
 CC sequence Cys-Xaa1-Xaa2-Gly-Pro-Xaa3-Thr-Tyr-Xaa4-Cys, where Xaa1 = Arg,  
 CC His, Leu or Tyr, Xaa2 = Met, Phe or Ile, Xaa3 = 1 of the 20 genetically  
 CC coded L-amino acids, and Xaa4 = Asp, Glu, Ile, Leu or Val. Optionally,  
 CC the peptide may be cyclised or dimerised. The peptide can be used to  
 CC treat a patient having a disorder characterised by a deficiency of EPO or  
 CC a low or defective red blood cell population. It can be used to treat end  
 CC stage renal failure or dialysis; anaemia associated with AIDS, autoimmune  
 CC disease, chronic inflammatory diseases or malignancy; beta-thalassemia;  
 CC cystic fibrosis; early anaemia of prematurity; spinal cord injury; acute  
 CC blood loss; aging; and neoplastic disease states accompanied by abnormal  
 CC erythropoiesis. The peptides can also be used as reagents for detecting  
 CC EPO receptors on living cells, in biological fluids, in tissue  
 CC homogenates, etc. Sequences AAY26352-548 are representative peptides  
 CC falling within the above peptide motif and isolated during the affinity  
 CC selection process  
 CC  
 XX  
 SQ Sequence 20 AA;  
 XX

Query Match 44.8%; Score 30; DB 8; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 4.7e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 44.8%; Score 30; DB 2; Length 20;  
 Best Local Similarity 42.9%; Pred. No. 4.9e+02;  
 Matches 3; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 4 NSPEC 8  
 DB 12 NSPEC 16

RESULT 15  
 AAY13684

ID AA13684 standard; peptide; 20 AA.  
 AC AA13684;  
 XX  
 DT 06-SEP-1999 (first entry)  
 XX  
 DE Erythropoietin receptor (EPO-R) binding peptide.  
 XX  
 KM Erythropoietin; EPO; receptor; EPO deficiency; renal failure; AIDS;  
 KM dialysis; anaemia; autoimmune disease; chronic inflammatory disease;  
 KM malignancy; beta-thalassemia; cystic fibrosis; prematurity; blood loss;  
 KM spinal cord injury; aging; neoplastic disease; erythropoiesis; EPO-R.  
 XX  
 OS Synthetic.  
 XX  
 PN MO9640749-A1.  
 PD 19-DEC-1996.  
 XX  
 PF 07-JUN-1996; 96MO-US009810.  
 XX  
 PR 07-JUN-1995; 95US-00484631.  
 PR 07-JUN-1995; 95US-00484635.  
 XX  
 PA (JOHN ) JOHNSON & JOHNSON CORP.  
 PA (AFRY-) AFRYMAX TECHNOLOGIES NV.  
 PI Wrighton NC, Dower WJ, Chang RS, Kashyap AK, Jolliffe LK;  
 PI Johnson D, Mulcahy L;  
 XX  
 DR WPI; 1997-052225/05.  
 XX  
 PT Erythropoietin receptor binding peptide - useful for treating disorders  
 PT characterised by deficiency of EPO, or low or defective red blood cell  
 PT population.  
 XX  
 PS Disclosure; Fig 2; 95pp; English.  
 XX  
 CC The invention describes a peptide of 10-40 amino acid residues which  
 CC binds to erythropoietin (EPO) receptor and which includes the amino acid  
 CC sequence Cys-Xaa1-Xaa2-Gly-Pro-Xaa3-Thr-Tyr-Xaa4-Cys, where Xaa1 = Arg,  
 CC His, Leu or Trp, Xaa2 = Met, Phe or Ile, Xaa3 = 1 of the 20 genetically  
 CC coded L-amino acids, and Xaa4 = Asp, Glu, Ile, Leu or Val. Optionally,  
 CC the peptide may be cyclised or dimerised. The peptide can be used to  
 CC treat a patient having a disorder characterised by a deficiency of EPO or  
 CC a low or defective red blood cell population. It can be used to treat end  
 CC stage renal failure or dialysis; anaemia associated with AIDS; autoimmune  
 CC disease; chronic inflammatory diseases or malignancy; beta-thalassemia;  
 CC cystic fibrosis; early anaemia of prematurity; spinal cord injury; acute  
 CC blood loss; aging; and neoplastic disease states accompanied by abnormal  
 CC erythropoiesis. The peptides can also be used as reagents for detecting  
 CC EPO receptors on living cells, in biological fluids, in tissue  
 CC homogenates, etc. Sequences AA13682-735 are representative peptides of  
 CC the invention  
 CC  
 SQ Sequence 20 AA;  
 XX

Query Match 44.8%; Score 30; DB 2; Length 20;  
 Best Local Similarity 42.9%; Pred. No. 4.9e+02;  
 Matches 3; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 6 PRCILGP 12  
 ::||:|  
 DB 4 YKCLMGP 10

RESULT 16  
 AA026998  
 ID AA026998 standard; peptide; 20 AA.  
 XX  
 AC AA026998;  
 XX  
 DT 11-NOV-1997 (first entry)

XX  
 DE Monomer subunit of erythropoietin receptor binding dimer.  
 XX  
 KM Monomer; erythropoietin; EPO; receptor; binding; dimer; activation;  
 KM treatment; disorder; deficiency; low; defective; red blood cell;  
 KM erythrocyte; population; cell surface; agonist; end stage; renal;  
 KM failure; dialysis; anaemia; anemia; AIDS; chronic; inflammatory; disease;  
 KM rheumatoid arthritis; bowel inflammation; autoimmune; transfusion.  
 XX  
 OS Synthetic.  
 XX  
 PN MO9640772-A2.  
 PD 19-DEC-1996.  
 XX  
 PF 06-JUN-1996; 96MO-US009469.  
 XX  
 PR 07-JUN-1995; 95US-00484135.  
 XX  
 PA (JOHN ) JOHNSON & JOHNSON.  
 PA Johnson DL, Zivin RA;  
 XX  
 DR WPI; 1997-099920/09.  
 XX  
 PT Activating cell surface receptors using peptide dimer agonists - also,  
 PT new dimers of erythropoietin receptor binding peptide(s) useful for  
 PT treating patient having disorder characterised by EPO deficiency.  
 XX  
 PS Disclosure; Fig 9; 110pp; English.  
 XX  
 CC The present peptide is a specific example of a claimed generic monomer  
 CC subunit of an erythropoietin (EPO) receptor binding dimer, which  
 CC comprises 2 EPO receptor binding monomers of 10 to 40 amino acids, and  
 CC activates or improves the bioactivity of the EPO cell surface receptor.  
 CC The dimer can be used to treat disorders resulting from EPO deficiency by  
 CC improving the activity of its cell surface receptor, e.g. end stage renal  
 CC failure/dialysis, anaemia associated with AIDS or chronic inflammatory  
 CC diseases such as rheumatoid arthritis and chronic bowel inflammation and  
 CC autoimmune disease. It can also be used to boost the red cell count of a  
 CC patient prior to surgery or as pretreatment to transfusion. The dimer  
 CC peptide exhibits increased biological potency in vitro and in vivo  
 CC relative to its component monomeric agonists. Dimerisation may also  
 CC convert cell surface receptor antagonists into agonists  
 CC  
 SQ Sequence 20 AA;  
 XX

Query Match 44.8%; Score 30; DB 2; Length 20;  
 Best Local Similarity 42.9%; Pred. No. 4.9e+02;  
 Matches 3; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 6 PRCILGP 12  
 ::||:|  
 DB 4 YKCLMGP 10

RESULT 17  
 AA005347  
 ID AA005347 standard; peptide; 20 AA.  
 XX  
 AC AA005347;  
 XX  
 DT 24-OCT-2001 (first entry)  
 XX  
 DE R1 and R2 peptide #41 useful as erythropoietin receptor agonist.  
 XX  
 KM Human; erythropoietin receptor; EPO-R; EPO agonist; EPO deficiency;  
 KM renal failure; anaemia; chronic inflammatory disease; autoimmune disease;  
 KM malignancy; red blood count.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200138342-A2.

```
XX 31-MAY-2001.
PD
XX
PR 24-NOV-2000; 2000WO-US032224.
XX
XX 24-NOV-1999; 99US-00449064.
XX
XX (GLAXO ) GLAXO GROUP LTD.
XX
XX Balu P;
XX
XX WPI; 2001-417749/44.
XX
XX Synthesizing peptide dimer useful as erythropoietin receptor agonist by
XX binding linking group with functional groups as initiation sites for
XX peptide synthesis to support and synthesizing peptide segments.
XX
XX Disclosure; Fig 1; 43pp; English.
XX
XX The present sequence for potential R1 and R2 peptide #41 can be used to
XX form a peptide dimer that binds and activates the erythropoietin receptor
XX (EPO-R). Various possible peptide sequences for R1 and R2 (AAU05301-
XX AAU05393) are described in the present invention. Also described is a
XX method for synthesizing such peptide dimers which act as EPO-R agonists.
XX The method is useful for synthesizing peptide dimers which are useful, in
XX vitro, as tools for understanding the biological role of EPO, in the
XX development of other compounds that bind to EPO-R, as commercial research
XX reagents for various medical research and diagnostic applications, for
XX detecting EPO receptors on living cells, for treatment of disorders
XX associated with a deficiency of EPO, such as end-stage renal
XX failure/dialysis, anemia associated with AIDS and chronic inflammatory
XX diseases, autoimmune diseases and malignancies, and for boosting the red
XX blood count of a patient prior to surgery
XX
XX Sequence 20 AA;

Query Match          44.8%; Score 30; DB 4; Length 20;
Best Local Similarity 42.9%; Pred. No. 4.9e+02;
Matches 3; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 6 PECTIAGP 12
   :::::
DB 4 YKCLMGP 10

RESULT 18
AAG88114
ID AAG88114 standard; peptide; 10 AA.
XX
XX AAG88114;
XX
XX 11-SEP-2001 (first entry)
XX
XX Saccharomyces cerevisiae peptide, SEQ ID NO: 3063.
XX
XX Saccharomyces cerevisiae; complementary peptide; peptide identification;
XX drug discovery; drug design.
XX
XX Saccharomyces cerevisiae.
XX
XX WO200142276-A1.
XX
XX 14-JUN-2001.
XX
XX 13-DEC-2000; 2000WO-GB004773.
XX
XX 13-DEC-1999; 99GB-00029471.
XX
XX (PROT-) PROTEOM LTD.
XX
XX Roberts GW, Heal JR;
XX
XX WPI; 2001-367863/38.
```

```
XX
XX Identifying complementary peptides by analysis of protein and nucleotide
XX sequence databases, useful in drug design.
XX
XX Example 5; Page 452; 488pp; English.
XX
XX The invention relates to the identification of complementary peptides by
XX analysis of protein and nucleotide sequence databases from higher
XX eukaryotic genomes, excluding human and plants. The specific
XX complementary peptides interact with their relevant target proteins
XX encoded in the eukaryote genome. The peptides may be used as reagents and
XX drugs for drug discovery and as lead ligands for drug design and
XX development. The present sequence is a complementary peptide from
XX Saccharomyces cerevisiae
XX
XX Sequence 10 AA;

Query Match          43.3%; Score 29; DB 4; Length 10;
Best Local Similarity 62.5%; Pred. No. 3.7e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 KNSPECTL 10
   :::::
DB 2 KNAPESVL 9

RESULT 19
AAG88115
ID AAG88115 standard; peptide; 10 AA.
XX
XX AAG88115;
XX
XX 11-SEP-2001 (first entry)
XX
XX Saccharomyces cerevisiae peptide, SEQ ID NO: 3064.
XX
XX Saccharomyces cerevisiae; complementary peptide; peptide identification;
XX drug discovery; drug design.
XX
XX Saccharomyces cerevisiae.
XX
XX WO200142276-A1.
XX
XX 14-JUN-2001.
XX
XX 13-DEC-2000; 2000WO-GB004773.
XX
XX 13-DEC-1999; 99GB-00029471.
XX
XX (PROT-) PROTEOM LTD.
XX
XX Roberts GW, Heal JR;
XX
XX WPI; 2001-367863/38.
XX
XX Identifying complementary peptides by analysis of protein and nucleotide
XX sequence databases, useful in drug design.
XX
XX Example 5; Page 452; 488pp; English.
XX
XX The invention relates to the identification of complementary peptides by
XX analysis of protein and nucleotide sequence databases from higher
XX eukaryotic genomes, excluding human and plants. The specific
XX complementary peptides interact with their relevant target proteins
XX encoded in the eukaryote genome. The peptides may be used as reagents and
XX drugs for drug discovery and as lead ligands for drug design and
XX development. The present sequence is a complementary peptide from
XX Saccharomyces cerevisiae
XX
XX Sequence 10 AA;

Query Match          43.3%; Score 29; DB 4; Length 10;
Best Local Similarity 62.5%; Pred. No. 3.7e+02;
```

Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 KNSPECTL 10  
 ||:|:|:  
 Db 2 KNAFESVL 9

## RESULT 20

ADT40845  
 ID ADT40845 standard, peptide; 10 AA.

AC ADT40845;

DT 30-DEC-2004 (first entry)

DE hsARS virus peptide, SEQ ID 1834.

XX virucide; Severe Acute Respiratory Syndrome; SARS; vaccine.

XX SARS coronavirus.

XX WO2004085650-A1.

XX 07-OCT-2004.

PF 24-MAR-2004; 2004MO-CN000246.

XX 24-MAR-2003; 2003US-0457031P.

PR 26-MAR-2003; 2003US-0457730P.

PR 02-APR-2003; 2003US-045931P.

PR 03-APR-2003; 2003US-0460357P.

PR 08-APR-2003; 2003US-0461265P.

PR 14-APR-2003; 2003US-0462805P.

PR 23-APR-2003; 2003US-0464886P.

PR 25-APR-2003; 2003US-0465738P.

PR 14-MAY-2003; 2003US-0470935P.

XX (UYNK-) UNIV HONG KONG.

PI Chan K, Guan Y, Nicholls JM, Peiris JSM, Poon L, Yuen K;

PI Leung FC;

DR MPI; 2004-737326/72.

XX New nucleic acid molecule encoding nucleocapsid- or spike-gene protein of

PT a human Severe Acute Respiratory Syndrome (hsARS) virus, useful for

PT diagnosing and treating SARS.

PS Example; SEQ ID NO 1834; 200pp; English.

XX The present invention relates to novel human Severe Acute Respiratory

CC Syndrome (hsARS) viral nucleic acid and protein sequences derived from a

CC hsARS virus having China Center for Type Culture Collection Deposit

CC Accession No. CCTCC-V200303. The present invention also relates to novel

CC nucleic acid molecules (1; ADT41483 or ADT41485) encoding a nucleocapsid-

CC (N) or spike (S)-gene protein of a hsARS virus. Also disclosed are

CC methods for detecting the presence of a N- or S-gene of the hsARS virus

CC or of the protein in a biological sample and identifying a subject

CC infected with the hsARS virus. The hsARS virus, nucleic acid and protein

CC sequences are useful as vaccines for diagnosing or treating SARS. They

CC are also useful in clinical and scientific research applications. The

CC hsARS virus genome (ADT30027) was obtained and the amino acid sequences

CC of all three reading frames were deduced from the complementary strand.

CC ADT40120 is the full-length protein encoded by the first reading frame of

CC the complementary strand and ADT40121-ADT40601 are the peptides from the

CC first reading frame protein. ADT40602 is the full-length protein encoded

CC by the second reading frame of the complementary strand and ADT40603-

CC ADT40976 are the peptides from the second reading frame protein. ADT40977

CC is the full-length protein encoded by the third reading frame of the

CC complementary strand and ADT40978-ADT41482 are the peptides from the

CC third reading frame protein.

XX Sequence 10 AA;

Query Match 43.3%; Score 29; DB 8; Length 10;  
 Best Local Similarity 55.6%; Pred. No. 3.7e+02;  
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 EKNSPECTL 10  
 :|||:|:  
 Db 2 KKNSDHCVL 10

## RESULT 21

ADS80262  
 ID ADS80262 standard; protein; 10 AA.

AC ADS80262;

DT 30-DEC-2004 (first entry)

DE SARS virus complementary DNA strand reading frame 2 protein #244.

XX virucide; vaccine; detection; severe acute respiratory syndrome;

KW real-time quantitative polymerase chain reaction; SARS.

XX SARS coronavirus.

XX WO2004085455-A1.

XX 07-OCT-2004.

PF 24-MAR-2004; 2004MO-CN000247.

XX 24-MAR-2003; 2003US-0457031P.

PR 26-MAR-2003; 2003US-0457730P.

PR 02-APR-2003; 2003US-045931P.

PR 03-APR-2003; 2003US-0460357P.

PR 08-APR-2003; 2003US-0461265P.

PR 14-APR-2003; 2003US-0462805P.

PR 23-APR-2003; 2003US-0464886P.

PR 05-MAY-2003; 2003US-0468139P.

PR 16-MAY-2003; 2003US-0471200P.

XX (UYNK-) UNIV HONG KONG.

PI Chan K, Guan Y, Nicholls JM, Peiris JSM, Poon L, Yuen K;

PI MPI; 2004-737292/72.

XX New isolated nucleic acid molecule useful for detecting, treating,

PT ameliorating, or preventing the virus causing severe acute respiratory

PT syndrome in humans using a real-time quantitative polymerase chain

PT reaction assay.

PS Example; SEQ ID NO 1834; 183pp; English.

XX The invention relates to an isolated nucleic acid molecule consisting

CC essentially of, and/or hybridizes under stringent conditions to a fully

CC defined nucleotide sequence of 16-25 base pairs (bp); SEQ ID NO: 2471-

CC 2476), or its complement. The methods and compositions of the present

CC invention are useful for the detection of the virus causing Severe Acute

CC Respiratory Syndrome (SARS) in humans using a real-time quantitative

CC polymerase chain reaction (PCR) assay. They can also be used in treating,

CC ameliorating, managing or preventing SARS. This sequence corresponds to a

CC partial SARS protein sequence from the complementary reading frame 2.

XX Sequence 10 AA;

SO Query Match 43.3%; Score 29; DB 8; Length 10;  
 Best Local Similarity 55.6%; Pred. No. 3.7e+02;  
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 EKNSPECTL 10  
 :|||:|:  
 Db 2 KKNSDHCVL 10

RESULT 22  
ADT38375  
ID ADT38375 standard; peptide, 10 AA.  
XX  
XX ADT38375;  
AC  
XX  
XX 30-DEC-2004 (first entry)  
DT  
XX  
XX hsSARS virus peptide, SEQ ID 1834.  
DE  
XX  
XX Virucide; Severe Acute Respiratory Syndrome; SARS; vaccine.  
KW  
XX  
XX SARS coronavirus.  
OS  
XX  
XX WO2004085633-A1.  
PN  
XX  
XX 07-OCT-2004.  
PD  
XX  
XX 24-MAR-2004; 2004WO-CN000248.  
PP  
XX  
XX 24-MAR-2003; 2003US-0457031P.  
PR  
XX  
XX 26-MAR-2003; 2003US-0457730P.  
PR  
XX  
XX 02-APR-2003; 2003US-0459931P.  
PR  
XX  
XX 03-APR-2003; 2003US-0460357P.  
PR  
XX  
XX 08-APR-2003; 2003US-0461265P.  
PR  
XX  
XX 14-APR-2003; 2003US-0462805P.  
PR  
XX  
XX 23-APR-2003; 2003US-0464886P.  
XX  
XX  
XX (UYHK-) UNIV HONG KONG.  
PA  
XX  
XX  
PI Chan K, Guan Y, Nicholls JM, Petris JSM, Poon L, Yuen K;  
PI Leung PC;  
XX  
XX WPI; 2004-728736/71.  
DR  
XX  
XX  
PT New isolated human severe acute respiratory syndrome (hSARS) virus,  
PT useful as vaccine for diagnosing or treating SARS or in clinical and  
PT scientific research applications.  
XX  
XX  
XX Example; SEQ ID NO 1834; 176pp; English.  
PS  
XX  
XX  
XX The present invention relates to novel human Severe Acute Respiratory  
CC Syndrome (hSARS) viral nucleic acid and protein sequences derived from a  
CC hSARS virus having China Center for Type Culture Collection Deposit  
CC Accession No. CCTCC-V200303. The hSARS virus, nucleic acid and protein  
CC sequences are useful as vaccines for diagnosing or treating SARS. They  
CC are also useful in clinical and scientific research applications. The  
CC hSARS virus genome (ADT36557) was obtained and the amino acid sequences  
CC of all three reading frames were deduced from the complementary strand.  
CC ADT37650 is the full-length protein encoded by the first reading frame of  
CC the complementary strand and ADT37651-ADT38131 are the peptides from the  
CC first reading frame protein. ADT38132 is the full-length protein encoded  
CC by the second reading frame of the complementary strand and ADT38133-  
CC ADT38506 are the peptides from the second reading frame protein. ADT38507  
CC is the full-length protein encoded by the third reading frame of the  
CC complementary strand and ADT38508-ADT39012 are the peptides from the  
CC third reading frame protein.  
CC  
XX  
XX Sequence 10 AA;  
SQ

Query Match 43.3%; Score 29; DB 8; Length 10;  
Best Local Similarity 55.6%; Pred. No. 3.7e+02;  
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 EKNSFECIL 10  
:|||||:|  
Db 2 KKNSDHCVL 10

RESULT 23  
ABB77729

ID ABB77729 standard; peptide, 15 AA.  
XX  
XX  
XX ABB77729;  
AC  
XX  
XX 30-JUL-2002 (first entry)  
DT  
XX  
XX N-terminal of human class III MHC 61.  
DE  
XX  
XX Human; class III MHC 61; immunological disease; inflammation;  
KW organ transplantation; gene therapy.  
XX  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO200226828-A1.  
PN  
XX  
XX 04-APR-2002.  
PD  
XX  
XX 02-JUL-2001; 2001WO-CN001116.  
PP  
XX  
XX 07-JUL-2000; 2000CN-00117015.  
PR  
XX  
XX (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.  
PA  
XX  
XX Mao Y, Xie Y;  
PI  
XX  
XX WPI; 2002-281324/32.  
DR  
XX  
XX  
PT Human class III MHC 61 and encoding polynucleotide, used in diagnosis and  
PT treatment of immunological diseases and inflammation and in organ  
PT transplantation.  
XX  
XX  
XX Example 6; Page 14; 40pp; Chinese.  
PS  
XX  
XX  
XX The present sequence is derived from class III MHC 61. The polypeptide  
CC and polynucleotide are used in diagnosis and treatment of immunological  
CC diseases and inflammation and in organ transplantation. The  
CC polynucleotide may also be used for gene therapy  
XX  
XX  
XX Sequence 15 AA;  
SQ

Query Match 43.3%; Score 29; DB 5; Length 15;  
Best Local Similarity 80.0%; Pred. No. 5.6e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 CITGP 12  
:|||||  
Db 7 CVLGP 11

RESULT 24  
ADU91959  
ID ADU91959 standard; peptide, 17 AA.  
XX  
XX  
XX ADU91959;  
AC  
XX  
XX 10-FEB-2005 (first entry)  
DT  
XX  
XX EPO-R agonist SEQ ID NO 100.  
DE  
XX  
XX erythropoietin receptor; EPO-R; erythropoietin; renal failure;  
KW autoimmune disease; cystic fibrosis; anemia; inflammation;  
KW spinal cord injury; aging; neurological disease; nephrotropic;  
KW antianemic; immunosuppressive; CNS-gen.; neuroprotective;  
KW respiratory-gen.; antiinflammatory; vulnary; nootropic; cyrostatic;  
KW hemostatic; cyclic.  
XX  
XX  
XX Synthetic.  
OS  
XX  
XX  
FH Key Location/Qualifiers  
FT Modified-site 1  
FT Disulfide-bond 4. .13  
FT Modified-site 17



FT /note= "C-terminal amide"  
 XX  
 PN WO2004101611-A2.  
 XX  
 PD 25-NOV-2004.  
 XX  
 PF 12-MAY-2004; 2004MO-US014886.  
 XX  
 PR 12-MAY-2003; 2003US-0470245P.  
 XX  
 PA (AFY-) AFFYMAX INC.  
 XX  
 PI Yln K, Holmes C, Lalonde G, Balu P, Schatz PJ, Tumelty D;  
 XX WPI, 2005-039329/04.  
 DR  
 XX  
 PT New peptide comprising specified sequence of amino acid is erythropoietin  
 PT receptor agonist useful for treating e.g. anemia, beta-thalassemia, renal  
 PT disorders.  
 XX  
 PS Disclosure; SEQ ID NO 100; 83pp; English.  
 XX  
 CC This invention describes a novel peptide which is an erythropoietin  
 CC receptor (EPO-R) activator. The peptide forms a dimer comprising a  
 CC linking moiety connecting two peptide chains composed of ADU91861. The N-  
 CC terminal of the peptide is acetylated. The EPO-R activator further  
 CC comprises at least one water soluble polymer, preferably polyethylene  
 CC glycol (PEG) covalently bound to the peptide and a spacer moiety. The  
 CC products of the invention are used for treating disorders associated with  
 CC deficiency of erythropoietin or low or defective red blood cell  
 CC population, end stage renal failure or dialysis, anemia associated with  
 CC AIDS, autoimmune disease or malignancy, beta-thalassemia, cystic  
 CC fibrosis, early anemia of prematurity, anemia associated with chronic  
 CC inflammatory disease, spinal cord injury, acute blood loss, aging and  
 CC neoplastic disease states accompanied by abnormal erythropoiesis. The  
 CC peptide compounds are potent agonists of erythropoietin receptor and have  
 CC nephrotropic, antianemic, immunosuppressive, CNS-Gen., neuroprotective,  
 CC respiratory-Gen., antiinflammatory, vulnerary, nootropic, cyostatic and  
 CC hemostatic activity. This sequence represents a peptide which acts as an  
 CC erythropoietin receptor (EPO-R) agonist.  
 XX  
 SQ Sequence 17 AA;  
 XX  
 Query Match 43.3%; Score 29; DB 9; Length 17;  
 Best Local Similarity 57.1%; Pred. No. 6.3e+02;  
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 QY 6 FPCITLGP 12  
 : : : : :  
 Db 2 YRCRMGP 8  
 RESULT 25  
 ADU91965  
 ID ADU91965 standard; peptide; 17 AA.  
 XX  
 AC ADU91965;  
 XX  
 DT 10-FEB-2005 (first entry)  
 XX  
 DE EPO-R agonist SEQ ID NO 106.  
 XX  
 XX erythropoietin receptor; EPO-R; erythropoietin; renal failure;  
 KW autoimmune disease; cystic fibrosis; anemia; inflammation;  
 KW spinal cord injury; aging; neurological disease; nephrotropic;  
 KW antianemic; immunosuppressive; CNS-Gen.; neuroprotective;  
 KW respiratory-Gen.; antiinflammatory; vulnerary; nootropic; cyostatic;  
 KW hemostatic; cyclic.  
 XX  
 OS Synthetic.  
 XX  
 Key Location/Qualifiers  
 FT Modified-site 1

FT /note= "Acetylated residue"  
 FT Disulfide-bond 4. .13  
 FT Modified-site 17  
 FT /note= "C-terminal amide"  
 XX  
 PN WO2004101611-A2.  
 XX  
 PD 25-NOV-2004.  
 XX  
 PF 12-MAY-2004; 2004MO-US014886.  
 XX  
 PR 12-MAY-2003; 2003US-0470245P.  
 XX  
 PA (AFY-) AFFYMAX INC.  
 XX  
 PI Yln K, Holmes C, Lalonde G, Balu P, Schatz PJ, Tumelty D;  
 XX WPI, 2005-039329/04.  
 DR  
 XX  
 PT New peptide comprising specified sequence of amino acid is erythropoietin  
 PT receptor agonist useful for treating e.g. anemia, beta-thalassemia, renal  
 PT disorders.  
 XX  
 PS Disclosure; SEQ ID NO 106; 83pp; English.  
 XX  
 CC This invention describes a novel peptide which is an erythropoietin  
 CC receptor (EPO-R) activator. The peptide forms a dimer comprising a  
 CC linking moiety connecting two peptide chains composed of ADU91861. The N-  
 CC terminal of the peptide is acetylated. The EPO-R activator further  
 CC comprises at least one water soluble polymer, preferably polyethylene  
 CC glycol (PEG) covalently bound to the peptide and a spacer moiety. The  
 CC products of the invention are used for treating disorders associated with  
 CC deficiency of erythropoietin or low or defective red blood cell  
 CC population, end stage renal failure or dialysis, anemia associated with  
 CC AIDS, autoimmune disease or malignancy, beta-thalassemia, cystic  
 CC fibrosis, early anemia of prematurity, anemia associated with chronic  
 CC inflammatory disease, spinal cord injury, acute blood loss, aging and  
 CC neoplastic disease states accompanied by abnormal erythropoiesis. The  
 CC peptide compounds are potent agonists of erythropoietin receptor and have  
 CC nephrotropic, antianemic, immunosuppressive, CNS-Gen., neuroprotective,  
 CC respiratory-Gen., antiinflammatory, vulnerary, nootropic, cyostatic and  
 CC hemostatic activity. This sequence represents a peptide which acts as an  
 CC erythropoietin receptor (EPO-R) agonist.  
 XX  
 SQ Sequence 17 AA;  
 XX  
 Query Match 43.3%; Score 29; DB 9; Length 17;  
 Best Local Similarity 42.9%; Pred. No. 6.3e+02;  
 Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
 QY 6 FPCITLGP 12  
 : : : : :  
 Db 2 YRCRMGP 8  
 RESULT 26  
 ADU92009  
 ID ADU92009 standard; peptide; 17 AA.  
 XX  
 AC ADU92009;  
 XX  
 DT 10-FEB-2005 (first entry)  
 XX  
 DE EPO-R agonist SEQ ID NO 150.  
 XX  
 XX erythropoietin receptor; EPO-R; erythropoietin; renal failure;  
 KW autoimmune disease; cystic fibrosis; anemia; inflammation;  
 KW spinal cord injury; aging; neurological disease; nephrotropic;  
 KW antianemic; immunosuppressive; CNS-Gen.; neuroprotective;  
 KW respiratory-Gen.; antiinflammatory; vulnerary; nootropic; cyostatic;  
 KW hemostatic; cyclic.  
 XX  
 OS Synthetic.

```

XX Key Location/Qualifiers
FH Modified-site 1
PT Disulfide-bond 4, .13
PT Modified-site 17
PT Modified-site /note="C-terminal amide"
XX
XX WO2004101611-A2.
XX
XX 25-NOV-2004.
XX
XX 12-MAY-2004; 2004WO-US014886.
XX
XX 12-MAY-2003; 2003US-0470245P.
XX
XX (AFPMY-) AFPMYMAX INC.
XX
XX Yin K, Holmes C, Lalonde G, Balu P, Schatz PJ, Tumelty D;
XX WPI; 2005-039329/04.
XX
XX New peptide comprising specified sequence of amino acid is erythropoietin
XX receptor agonist useful for treating e.g. anemia, beta-thalassemia, renal
XX disorders.
XX
XX Disclosure; SEQ ID NO 150; 83pp; English.
XX
XX This invention describes a novel peptide which is an erythropoietin
XX receptor (EPO-R) activator. The peptide forms a dimer comprising a
XX linking moiety connecting two peptide chains composed of AD91861. The N-
XX terminal of the peptide is acetylated. The EPO-R activator further
XX comprises at least one water soluble polymer, preferably polyethylene
XX glycol (PEG) covalently bound to the peptide and a spacer moiety. The
XX products of the invention are used for treating disorders associated with
XX deficiency of erythropoietin or low or defective red blood cell
XX population, end stage renal failure or dialysis, anemia associated with
XX AIDS, autoimmune disease or malignancy, beta-thalassemia, cystic
XX fibrosis, early anemia of prematurity, anemia associated with chronic
XX inflammatory disease, spinal cord injury, acute blood loss, aging and
XX neoplastic disease states accompanied by abnormal erythropoiesis. The
XX peptide compounds are potent agonists of erythropoietin receptor and have
XX nephroprotective, anti-anemic, immunosuppressive, CNS-Gen., neuroprotective,
XX respiratory-Gen., anti-inflammatory, vulnerary, nociceptive, cytoprotective,
XX and hemostatic activity. This sequence represents a peptide which acts as an
XX erythropoietin receptor (EPO-R) agonist.
XX
XX Sequence 17 AA;
SQ
XX
XX Query Match 43.3%; Score 29; DB 9; Length 17;
XX Best Local Similarity 42.9%; Pred. No. 6.3e+02;
XX Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 6 PECTILGP 12
XX :|:|:|
DB 2 YSCLMGP 8
XX
XX
XX RESULT 27
XX ID AAY26490 standard; peptide, 19 AA.
XX
XX AAY26490;
XX
XX 06-SEP-1999 (first entry)
XX
XX Erythropoietin receptor (EPO-R) binding peptide.
XX
XX Erythropoietin receptor (EPO-R) binding peptide.
XX
XX Erythropoietin receptor; EPO deficiency; renal failure; AIDS;
XX dialysis; anemia; autoimmune disease; chronic inflammatory disease;
XX malignancy; beta-thalassemia; cystic fibrosis; prematurity; blood loss;
XX spinal cord injury; aging; neoplastic disease; erythropoiesis; EPO-R.
XX

```

```

OS Synthetic.
XX
XX WO9640749-A1.
XX
XX 19-DEC-1996.
XX
XX 07-JUN-1996; 96WO-US009810.
XX
XX 07-JUN-1995; 95US-00484631.
XX
XX 07-JUN-1995; 95US-00484635.
XX
XX (JOHJ) JOHNSON & JOHNSON CORP.
XX (AFPMY-) AFPMYMAX TECHNOLOGIES NV.
XX
XX Wrighton NC, Dower WJ, Chang RS, Kashyap AK, Joliffe LK;
XX Johnson D, Mulcahy L;
XX WPI; 1997-052225/05.
XX
XX Erythropoietin receptor binding peptide - useful for treating disorders
XX characterised by deficiency of EPO, or low or defective red blood cell
XX population.
XX
XX Disclosure; Page 23; 95pp; English.
XX
XX The invention describes a peptide of 10-40 amino acid residues which
XX binds to erythropoietin (EPO) receptor and which includes the amino acid
XX sequence Cys-Xaa1-Xaa2-Gly-Pro-Xaa3-Thr-Trip-Xaa4-Cys, where Xaa1 = Arg,
XX His, Leu or Trp, Xaa2 = Met, Phe or Ile, Xaa3 = 1 of the 20 genetically
XX coded L-amino acids, and Xaa4 = Asp, Glu, Ile, Leu or Val. Optionally,
XX the peptide may be cyclised or dimerised. The peptide can be used to
XX treat a patient having a disorder characterised by a deficiency of EPO or
XX a low or defective red blood cell population. It can be used to treat end
XX stage renal failure or dialysis; anemia associated with AIDS, autoimmune
XX disease, chronic inflammatory diseases or malignancy; beta-thalassemia;
XX cystic fibrosis; early anaemia or prematurity; spinal cord injury; acute
XX blood loss; aging; and neoplastic disease states accompanied by abnormal
XX erythropoiesis. The peptides can also be used as reagents for detecting
XX EPO receptors on living cells, in biological fluids, in tissue
XX homogenates, etc. Sequences AAY26352-548 are representative peptides
XX falling within the above peptide motif and isolated during the affinity
XX selection process
XX
XX Sequence 19 AA;
SQ
XX
XX Query Match 43.3%; Score 29; DB 2; Length 19;
XX Best Local Similarity 40.0%; Pred. No. 7e+02;
XX Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
QY 3 KNSPECTILGP 12
XX :|:|:|
DB 2 KTKVRCMGMP 11
XX
XX
XX RESULT 28
XX ID ADS33404 standard; peptide, 19 AA.
XX
XX ADS33404;
XX
XX 02-DEC-2004 (first entry)
XX
XX CMET-HGF binding peptide #57.
XX
XX cytostatic; hepatocyte growth factor receptor; CMET; HGF; tumor;
XX glioblastoma; malignant mesothelioma; colorectal tumor;
XX hepatocellular tumor; hepatobiliary tumor; renal tumor; osteosarcoma;
XX cervical tumors; diagnostic imaging; cellular proliferation;
XX angiogenesis; hyperproliferation; cancer; solid phase matrix;
XX chromatography.
XX
XX Synthetic.
XX

```

PN WO2004078778-A2.  
 XX 16-SEP-2004.  
 PD  
 XX  
 PF 03-MAR-2004, 2004WO-US006473.  
 XX  
 PR 03-MAR-2003, 2003US-0451588P.  
 XX  
 PA (DYAX-) DYAX CORP.  
 PA (BRAC) BRACCO INT BV.  
 XX  
 PI Sato AK, Dransfield DT, Ladner RC, Shrivastava A, Nanjappan P;  
 PI WPI, 2004-668601/65.  
 DR  
 XX Hepatocyte growth factor receptor (cmet) binding polypeptide or  
 PT multimeric peptide construct, useful for diagnostic imaging of sites of  
 PT cellular proliferation and/or angiogenesis, and for treating cancer.  
 XX  
 PS Claim 7, SEQ ID NO 57, 174pp; English.  
 XX  
 CC The invention relates to a novel polypeptide or multimeric peptide  
 CC construct (I) which binds hepatocyte growth factor receptor (cmet) or a  
 CC complex comprising cmet and hepatocyte growth factor (HGF). (I) is useful  
 CC for detecting cmet or a complex of cmet and HGF in an animal or human  
 CC subject which involves providing (I), where (I) is labelled,  
 CC administering to the subject the labelled (I), and detecting labelled (I)  
 CC in the subject. The label is radioactive or paramagnetic. (I) is useful  
 CC for purifying cmet or a cmet and HGF complex from a solution containing  
 CC it which involves contacting the solution with at least one (I), and  
 CC separating the polypeptide or multimeric polypeptide from the solution.  
 CC (M1) is useful for treating conditions involving activation of cmet. The  
 CC disease is a solid tumor chosen from breast, thyroid, glioblastoma,  
 CC prostate, malignant mesothelioma, colorectal, hepatocellular,  
 CC hepatobiliary, renal, osteosarcoma and cervical tumors. (I) is useful for  
 CC diagnostic imaging of sites of cellular proliferation and/or  
 CC angiogenesis, thus useful in diagnosis of such hyperproliferative-related  
 CC and/or angiogenesis-related disorders. (I) is useful for targeting  
 CC therapeutic agents or delivering vehicles for therapeutics to sites of  
 CC hyperproliferation and/or angiogenesis or other tissue expressing cmet.  
 CC (I) is useful for detection and/or imaging of cmet in vitro or in vivo.  
 CC (I) is useful for treating cancer. (I) is used in gene therapy for  
 CC treating hyper proliferative disorders. cmet binding peptides were  
 CC synthesized on a solid phase matrix using 9-fluorenylmethoxycarbonyl  
 CC protocols. The peptides were purified with reverse chromatography. This  
 CC sequence corresponds to a peptide of the invention.  
 CC  
 XX SQ Sequence 19 AA;  
 Query Match 43.3%; Score 29; DB 8; Length 19;  
 Best Local Similarity 83.3%; Pred. No. 7e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 5 SPECIL 10  
 :|||:  
 Db 11 TPCIL 16  
 RESULT 29  
 AAY13694  
 ID AAY13694 standard; peptide; 20 AA.  
 AC AAY13694;  
 XX  
 XX 06-SRP-1999 (first entry)  
 XX  
 DE Erythropoietin receptor (EPO-R) binding peptide.  
 XX  
 KM Erythropoietin, EPO, receptor; EPO deficiency; renal failure; AIDS;  
 KM dialysis; anaemia; autoimmune disease; chronic inflammatory disease;  
 KM malignancy; beta-thalassemia; cystic fibrosis; prematurity; blood loss;  
 KM spinal cord injury; aging; neoplastic disease; erythropoietin; EPO-R.  
 XX

OS Synthetic.  
 PN WO9640749-A1.  
 XX  
 PD 19-DEC-1996.  
 XX  
 PF 07-JUN-1996; 96WO-US009810.  
 XX  
 PR 07-JUN-1995; 95US-00484631.  
 PR 07-JUN-1995; 95US-00484635.  
 XX  
 PA (JOHN) JOHNSON & JOHNSON CORP.  
 PA (AFFY-) AFFYMAX TECHNOLOGIES NV.  
 XX  
 PI WRIGHTSON NC, DOWER WJ, CHANG RS, KASHYAP AK, JOLLIFFE LK;  
 PI JOHNSON D, MULCANY L;  
 DR WPI, 1997-052225/05.  
 XX  
 PT Erythropoietin receptor binding peptide - useful for treating disorders  
 PT characterized by deficiency of EPO, or low or defective red blood cell  
 PT population.  
 XX  
 PS Disclosure; Fig 2; 95pp; English.  
 XX  
 CC The invention describes a peptide of 10-40 amino acid residues which  
 CC binds to erythropoietin (EPO) receptor and which includes the amino acid  
 CC sequence Cys-Xaa1-Xaa2-Gly-Pro-Xaa3-Thr-Tyr-Xaa4-Cys, where Xaa1 = Arg,  
 CC His, Leu or Tyr, Xaa2 = Met, Phe or Ile, Xaa3 = 1 of the 20 genetically  
 CC coded L-amino acids, and Xaa4 = Asp, Glu, Ile, Leu or Val. Optionally,  
 CC the peptide may be cyclised or dimerised. The peptide can be used to  
 CC treat a patient having a disorder characterised by a deficiency of EPO or  
 CC a low or defective red blood cell population. It can be used to treat end  
 CC stage renal failure or dialysis; anaemia associated with AIDS; autoimmune  
 CC disease; chronic inflammatory diseases or malignancy; beta-thalassemia;  
 CC cystic fibrosis; early anaemia of prematurity; spinal cord injury; acute  
 CC blood loss; aging; and neoplastic disease states accompanied by abnormal  
 CC erythropoiesis. The peptides can also be used as reagents for detecting  
 CC EPO receptors on living cells, in biological fluids, in tissue  
 CC homogenates, etc. Sequences AAY13662-735 are representative peptides of  
 CC the invention  
 XX  
 SQ Sequence 20 AA;  
 Query Match 43.3%; Score 29; DB 2; Length 20;  
 Best Local Similarity 57.1%; Pred. No. 7.4e+02;  
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 QY 6 FPCILGP 12  
 :|||:  
 Db 4 YECRMGP 10  
 RESULT 30  
 AAY13720  
 ID AAY13720 standard; peptide; 20 AA.  
 AC AAY13720;  
 XX  
 XX 06-SRP-1999 (first entry)  
 XX  
 DE Erythropoietin receptor (EPO-R) binding peptide.  
 XX  
 KM Erythropoietin, EPO, receptor; EPO deficiency; renal failure; AIDS;  
 KM dialysis; anaemia; autoimmune disease; chronic inflammatory disease;  
 KM malignancy; beta-thalassemia; cystic fibrosis; prematurity; blood loss;  
 KM spinal cord injury; aging; neoplastic disease; erythropoietin; EPO-R.  
 XX  
 OS Synthetic.  
 OS  
 PN WO9640749-A1.  
 XX  
 PD 19-DEC-1996.  
 XX

XX 07-JUN-1996; 96WO-US009810.  
 XX  
 XX 07-JUN-1995; 95US-00484631.  
 PR 07-JUN-1995; 95US-00484635.  
 XX  
 XX (JOHN J) JOHNSON & JOHNSON CORP.  
 PA (AFPY-) AFPMAX TECHNOLOGIES NV.  
 XX  
 PI Wrighton NC, Dower WJ, Chang RS, Kashyap AK, Jolliffe LK;  
 PI Johnson D, Mulcahy L;  
 DR WPI; 1997-052225/05.  
 XX  
 XX Erythropoietin receptor binding peptide - useful for treating disorders  
 PT characterised by deficiency of EPO, or low or defective red blood cell  
 PT population.  
 XX  
 PS Disclosure; Fig 2; 95pp; English.  
 XX  
 CC The invention describes a peptide of 10-40 amino acid residues which  
 CC binds to erythropoietin (EPO) receptor and which includes the amino acid  
 CC sequence Cys-Xaa1-Xaa2-Gly-Pro-Xaa3-Thr-Tyr-Xaa4-Cys, where Xaa1 = Arg,  
 CC His, Leu or Trp, Xaa2 = Met, Phe or Ile, Xaa3 = 1 of the 20 genetically  
 CC coded L-amino acids, and Xaa4 = Asp, Glu, Ile, Leu or Val. Optionally,  
 CC the peptide may be cyclised or dimerised. The peptide can be used to  
 CC treat a patient having a disorder characterised by a deficiency of EPO or  
 CC a low or defective red blood cell population. It can be used to treat end  
 CC stage renal failure or dialysis; anaemia associated with AIDS, autoimmune  
 CC disease, chronic inflammatory diseases or malignancy; beta-thalassemia;  
 CC cystic fibrosis; early anaemia of prematurity; spinal cord injury; acute  
 CC blood loss; aging; and neoplastic disease states accompanied by abnormal  
 CC erythropoiesis. The peptides can also be used as reagents for detecting  
 CC EPO receptors on living cells, in biological fluids, in tissue  
 CC homogenates, etc. Sequences AAY13662-735 are representative peptides of  
 CC the invention  
 CC  
 SQ Sequence 20 AA;  
 XX  
 XX  
 Query Match 43.3%; Score 29; DB 2; Length 20;  
 Best Local Similarity 42.9%; Pred. No. 7.4e+02;  
 Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
 QY 6 PECTIGP 12  
 : ||: ||  
 Db 4 YSCLMGP 10  
 XX  
 RESULT 31  
 AAY13685  
 ID AAY13685 standard; peptide; 20 AA.  
 XX  
 AC AAY13685;  
 XX  
 DT 06-SEP-1999 (first entry)  
 XX  
 DE Erythropoietin receptor (EPO-R) binding peptide.  
 XX  
 KW Erythropoietin; EPO; receptor; EPO deficiency; renal failure; AIDS;  
 KW dialysis; anaemia; autoimmune disease; chronic inflammatory disease;  
 KW malignancy; beta-thalassemia; cystic fibrosis; prematurity; blood loss;  
 KW spinal cord injury; aging; neoplastic disease; erythropoiesis; EPO-R.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9640749-A1.  
 XX  
 PD 19-DEC-1996.  
 XX  
 PP 07-JUN-1996; 96WO-US009810.  
 XX  
 XX 07-JUN-1995; 95US-00484631.  
 PR 07-JUN-1995; 95US-00484635.  
 XX

XX (JOHN J) JOHNSON & JOHNSON CORP.  
 PA (AFPY-) AFPMAX TECHNOLOGIES NV.  
 XX  
 XX Wrighton NC, Dower WJ, Chang RS, Kashyap AK, Jolliffe LK;  
 PI Johnson D, Mulcahy L;  
 DR WPI; 1997-052225/05.  
 XX  
 XX Erythropoietin receptor binding peptide - useful for treating disorders  
 PT characterised by deficiency of EPO, or low or defective red blood cell  
 PT population.  
 XX  
 PS Disclosure; Fig 2; 95pp; English.  
 XX  
 CC The invention describes a peptide of 10-40 amino acid residues which  
 CC binds to erythropoietin (EPO) receptor and which includes the amino acid  
 CC sequence Cys-Xaa1-Xaa2-Gly-Pro-Xaa3-Thr-Tyr-Xaa4-Cys, where Xaa1 = Arg,  
 CC His, Leu or Trp, Xaa2 = Met, Phe or Ile, Xaa3 = 1 of the 20 genetically  
 CC coded L-amino acids, and Xaa4 = Asp, Glu, Ile, Leu or Val. Optionally,  
 CC the peptide may be cyclised or dimerised. The peptide can be used to  
 CC treat a patient having a disorder characterised by a deficiency of EPO or  
 CC a low or defective red blood cell population. It can be used to treat end  
 CC stage renal failure or dialysis; anaemia associated with AIDS, autoimmune  
 CC disease, chronic inflammatory diseases or malignancy; beta-thalassemia;  
 CC cystic fibrosis; early anaemia of prematurity; spinal cord injury; acute  
 CC blood loss; aging; and neoplastic disease states accompanied by abnormal  
 CC erythropoiesis. The peptides can also be used as reagents for detecting  
 CC EPO receptors on living cells, in biological fluids, in tissue  
 CC homogenates, etc. Sequences AAY13662-735 are representative peptides of  
 CC the invention  
 CC  
 SQ Sequence 20 AA;  
 XX  
 XX  
 Query Match 43.3%; Score 29; DB 2; Length 20;  
 Best Local Similarity 42.9%; Pred. No. 7.4e+02;  
 Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
 QY 6 PECTIGP 12  
 : ||: ||  
 Db 4 YSCLMGP 10  
 XX  
 RESULT 32  
 AAY26375  
 ID AAY26375 standard; peptide; 20 AA.  
 XX  
 AC AAY26375;  
 XX  
 DT 06-SEP-1999 (first entry)  
 XX  
 DE Erythropoietin receptor (EPO-R) binding peptide.  
 XX  
 KW Erythropoietin; EPO; receptor; EPO deficiency; renal failure; AIDS;  
 KW dialysis; anaemia; autoimmune disease; chronic inflammatory disease;  
 KW malignancy; beta-thalassemia; cystic fibrosis; prematurity; blood loss;  
 KW spinal cord injury; aging; neoplastic disease; erythropoiesis; EPO-R.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9640749-A1.  
 XX  
 PD 19-DEC-1996.  
 XX  
 PP 07-JUN-1996; 96WO-US009810.  
 XX  
 XX 07-JUN-1995; 95US-00484631.  
 PR 07-JUN-1995; 95US-00484635.  
 XX  
 XX (JOHN J) JOHNSON & JOHNSON CORP.  
 PA (AFPY-) AFPMAX TECHNOLOGIES NV.  
 XX  
 XX Wrighton NC, Dower WJ, Chang RS, Kashyap AK, Jolliffe LK;

PI Johnson D, Mulcahy L;  
 XX WPI, 1997-052225/05.  
 XX  
 PT Erythropoietin receptor binding peptide - useful for treating disorders  
 PT characterised by deficiency of EPO, or low or defective red blood cell  
 PT population.  
 XX  
 PS Disclosure; Page 17; 95pp; English.  
 XX  
 CC The invention describes a peptide of 10-40 amino acid residues which  
 CC binds to erythropoietin (EPO) receptor and which includes the amino acid  
 CC sequence Cys-Xaa1-Xaa2-Gly-Pro-Xaa3-Thr-Tyr-Xaa4-Cys, where Xaa1 = Arg,  
 CC His, Leu or Tyr, Xaa2 = Met, Phe or Ile, Xaa3 = 1 of the 20 genetically  
 CC coded L-amino acids, and Xaa4 = Asp, Glu, Ile, Leu or Val. Optionally,  
 CC the peptide may be cyclised or dimerised. The peptide can be used to  
 CC treat a patient having a disorder characterised by a deficiency of EPO or  
 CC a low or defective red blood cell population. It can be used to treat end  
 CC stage renal failure or dialysis; anaemia associated with AIDS, autoimmune  
 CC disease, chronic inflammatory diseases or malignancy; beta-thalassemia;  
 CC cystic fibrosis; early anaemia of prematurity; spinal cord injury; acute  
 CC blood loss; aging; and neoplastic disease states accompanied by abnormal  
 CC erythropoiesis. The peptides can also be used as reagents for detecting  
 CC EPO receptors on living cells, in biological fluids, in tissue  
 CC homogenates, etc. Sequences AAY26352-548 are representative peptides  
 CC falling within the above peptide motif and isolated during the affinity  
 CC selection process  
 CC  
 SO Sequence 20 AA;  
 XX  
 XX  
 Query Match 43.3%; Score 29; DB 2; Length 20;  
 Best Local Similarity 42.9%; Pred. No. 7.4e+02;  
 Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
 QY 6 FRCILGP 12  
 : : : : :  
 Db 4 YSCIMGP 10  
 XX  
 XX  
 RESULT 33  
 AAY26374  
 ID AAY26374 standard; peptide; 20 AA.  
 XX  
 AC AAY26374;  
 XX  
 DT 06-SEP-1999 (first entry)  
 XX  
 DE Erythropoietin receptor (EPO-R) binding peptide.  
 XX  
 KW Erythropoietin; EPO; receptor; EPO deficiency; renal failure; AIDS;  
 KW dialysis; anaemia; autoimmune disease; chronic inflammatory disease;  
 KW malignancy; beta-thalassemia; cystic fibrosis; prematurity; blood loss;  
 KW spinal cord injury; aging; neoplastic disease; erythropoiesis; EPO-R.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9640749-A1.  
 XX  
 PD 19-DEC-1996.  
 XX  
 PF 07-JUN-1996; 96WO-US009810.  
 XX  
 PR 07-JUN-1995; 95US-00484631.  
 PR 07-JUN-1995; 95US-00484635.  
 XX  
 PA (JOHN J) JOHNSON & JOHNSON CORP.  
 PA (APFY-) APFYMAY TECHNOLOGIES NV.  
 XX  
 PI Wrighton NC, Dower WJ, Chang RS, Kashyap AK, Jolliffe LK;  
 PI Johnson D, Mulcahy L;  
 XX  
 XX WPI, 1997-052225/05.  
 XX

PT Erythropoietin receptor binding peptide - useful for treating disorders  
 PT characterised by deficiency of EPO, or low or defective red blood cell  
 PT population.  
 XX  
 PS Disclosure; Page 17; 95pp; English.  
 XX  
 CC The invention describes a peptide of 10-40 amino acid residues which  
 CC binds to erythropoietin (EPO) receptor and which includes the amino acid  
 CC sequence Cys-Xaa1-Xaa2-Gly-Pro-Xaa3-Thr-Tyr-Xaa4-Cys, where Xaa1 = Arg,  
 CC His, Leu or Tyr, Xaa2 = Met, Phe or Ile, Xaa3 = 1 of the 20 genetically  
 CC coded L-amino acids, and Xaa4 = Asp, Glu, Ile, Leu or Val. Optionally,  
 CC the peptide may be cyclised or dimerised. The peptide can be used to  
 CC treat a patient having a disorder characterised by a deficiency of EPO or  
 CC a low or defective red blood cell population. It can be used to treat end  
 CC stage renal failure or dialysis; anaemia associated with AIDS, autoimmune  
 CC disease, chronic inflammatory diseases or malignancy; beta-thalassemia;  
 CC cystic fibrosis; early anaemia of prematurity; spinal cord injury; acute  
 CC blood loss; aging; and neoplastic disease states accompanied by abnormal  
 CC erythropoiesis. The peptides can also be used as reagents for detecting  
 CC EPO receptors on living cells, in biological fluids, in tissue  
 CC homogenates, etc. Sequences AAY26352-548 are representative peptides  
 CC falling within the above peptide motif and isolated during the affinity  
 CC selection process  
 CC  
 SO Sequence 20 AA;  
 XX  
 XX  
 Query Match 43.3%; Score 29; DB 2; Length 20;  
 Best Local Similarity 57.1%; Pred. No. 7.4e+02;  
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 QY 6 FRCILGP 12  
 : : : : :  
 Db 4 YRCRMGP 10  
 XX  
 XX  
 RESULT 34  
 AAW27034  
 ID AAW27034 standard; peptide; 20 AA.  
 XX  
 AC AAW27034;  
 XX  
 DT 11-NOV-1997 (first entry)  
 XX  
 DE Monomer subunit of erythropoietin receptor binding dimer.  
 XX  
 KW Monomer; erythropoietin; EPO; receptor; binding; dimer; activation;  
 KW treatment; disorder; deficiency; low; defective; red blood cell;  
 KW erythrocyte; population; cell surface; agonist; end stage; renal;  
 KW failure; dialysis; anaemia; anemia; AIDS; chronic; inflammatory; disease;  
 KW rheumatoid arthritis; bowel inflammation; autoimmune; transfusion.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9640772-A2.  
 XX  
 PD 19-DEC-1996.  
 XX  
 PF 06-JUN-1996; 96WO-US009469.  
 XX  
 PR 07-JUN-1995; 95US-00484135.  
 XX  
 PA (JOHN J) JOHNSON & JOHNSON.  
 PA Johnson DL, Zivin RA;  
 XX  
 PI WPI, 1997-099920/09.  
 XX  
 DR  
 XX  
 PT Activating cell surface receptors using peptide dimer agonists - also,  
 PT new dimers of erythropoietin receptor binding peptide(s) useful for  
 PT treating patient having disorder characterised by EPO deficiency.  
 XX  
 PS Disclosure; Fig 9; 110pp; English.  
 XX

CC The present peptide is a specific example of a claimed generic monomer  
CC subunit of an erythropoietin (EPO) receptor binding dimer, which  
CC comprises 2 EPO receptor binding monomers of 10 to 40 amino acids, and  
CC activates or improves the bioactivity of the EPO cell surface receptor.  
CC The dimer can be used to treat disorders resulting from EPO deficiency by  
CC improving the activity of its cell surface receptor, e.g. end stage renal  
CC failure/dialysis, anaemia associated with AIDS or chronic inflammatory  
CC diseases such as rheumatoid arthritis and chronic bowel inflammation and  
CC autoimmune disease. It can also be used to boost the red cell count of a  
CC patient prior to surgery or as pretreatment to transfusion. The dimer  
CC peptide exhibits increased biological potency in vitro and in vivo  
CC relative to its component monomeric agonists. Dimerisation may also  
CC convert cell surface receptor antagonists into agonists  
XX  
SQ Sequence 20 AA;  
XX  
Query Match 43.3%; Score 29; DB 2; Length 20;  
Best Local Similarity 42.9%; Pred. No. 7.4e+02;  
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
XX  
QY 6 PECTIGP 12  
: || : ||  
Db 4 YECRMGP 10  
XX  
RESULT 35  
AAW27008  
ID AAW27008 standard; peptide; 20 AA.  
XX  
AC AAW27008;  
XX  
DT 11-NOV-1997 (first entry)  
XX  
DE Monomer subunit of erythropoietin receptor binding dimer.  
XX  
KW Monomer; erythropoietin; EPO; receptor; binding; dimer; activation;  
KW treatment; disorder; deficiency; low; defective; red blood cell;  
KW erythrocyte; population; cell surface; agonist; end stage; renal;  
KW failure; dialysis; anaemia; anemia; AIDS; chronic; inflammatory; disease;  
KW rheumatoid arthritis; bowel inflammation; autoimmune; transfusion.  
XX  
OS Synthetic.  
XX  
PN WO9640772-A2.  
XX  
PD 19-DEC-1996.  
XX  
PF 06-JUN-1996; 96WO-US009469.  
XX  
PR 07-JUN-1995; 95US-00484135.  
XX  
PA (JOHN ) JOHNSON & JOHNSON.  
XX  
PI Johnson DL, Zivin RA;  
XX  
DR WPI; 1997-099920/09.  
XX  
PT Activating cell surface receptors using peptide dimer agonists - also,  
PT new dimers of erythropoietin receptor binding peptide(s) useful for  
PT treating patient having disorder characterised by EPO deficiency.  
XX  
PS Disclosure; Fig 9; 110pp; English.  
XX  
CC The present peptide is a specific example of a claimed generic monomer  
CC subunit of an erythropoietin (EPO) receptor binding dimer, which  
CC comprises 2 EPO receptor binding monomers of 10 to 40 amino acids, and  
CC activates or improves the bioactivity of the EPO cell surface receptor.  
CC The dimer can be used to treat disorders resulting from EPO deficiency by  
CC improving the activity of its cell surface receptor, e.g. end stage renal  
CC failure/dialysis, anaemia associated with AIDS or chronic inflammatory  
CC diseases such as rheumatoid arthritis and chronic bowel inflammation and  
CC autoimmune disease. It can also be used to boost the red cell count of a  
CC patient prior to surgery or as pretreatment to transfusion. The dimer

CC peptide exhibits increased biological potency in vitro and in vivo  
CC relative to its component monomeric agonists. Dimerisation may also  
CC convert cell surface receptor antagonists into agonists  
XX  
SQ Sequence 20 AA;  
XX  
Query Match 43.3%; Score 29; DB 2; Length 20;  
Best Local Similarity 57.1%; Pred. No. 7.4e+02;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
XX  
QY 6 PECTIGP 12  
: || : ||  
Db 4 YECRMGP 10  
XX  
RESULT 36  
AAW26999  
ID AAW26999 standard; peptide; 20 AA.  
XX  
AC AAW26999;  
XX  
DT 11-NOV-1997 (first entry)  
XX  
DE Monomer subunit of erythropoietin receptor binding dimer.  
XX  
KW Monomer; erythropoietin; EPO; receptor; binding; dimer; activation;  
KW treatment; disorder; deficiency; low; defective; red blood cell;  
KW erythrocyte; population; cell surface; agonist; end stage; renal;  
KW failure; dialysis; anaemia; anemia; AIDS; chronic; inflammatory; disease;  
KW rheumatoid arthritis; bowel inflammation; autoimmune; transfusion.  
XX  
OS Synthetic.  
XX  
PN WO9640772-A2.  
XX  
PD 19-DEC-1996.  
XX  
PF 06-JUN-1996; 96WO-US009469.  
XX  
PR 07-JUN-1995; 95US-00484135.  
XX  
PA (JOHN ) JOHNSON & JOHNSON.  
XX  
PI Johnson DL, Zivin RA;  
XX  
DR WPI; 1997-099920/09.  
XX  
PT Activating cell surface receptors using peptide dimer agonists - also,  
PT new dimers of erythropoietin receptor binding peptide(s) useful for  
PT treating patient having disorder characterised by EPO deficiency.  
XX  
PS Disclosure; Fig 9; 110pp; English.  
XX  
CC The present peptide is a specific example of a claimed generic monomer  
CC subunit of an erythropoietin (EPO) receptor binding dimer, which  
CC comprises 2 EPO receptor binding monomers of 10 to 40 amino acids, and  
CC activates or improves the bioactivity of the EPO cell surface receptor.  
CC The dimer can be used to treat disorders resulting from EPO deficiency by  
CC improving the activity of its cell surface receptor, e.g. end stage renal  
CC failure/dialysis, anaemia associated with AIDS or chronic inflammatory  
CC diseases such as rheumatoid arthritis and chronic bowel inflammation and  
CC autoimmune disease. It can also be used to boost the red cell count of a  
CC patient prior to surgery or as pretreatment to transfusion. The dimer  
CC peptide exhibits increased biological potency in vitro and in vivo  
CC relative to its component monomeric agonists. Dimerisation may also  
CC convert cell surface receptor antagonists into agonists  
XX  
SQ Sequence 20 AA;  
XX  
Query Match 43.3%; Score 29; DB 2; Length 20;  
Best Local Similarity 42.9%; Pred. No. 7.4e+02;  
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 6 PECTILGP 12  
: ||: ||  
Db 4 YSCLMGP 10

RESULT 37  
AAU05356  
ID AAU05356 standard; peptide; 20 AA.

XX AAU05356;

DT 24-OCT-2001 (first entry)

DE R1 and R2 peptide #50 useful as erythropoietin receptor agonist.

XX Human; erythropoietin receptor; EPO-R; EPO agonist; EPO deficiency;  
KM renal failure; anaemia; chronic inflammatory disease; autoimmune disease;  
KW malignancy; red blood count.

XX Homo sapiens.

XX WO200138342-A2.

XX 31-MAY-2001.

XX 24-NOV-2000; 2000WO-US032224.

XX 24-NOV-1999; 99US-00449064.

XX (GLAX ) GLAXO GROUP LTD.

XX Balu P;

XX WPI; 2001-417749/44.

XX Synthesizing peptide dimer useful as erythropoietin receptor agonist by  
PT binding linking group with functional groups as initiation sites for  
PT peptide synthesis to support and synthesizing peptide segments.

XX Disclosure; Fig 1; 43pp; English.

XX The present sequence for potential R1 and R2 peptide #50 can be used to  
CC form a peptide dimer that binds and activates the erythropoietin receptor  
CC (EPO-R). Various possible peptide sequences for R1 and R2 (AAU05301-  
CC AAU05393) are described in the present invention. Also described is a  
CC method for synthesizing such peptide dimers which act as EPO-R agonists.  
CC The method is useful for synthesizing peptide dimers which are useful, in  
CC vitro, as tools for understanding the biological role of EPO, in the  
CC development of other compounds that bind to EPO-R, as commercial research  
CC reagents for various medical research and diagnostic applications, for  
CC detecting EPO receptors on living cells, for treatment of disorders  
CC associated with a deficiency of EPO, such as end-stage renal  
CC failure/dialysis, anaemia associated with AIDS and chronic inflammatory  
CC diseases, autoimmune diseases and malignancies, and for boosting the red  
CC blood count of a patient prior to surgery

XX Sequence 20 AA;

Query Match 43.3%; Score 29; DB 4; Length 20;  
Best Local Similarity 57.1%; Pred. No. 7.4e+02;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 6 PECTILGP 12  
: ||: ||  
Db 4 YECRMGP 10

RESULT 38  
AAU05348  
ID AAU05348 standard; peptide; 20 AA.

XX AAU05348;  
XX

DT 24-OCT-2001 (first entry)

DE R1 and R2 peptide #42 useful as erythropoietin receptor agonist.

XX Human; erythropoietin receptor; EPO-R; EPO agonist; EPO deficiency;  
KM renal failure; anaemia; chronic inflammatory disease; autoimmune disease;  
KW malignancy; red blood count.

XX Homo sapiens.

XX WO200138342-A2.

XX 31-MAY-2001.

XX 24-NOV-2000; 2000WO-US032224.

XX 24-NOV-1999; 99US-00449064.

XX (GLAX ) GLAXO GROUP LTD.

XX Balu P;

XX WPI; 2001-417749/44.

XX Synthesizing peptide dimer useful as erythropoietin receptor agonist by  
PT binding linking group with functional groups as initiation sites for  
PT peptide synthesis to support and synthesizing peptide segments.

XX Disclosure; Fig 1; 43pp; English.

XX The present sequence for potential R1 and R2 peptide #42 can be used to  
CC form a peptide dimer that binds and activates the erythropoietin receptor  
CC (EPO-R). Various possible peptide sequences for R1 and R2 (AAU05301-  
CC AAU05393) are described in the present invention. Also described is a  
CC method for synthesizing such peptide dimers which act as EPO-R agonists.  
CC The method is useful for synthesizing peptide dimers which are useful, in  
CC vitro, as tools for understanding the biological role of EPO, in the  
CC development of other compounds that bind to EPO-R, as commercial research  
CC reagents for various medical research and diagnostic applications, for  
CC detecting EPO receptors on living cells, for treatment of disorders  
CC associated with a deficiency of EPO, such as end-stage renal  
CC failure/dialysis, anaemia associated with AIDS and chronic inflammatory  
CC diseases, autoimmune diseases and malignancies, and for boosting the red  
CC blood count of a patient prior to surgery

XX Sequence 20 AA;

Query Match 43.3%; Score 29; DB 4; Length 20;  
Best Local Similarity 42.9%; Pred. No. 7.4e+02;  
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 6 PECTILGP 12  
: ||: ||  
Db 4 YSCLMGP 10

RESULT 39  
AAU05381  
ID AAU05381 standard; peptide; 20 AA.

XX AAU05381;

DT 24-OCT-2001 (first entry)

DE R1 and R2 peptide #75 useful as erythropoietin receptor agonist.

XX Human; erythropoietin receptor; EPO-R; EPO agonist; EPO deficiency;  
KM renal failure; anaemia; chronic inflammatory disease; autoimmune disease;  
KW malignancy; red blood count.

XX Homo sapiens.

XX WO200138342-A2.

[illegible]

Pt	Firat H, Langlade-Demoyan P, Vilmer E, Lemonnier F, Rohrllich P;
Pt	Yocunda P;
Dx	WP1; 2002-471825/50.
Pt	New mutated peptide from fusion protein TEL/AML1, useful for vaccination
Pt	against acute lymphoblastic leukemia, also related nucleic acid and
Pt	transfected tumor cells.
Pt	
Pt	Example 1; Page 20; 47pp; French.
Sq	
Cc	The present invention relates to mutated immunogenic peptides (ABB83233-
Cc	ABB83238), derived from wild-type human fusion protein TEL/AML1 peptide
Cc	R9M (TEL: Translocation BRS Leukaemia; AML1: Acute Myeloid Leukemia-1,
Cc	ABB83232). The mutated immunogenic peptides can induce an immune response
Cc	against development of lymphoblastic tumour cells, specifically B-type
Cc	acute lymphoblastic leukaemia (ALL) cells associated with the t(12/21)
Cc	translocation (TEL is located on chromosome 12 and AML1 is located on
Cc	chromosome 21). The present peptide was used in an example from the
Cc	invention
Sq	
Sq	Sequence 9 AA;
Cy	
Cy	Query Match                      41.8%; Score 28; DB 5; Length 9;
Cy	Best Local Similarity    100.0%; Pred.No. 2e+06;
Cy	Matches       5; Conservative     0; Mismatches     0; Indels       0; Gaps
Cy	7 ECITG 11
Cy	
Cy	Db               4 ECITG 8
Result	41
ID	ABB83232
AC	ABB83232 standard; peptide; 9 AA.
XX	
AC	ABB83232;
XX	
DT	19-AUG-2002 (first entry)
DE	
DE	Wild-type human TEL/AML1 fusion protein peptide R9M.
KX	
KX	Human, TEL/AML1 fusion protein; cytosatic; immunogenic peptide;
KW	Lymphoblastic tumour; B-type acute lymphoblastic leukaemia; TEL;
KW	Translocation BRS leukaemia; AML1; Acute Myeloid Leukemia-1.
XX	
OS	Homo sapiens.
PN	
PN	WO200244202-A2.
XX	
PD	06-JUN-2002.
XX	
PF	29-NOV-2001; 2001MO-FR003779.
XX	
PR	01-DEC-2000; 2000CA-02325666.
XX	
PA	(INSP ) INST PASTEUR.
PA	(INSRM ) INSERM INST NAT SANTE & RECH MEDICALE.
XX	(ASSI-) ASSISTANCE PUBLIQUE HOPITAUX PARIS.
XX	
PI	Firat H, Langlade-Demoyan P, Vilmer E, Lemonnier F, Rohrllich P;
PI	Yocunda P;
XX	
DR	WP1; 2002-471825/50.
DR	N-PSDB; ABN83397.
PT	New mutated peptide from fusion protein TEL/AML1, useful for vaccination
PT	against acute lymphoblastic leukemia, also related nucleic acid and
PT	transfected tumor cells.
XX	
XX	Claim 1; Page 6; 47pp; French.
CC	The present invention relates to mutated immunogenic peptides (ABB83233-



CC ABB83238), derived from the present peptide: wild-type human fusion  
CC protein TR/AML peptide R9M (TR: Translocation B15 Leukaemia; AML1:  
CC Acute Myeloid Leukemia-1). The mutated immunogenic peptides can induce  
CC an immune response against development of lymphoblastic tumour cells,  
CC specifically B-type acute lymphoblastic leukaemia (ALL) cells associated  
CC with the t(12;21) translocation (TR) is located on chromosome 12 and AML1  
CC is located on chromosome 21)  
XX  
XX  
SQ Sequence 9 AA;  
Query Match 41.8%; Score 28; DB 5; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 7 ECTIG 11  
DB 4 ECTIG 8  
RESULT 42  
ADCS9364  
ID ADCS9364 standard; peptide; 9 AA.  
XX  
XX ADCS9364;  
AC  
XX  
XX 18-DEC-2003 (first entry)  
DT  
XX  
XX GST binding peptide #11.  
DE  
XX  
XX Glutathione-S-transferase pI; GST pI; GST pI inhibitory peptide;  
KM inhibitory peptide; drug metabolising enzyme; GST binding protein;  
KM drug resistance; cancer; cytotoxic effect; cytostatic.  
XX  
XX  
OS Unidentified.  
XX  
XX JP2002371100-A.  
PN  
XX  
XX 26-DEC-2002.  
PD  
XX  
XX 11-JUN-2001; 2001JP-00176265.  
PF  
XX  
XX 11-JUN-2001; 2001JP-00176265.  
PR  
XX  
XX (TAMA-) TAMA TLO KK.  
PA  
XX  
XX WPI; 2003-472866/45.  
DR  
XX  
XX Glutathione-S-transferase (GST) binding peptides and a process for their  
PT preparation for GST-pai inhibitors without substantial adverse reaction.  
PT  
XX  
XX Claim 2; Page 2; 6pp; Japanese.  
PS  
XX  
XX The invention discloses glutathione-S-transferase (GST) pI inhibitory  
CC peptides which are useful as drug metabolising enzymes. The GST binding  
CC proteins are prepared by culture of a transformant obtained from GST  
CC plasmid and purification of resultant GST binding peptide,  
CC preparation of a peptide library, recovery of a phage expressing GST  
CC binding peptide, purification of the phage from single plaque and  
CC determination of the peptide sequence of GST binding phage. The agents  
CC overcome drug resistance of cancers. The peptides improvement of drug  
CC sensitivity of cancer cells providing elevated cytotoxic effect. The  
CC sequence presented is a GST binding peptide of the invention.  
XX  
XX  
SQ Sequence 9 AA;  
Query Match 41.8%; Score 28; DB 7; Length 9;  
Best Local Similarity 80.0%; Pred. No. 2e+06;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 8 CILGP 12  
DB 1 CILGP 5

RESULT 43  
ADG20335  
ID ADG20335 standard; peptide; 9 AA.  
XX  
XX  
XX ADG20335;  
AC  
XX  
XX 11-MAR-2004 (first entry)  
DT  
XX  
XX  
DE Antigenic peptide SEQ ID NO:11.  
XX  
XX  
XX double-chimeric beta 2-microglobulin; antigenic peptide;  
KM antigen-presenting cell; beta 2-microglobulin;  
KM major histocompatibility complex class I epitope; MHC class I epitope;  
KM cytostatic; antibacterial; virucide; fungicide; protozoacide; vaccine;  
KM cytotoxic T lymphocyte induction; cancer; pathogenic organism;  
KM tumour associated antigen; pathogenic antigen.  
XX  
XX  
XX Synthetic.  
OS  
XX  
XX WO2003106616-A2.  
PN  
XX  
XX 24-DEC-2003.  
PD  
XX  
XX 12-JUN-2003; 2003WO-11000501.  
PF  
XX  
XX 12-JUN-2002; 2002US-0388273P.  
PR  
XX  
XX (GAVI-) GAVISH-GALILEE BIO APPL LTD.  
PA  
XX  
XX Gross G, Margalit A;  
PI  
XX  
XX WPI; 2004-071554/07.  
DR  
XX  
XX Novel double-chimeric beta2-microglobulin polynucleotide useful for  
PT treating cancer, comprising sequence encoding polypeptide capable of  
PT presentation of antigenic peptides.  
PT  
XX  
XX Claim 16; SEQ ID NO 11; 86pp; English.  
PS  
XX  
XX The present invention describes a double-chimeric beta 2-microglobulin  
CC polynucleotide (I) comprising a sequence encoding a polypeptide (II) that  
CC is capable of high level presentation of antigenic peptides on antigen-  
CC presenting cells, where (II) comprising a beta 2-microglobulin molecule  
CC that is linked through its carboxyl terminal to a polypeptide stretch  
CC which allows the anchorage of the beta 2-microglobulin molecule to the  
CC cell membrane, and through its amino terminal to an antigenic peptide  
CC comprising major histocompatibility complex (MHC) class I epitope. The  
CC antigenic peptide is not related to an autoimmune disease. Also  
CC described: (1) an expression vector (III) comprising (I) and is a  
CC recombinant viral vector; (2) an antigen-presenting cell (IV) transfected  
CC with (I); (3) a DNA vaccine (V) comprising a (I) or (III); (4) a cellular  
CC vaccine (VI) for the prevention or treatment of cancer comprising (IV)  
CC which express (I) or tumour cells transfected with (II), where the cells  
CC have been pulsed with an antigenic peptide derived from one tumour  
CC associated antigen; and (5) a pharmaceutical composition (VII) comprising  
CC (I), (III) or (IV) as an active ingredient and carrier. (I) has  
CC cytostatic, antibacterial, virucide, fungicide and protozoacide  
CC activities, and can be used in vaccines, and for inducing cytotoxic T  
CC lymphocytes. (I) and (V) can be used for the prevention or treatment of  
CC cancer or for a disease caused by a pathogenic organism. (VI) is useful  
CC for prevention or treatment of cancer, or disease caused by a pathogenic  
CC organism, where (VI) presents one tumour associated antigen, or  
CC pathogenic antigen. (VI) is also useful for immunising a mammal against a  
CC tumour-associated antigen or a disease caused by a pathogenic organism,  
CC which involves immunising the mammal with (VI). (I) is useful for  
CC inducing class I-restricted CTL response in a mammal. The present  
CC sequence is used in the exemplification of the present invention.  
XX  
XX  
SQ Sequence 9 AA;  
Query Match 41.8%; Score 28; DB 8; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2e+06;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 ECTIG 11  
 |||||  
 Db 4 ECTIG 8

RESULT 44  
 ADX08674  
 ID ADX08674 standard; peptide; 9 AA.

AC ADX08674;  
 XX  
 XX  
 XX 21-APR-2005 (first entry)  
 XX  
 DE HLA class I restricted epitope (derived from fusion protein) peptide #10.

KW vaccine; infection; viral infections; vitruclide; bacterial infection;  
 KW antibacterial; yeast infection; fungicide; fungal infection;  
 KW protozoal infection; protozoacide; cancer; cytostatic; melanoma;  
 KW lung tumor; colon tumor; breast tumor; leukemia; autoimmune disease;  
 KW multiple sclerosis; neuroprotective; rheumatoid arthritis; antiarthritic;  
 KW antineumatic; systemic lupus erythematosus; antiinflammatory;  
 KW dermatological; immunosuppressive.

XX  
 OS Unidentified.  
 XX  
 PN WO2005011730-A1.  
 XX  
 PD 10-FEB-2005.  
 XX  
 PF 30-JUL-2004; 2004WO-GB003285.  
 XX  
 PR 01-AUG-2003; 2003GB-00018096.

XX  
 PA (UNIO ) QUEEN MARY & WESTFIELD COLLEGE.  
 XX  
 PI Wang P, Li S;  
 XX  
 DR WPI; 2005-152360/16.

XX  
 PT New vaccine composition comprises inverted microsomes from animal cells  
 PT with an externally disposed peptide antigen and a protein of the Major  
 PT Histocompatibility Complex (MHC), useful for treating or preventing, e.g.  
 PT cancer.

PS Disclosure; Page 60; 83pp; English.  
 XX  
 XX The invention comprises a vaccine composition that consists of isolated  
 CC inverted microsomes from an animal cell (or its membrane fragments), in  
 CC association with an externally disposed peptide antigen and a protein of  
 CC the MHC. The vaccine composition of the invention is useful for the  
 CC prophylaxis or treatment of: infection (e.g. viral, bacterial, yeast,  
 CC cancer, breast cancer or leukemia), autoimmune disease (e.g. multiple  
 CC sclerosis, rheumatoid arthritis or systemic lupus erythematosus). The  
 CC present amino acid sequence represents an HLA class I restricted epitope  
 CC derived from a fusion protein.

XX  
 SQ Sequence 9 AA;

Query Match 41.8%; Score 28; DB 9; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 2e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 ECTIG 11  
 |||||  
 Db 4 ECTIG 8

RESULT 45  
 AAW98996  
 ID AAW98996 standard; peptide; 10 AA.

XX  
 AC AAW98996;  
 XX  
 DT 11-MAY-1999 (first entry)  
 XX  
 DE I domain peptide P1.  
 XX  
 KW Cyclic integrin binding peptide; integrin alpha-2i domain; inhibitor;  
 KW collagen I; collagen IV; laminin-1; cell migration; cancer;  
 KW cardiovascular disease; periodontal disease.

XX  
 OS Synthetic.  
 XX  
 PN WO9902551-A1.  
 XX  
 PD 21-JAN-1999.  
 XX  
 PF 09-JUL-1998; 98WO-FI000579.  
 XX  
 PR 11-JUL-1997; 97US-00893526.

XX  
 PA (HEIN/) HEINO J.  
 PA (IVAS/) IVASKA J.  
 PA (KAP/) KAPRYLAE J.

XX  
 PI Heino J, Ivaaka J, Kaepylae J;  
 XX  
 DR WPI; 1999-120775/10.

XX  
 PT Cyclin integrin binding peptides - used to inhibit integrin-dependant  
 PT cell migration.  
 XX  
 PS Example 3; Page 24; 59pp; English.

XX  
 CC The present sequence invention describes cyclic integrin binding peptides  
 CC comprising the amino acid sequence RKK, preferably RKKH. Also described  
 CC in the present invention are: (1) a cyclic peptide comprising the amino  
 CC acid sequence XIRKKHX2Xn where X is any amino acid and n=1-4; (2) a  
 CC cyclic integrin binding peptide comprising the amino acid sequence  
 CC CTRKKHNC or CTRKKHNAQC; (3) a pharmaceutical composition comprising one  
 CC of the above integrin binding peptides; and (4) a binding assay for  
 CC identifying integrin binding agents, comprising: (a) biotinylating the  
 CC integrin binding agent to be assayed; (b) reacting the biotinylated agent  
 CC with an immobilised recombinant alpha 2i domain or domain-derived  
 CC peptide in conditions suitable for binding; (c) washing the solid  
 CC support carrying the bound agent; (d) adding a labelled biotin-binding  
 CC agent; and (e) detecting any bound integrin binding agent. The integrin  
 CC binding peptides can be used for inhibiting integrins. They can also be  
 CC used for inhibiting integrin-dependent cell migration, such as associated  
 CC with cancer, cardiovascular disease or a periodontitis condition. They can  
 CC also be used for inhibiting the adhesion of platelets to collagen or  
 CC collagen induced platelet aggregation in a patient. The present sequence  
 CC represents a peptide from the present invention

XX  
 SQ Sequence 10 AA;

Query Match 41.8%; Score 28; DB 2; Length 10;  
 Best Local Similarity 62.5%; Pred. No. 5.6e+02;  
 Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 DEKNSFEC 8  
 |||||  
 Db 3 DESNSIYC 10

RESULT 46  
 ABR91275  
 ID ABR91275 standard; peptide; 13 AA.

AC ABR91275;  
 XX  
 DT 10-SEP-2003 (first entry)  
 XX

DE P. papataei salivary polypeptide immunogenic peptide SEQ ID NO:109.  
 XX  
 XX Phlebotomus papataei; salivary polypeptide; antigenic; immunogenic;  
 KM protozoacide; immunostimulant; vaccine; immune response; Leishmaniasis.  
 XX  
 OS Phlebotomus papataei.  
 OS Synthetic.  
 XX  
 PN WO2002109324-A2.  
 XX  
 PD 27-DEC-2002.  
 XX  
 PF 18-JUN-2002; 2002WO-US019663.  
 XX  
 PR 19-JUN-2001; 2001US-0299391P.  
 XX  
 PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 XX  
 PI Valenzuela JG, Belkaid Y, Kamhawi S, Sacks D, Ribeiro JMC;  
 XX  
 DR WPI; 2003-157000/15.  
 XX  
 PT Novel isolated salivary polypeptide of Phlebotomus papataei, useful for  
 PT producing an immune response in a subject or for preventing Leishmaniasis  
 PT in a subject.  
 XX  
 PS Claim 10; Page 93; 279pp; English.  
 XX  
 CC The present invention describes an isolated salivary polypeptide (I), of  
 CC Phlebotomus papataei. Also described: (1) an isolated nucleic acid (II)  
 CC encoding (I); (2) an isolated fragment (III) of (II), where the fragment  
 CC encodes the polypeptide fragment specific for a polypeptide such as  
 CC Phlebotomus papataei salivary polypeptide (PSP) 12, PSP14, PSP15,  
 CC PSP30, PSP32, PSP36, PSP42 or PSP44; (3) an isolated antigenic or  
 CC immunogenic fragment (IV) of (I); (4) a nucleic acid (V) that hybridises  
 CC under stringent conditions to (II); (5) a vector (VI) comprising (II) or  
 CC (III); and (6) a composition (VII) comprising (I) or its fragment, (IV)  
 CC or (VI), and a pharmaceutically acceptable carrier. (I) has protozoacide  
 CC and immunostimulant activities, and can be used in vaccines. (VII) is  
 CC useful for producing an immune response in a subject or for preventing  
 CC Leishmaniasis in a subject. (II) is also useful for preventing  
 CC Leishmaniasis in a subject. (VI) is useful as a vaccine. ACC79987 to  
 CC ACC79999 and ABR91176 to ABR92046 represent sequences used in the  
 CC exemplification of the present invention  
 CC  
 XX  
 SQ Sequence 13 AA;  
 Query Match 41.8%; Score 28; DB 6; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 7.3e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 6 FPCIL 10  
 XX  
 DB 5 FPCIL 9  
 XX  
 RESULT 47  
 AB000601 standard; peptide; 14 AA.  
 ID AB000601  
 XX  
 AC AB000601,  
 XX  
 DT 05-SEP-2002 (first entry)  
 XX  
 DE B lymphocyte stimulator protein binding peptide #45.  
 XX  
 KM B lymphocyte stimulator protein binding protein; BlyS; immune disease;  
 KM allergy; proliferative disease; infectious disease; arteriosclerosis;  
 KM inflammatory disorder; hypergammaglobulinaemia; blood clotting;  
 KM leukaemia; graft-versus-host disease; neurodegenerative disease;  
 KM immunosuppressive; nephrotropic; antineumatic; antiarthritic;  
 KM neuroprotective; cytotoxic; immunostimulant; antitumour; anti-HIV;  
 KM antilesthetic; antiallergic; thyromimetic; antianemic; haemostatic;

KM dermatological; antiinflammatory; cardiac; ophthalmological; uropathic;  
 KM antidiabetic; antithyroid; antidepressant; hepatotropic.  
 XX  
 OS Unidentified.  
 OS  
 XX  
 PN WO200216411-A2.  
 XX  
 PD 28-FEB-2002.  
 XX  
 PF 17-AUG-2001; 2001WO-US025850.  
 XX  
 PR 18-AUG-2000; 2000US-0226700P.  
 XX  
 PA (HDMA-) HUMAN GENOME SCI INC.  
 XX  
 PI Belzer JP, Potter DM, Fleming TL, Rosen CA;  
 XX  
 DR WPI; 2002-499775/53.  
 XX  
 PT The treatment of various diseases e.g. rheumatoid arthritis, comprises  
 PT administering B lymphocyte stimulator binding polypeptide.  
 XX  
 PS Claim 70; Page 192; 387pp; English.  
 XX  
 CC The present invention relates to the treatment, prevention or  
 CC amelioration of a disease or disorder associated with: aberrant B  
 CC lymphocyte stimulator (BlyS), BlyS receptor expression or activity; cells  
 CC of hematopoietic origin; or proliferative disease; and reducing,  
 CC inhibiting or stimulating immunoglobulin production, B cell proliferation  
 CC and graft rejection involving administration of BlyS binding polypeptide.  
 CC The BlyS binding polypeptides are used in the treatment, prevention or  
 CC amelioration of diseases such as immune system diseases, proliferative  
 CC diseases, diseases of cells of hematopoietic origin, graft rejection,  
 CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,  
 CC hypergammaglobulinaemia, blood clotting disorders, ischaemia, and  
 CC neurodegenerative diseases. The present sequence is a B lymphocyte  
 CC stimulator protein binding peptide  
 CC  
 XX  
 SQ Sequence 14 AA;  
 Query Match 41.8%; Score 28; DB 5; Length 14;  
 Best Local Similarity 57.1%; Pred. No. 7.8e+02;  
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 QY 6 FPCILGP 12  
 XX  
 DB 2 FPCILGP 8  
 XX  
 RESULT 48  
 ABG33462 standard; peptide; 14 AA.  
 ID ABG33462  
 XX  
 AC ABG33462;  
 XX  
 DT 15-UTL-2002 (first entry)  
 XX  
 DE B lymphocyte stimulator (BlyS) binding peptide #50.  
 XX  
 KM B lymphocyte stimulator protein; B lymphocyte stimulator binding peptide;  
 KM BlyS; biological fluid; serum; plasma; lymph; blood; urine; spinal fluid;  
 KM synovial fluid; saliva; mucus.  
 XX  
 OS Synthetic.  
 OS  
 XX  
 PN WO200216412-A2.  
 XX  
 PD 28-FEB-2002.  
 XX  
 PF 17-AUG-2001; 2001WO-US025891.  
 XX  
 PR 18-AUG-2000; 2000US-0226489P.  
 XX

PA (DYAX-) DYAX CORP.  
 XX Belzer JP, Potter MD, Fleming TJ, Ladner RC;  
 XX WPI, 2002-351647/38.  
 DR  
 XX New B-lymphocyte stimulator binding polypeptide useful in detecting or  
 PT isolating Blys or Blys-like polypeptide complexes a specified amino acid  
 PT sequence.  
 XX  
 PS Claim 13; Page 72; 269pp; English.  
 XX  
 CC The invention relates to a B lymphocyte stimulator (Blys) binding  
 CC polypeptide. Blys binding peptides bind Blys or Blys-like proteins  
 CC reversibly or irreversibly. The binding peptides are used in detection,  
 CC isolation and/or purification of Blys in a solution such as water or a  
 CC buffer solution, as well as any fluid and/or cell obtained from an  
 CC individual biological fluid, body tissue, body cell, cell line, tissue  
 CC culture or other source containing Blys or Blys-like polypeptides. The  
 CC biological fluids include sera, plasma, lymph, blood, blood fraction,  
 CC urine, synovial fluid, spinal fluid, saliva and mucous. Sequences  
 CC ABG33406-33415, ABG33423-33575, ABG33588-33846, ABG33848-33850 and  
 CC ABG33852-33862 represent Blys binding peptides of the invention  
 CC  
 SQ Sequence 14 AA;  
 XX  
 Query Match 41.8%; Score 28; DB 5; Length 14;  
 Best Local Similarity 57.1%; Pred. No. 7.8e+02;  
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 Qy 6 FPCILGP 12  
 Db 2 FDCCLKP 8  
 XX  
 RESULT 49  
 ADB48057  
 ID ADB48057 standard; protein; 14 AA.  
 XX  
 AC ADB48057;  
 XX  
 DT 04-DEC-2003 (first entry)  
 XX  
 DE Novel human secreted protein associated polypeptide #136.  
 XX  
 KW human; secreted protein; insulin; haemoglobin S; haemoglobin B;  
 KW superoxide; SOD; catalase; DNA repair protein; oncogene;  
 KW tumour suppressor; tumour necrosis factor; TNF; inflammation;  
 KW blood vessel growth inhibition; immune response; immune system disorder;  
 KW hyperproliferative disorder; neoplasm; cardiovascular disorder;  
 KW peripheral artery disease; limb ischaemia; arterio-arterial fistula;  
 KW arteriovenous fistula; congenital heart defect;  
 KW neovascularisation disorder; wound healing;  
 KW epithelial cell proliferation; neurological disease; Alzheimer's disease;  
 KW Parkinson's disease; Huntington's disease; mania; dementia;  
 KW infectious disease.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US200305443-A1.  
 XX  
 PD 20-MAR-2003.  
 XX  
 PF 04-OCT-2001; 2001US-00966730.  
 XX  
 XX 05-AUG-1997; 97US-0054798P.  
 PR 05-AUG-1997; 97US-0054803P.  
 PR 05-AUG-1997; 97US-0054804P.  
 PR 05-AUG-1997; 97US-0054806P.  
 PR 05-AUG-1997; 97US-0054807P.  
 PR 05-AUG-1997; 97US-0054808P.  
 PR 05-AUG-1997; 97US-0054809P.  
 PR 05-AUG-1997; 97US-0055309P.

PR 05-AUG-1997; 97US-0055310P.  
 PR 05-AUG-1997; 97US-0055311P.  
 PR 05-AUG-1997; 97US-0055312P.  
 PR 05-AUG-1997; 97US-0055386P.  
 PR 18-AUG-1997; 97US-0055970P.  
 PR 18-AUG-1997; 97US-0055986P.  
 PR 19-AUG-1997; 97US-0056364P.  
 PR 19-AUG-1997; 97US-0056365P.  
 PR 19-AUG-1997; 97US-0056366P.  
 PR 19-AUG-1997; 97US-0056367P.  
 PR 19-AUG-1997; 97US-0056370P.  
 PR 19-AUG-1997; 97US-0056371P.  
 PR 19-AUG-1997; 97US-0056557P.  
 PR 19-AUG-1997; 97US-0056563P.  
 PR 19-AUG-1997; 97US-0056731P.  
 PR 19-AUG-1997; 97US-0056732P.  
 PR 04-AUG-1998; 98WO-08016235.  
 PR 04-FEB-1999; 99US-00244112.  
 PR 06-OCT-2000; 2000US-0238291P.  
 PR 01-FEB-2001; 2001US-00774639.  
 XX  
 PA (RUBE/) RUBEN S M.  
 PA (SOP/) SOPPET D R.  
 PA (EBNE/) EBNER R.  
 PA (OLSE/) OLSEN H S.  
 PA (YOUN/) YOUNG P E.  
 PA (GREE/) GREENE J M.  
 PA (FERR/) FERRIE A M.  
 PA (YUOJ/) YU G.  
 PA (NIJU/) NI J.  
 PA (ROSE/) ROSEN C A.  
 PA (BREM/) BREWER L A.  
 PA (JANA/) JANAT F.  
 PA (BIRS/) BIRSE C E.  
 XX  
 PI Ruben SM, Soppet DR, Ebner R, Olsen HS, Young PE, Greene JM;  
 PI Ferrie AM, Yu G, Ni J, Rosen CA, Brewer LA, Janat F, Birse CE;  
 XX WPI; 2003-695903/66.  
 XX  
 DR  
 XX  
 PT Novel human secreted proteins useful for treating and/or diagnosing  
 PT disorders of immune system, cardiovascular disorders such as peripheral  
 PT artery disease, neurological diseases such as Alzheimer's disease.  
 XX  
 PS Disclosure; Page 61; 333pp; English.  
 XX  
 CC The invention relates to novel human secreted proteins. The protein is  
 CC useful for preventing, treating or ameliorating a medical condition. The  
 CC protein is useful for diagnosing a pathological condition or  
 CC susceptibility to a pathological condition in a subject. The protein is  
 CC useful for identifying a binding partner. The nucleic acid is useful for  
 CC diagnosing pathological condition or a susceptibility to pathological  
 CC condition in a subject. The protein is useful as reagents for  
 CC differential identification of the tissues or cell types present in a  
 CC biological sample. The protein can be administered to patients having  
 CC absent or decreased levels of polypeptides e.g. insulin, to supplement  
 CC for haemoglobin B, superoxide (SOD), catalase, DNA repair protein, to  
 CC inhibit the activity of a polypeptide e.g. an oncogene or tumour  
 CC suppressor, to activate the activity of polypeptide e.g. by binding to a  
 CC receptor, to reduce the activity of membrane bound receptor by competing  
 CC with it for free ligand e.g. soluble tumour necrosis factor (TNF)  
 CC receptors used in reducing inflammation, or to bring about a desired  
 CC response e.g. blood vessel growth inhibition, enhancement of immune  
 CC response to proliferative cells or tissues. The protein and the nucleic  
 CC acid are useful for treating, preventing, detecting, diagnosing disorders  
 CC of immune system involving abnormal growth of specific types of cells as  
 CC well as of other cell types where expression has been observed. The  
 CC protein, the nucleic acid and antibodies are useful for treating,  
 CC preventing and/or diagnosing diseases, disorders and/or conditions of  
 CC immune system, hyperproliferative disorders including neoplasms,  
 CC cardiovascular disorders (such as peripheral artery disease, limb  
 CC ischaemia, arterio-arterial fistula, arteriovenous fistula, congenital

CC heart defects, etc), neovascularisation disorders, wound healing and  
 CC epithelial cell proliferation, neurological diseases (such as Alzheimer's  
 CC disease, Parkinson's disease, Huntington's disease, mania, dementia,  
 CC etc), infectious diseases caused by virus, bacteria, fungi, etc. The  
 CC present sequence represents the amino acid sequence of a novel human  
 CC secreted protein associated polypeptide.

SO Sequence 14 AA;

Query Match 41.8%; Score 28; DB 7; Length 14;  
 Best Local Similarity 55.6%; Pred. No. 7.8e+02;  
 Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 3 KNSPECTIG 11  
 |  
 3 KQDLHCITG 11

RESULT 50

ADJ55612 standard; protein; 14 AA.

ADJ55612/

06-MAY-2004 (first entry)

Novel human secreted protein fragment #136.

neuroprotective; nootropic; antiparkinsonian; anticonvulsant;  
 antidiabetic; antirheumatic; antiarthritic; dermatological;

antiinflammatory; immunosuppressive; antichyroid; antianemic;  
 vasotropic; anti-HIV; hepatotropic; vitruclide; antibacterial; fungicide;

antiparasitic; muscular; gynecological; gastrointestinal; respiratory;  
 cardiovascular; litholytic; cytoskeletal; antiarrhythmic; cardiac;

nephrotropic; litholytic; cytoskeletal; gene therapy; neural disorder;  
 Alzheimer's disease; Parkinson's disease; Huntington's chorea;

amyotrophic lateral sclerosis; multiple sclerosis;  
 immune system disorder; diabetes; rheumatoid arthritis;

systemic lupus erythematosus; autoimmune thyroiditis; haemolytic anemia;  
 inflammatory bowel disease; Crohn's disease; infectious disease;

infection; muscular disorder; reproductive disorder;  
 gastrointestinal disorder; pulmonary disorder; cardiovascular disorder;

atherosclerosis; arrhythmia; myocarditis; renal disorder;  
 acute glomerulonephritis; pyelonephritis; renal lithiasis;

hyperproliferative disorder; cancer; human.

Homo sapiens.

US2004023283-A1.

05-FEB-2004.

18-JUL-2003; 2003US-00621363.

05-AUG-1997; 97US-0054798P.  
 05-AUG-1997; 97US-0054803P.  
 05-AUG-1997; 97US-0054804P.  
 05-AUG-1997; 97US-0054806P.  
 05-AUG-1997; 97US-0054807P.  
 05-AUG-1997; 97US-0054808P.  
 05-AUG-1997; 97US-0054809P.  
 05-AUG-1997; 97US-0055309P.  
 05-AUG-1997; 97US-0055310P.  
 05-AUG-1997; 97US-0055311P.  
 05-AUG-1997; 97US-0055312P.  
 05-AUG-1997; 97US-0055386P.  
 05-AUG-1997; 97US-0055370P.  
 05-AUG-1997; 97US-0055586P.  
 05-AUG-1997; 97US-0056364P.  
 05-AUG-1997; 97US-0056365P.  
 05-AUG-1997; 97US-0056366P.  
 05-AUG-1997; 97US-0056367P.

PR 19-AUG-1997; 97US-0056370P.  
 PR 19-AUG-1997; 97US-0056371P.  
 PR 19-AUG-1997; 97US-0056557P.  
 PR 19-AUG-1997; 97US-0056563P.  
 PR 19-AUG-1997; 97US-0056731P.  
 PR 19-AUG-1997; 97US-0056732P.  
 PR 04-FEB-1999; 98WO-US016235.  
 PR 06-OCT-2000; 2000US-0238291P.  
 PR 01-FEB-2001; 2001US-00774639.  
 PR 04-OCT-2001; 2001US-00969730.

(HUMA-) HUMAN GENOME SCI INC.

PR Ruben SM, Soppet DR, Edner R, Olsen HS, Young PE, Greene JM,  
 PI Ferlie AM, Yu G, Ni J, Rosen CA, Brewer L, Janat F, Birse CB,  
 XX WPI; 2004-142651/14.

DR WPI; 2004-142651/14.

XX New human secreted proteins and nucleic acid molecules, useful for

PT detecting, preventing, diagnosing, treating or ameliorating medical

PT conditions, e.g. immune system disorders, reproductive disorders or

PT infectious diseases.

XX Disclosure; SEQ ID NO 340; 333bp; English.

PS The invention describes an isolated, secreted polypeptide comprising an

CC amino acid sequence at least 95% identical to: a polypeptide fragment,

CC domain or epitope, a full-length protein, or a secreted form of any one

CC of 97 sequences of 8-457 amino acids (I), given in the specification, or

CC the encoded sequence included in any one of the American Type Culture

CC Collection (ATCC) deposit numbers (II) given in the specification; a

CC polypeptide fragment of (I), or the encoded sequence included in (II),

CC having biological activity; or a variant, allelic variant, or a species

CC homologue of (I). The polypeptides, nucleic acid molecules and antibodies

CC are useful for detecting, preventing, diagnosing, prognosticating,

CC treating or ameliorating medical conditions such as neural disorders,

CC e.g. Alzheimer's disease, Parkinson's disease, Huntington's chorea,

CC amyotrophic lateral sclerosis or multiple sclerosis, immune system

CC disorders, e.g. diabetes, rheumatoid arthritis, systemic lupus

CC erythematosus, autoimmune thyroiditis or haemolytic anemia, inflammatory

CC or Crohn's disease, infectious diseases such as HIV infection, hepatitis

CC infection, bacterial infection, fungal infection or parasitic infection,

CC muscular disorders, reproductive disorders, gastrointestinal disorders,

CC pulmonary disorders, cardiovascular disorders, e.g. atherosclerosis,

CC arrhythmia or myocarditis, renal disorders, e.g. acute

CC glomerulonephritis, pyelonephritis or renal lithiasis, hyperproliferative

CC disorders, or cancerous diseases or conditions. The nucleic acids are

CC also useful for chromosome identification, radiation hybrid mapping or

CC long-range restriction mapping, as molecular weight markers, or as

CC hybridization or diagnostic probes. This is the amino acid sequence of a

CC novel human secreted protein fragment.

SO Sequence 14 AA;

Query Match 41.8%; Score 28; DB 8; Length 14;  
 Best Local Similarity 55.6%; Pred. No. 7.8e+02;  
 Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 3 KNSPECTIG 11  
 |  
 3 KQDLHCITG 11

RESULT 51

ADJ59893 standard; peptide; 15 AA.

ADJ59893/

02-APR-2001 (first entry)

```

DE 63B internal peptide.
XX
XX 63B protein; formicidal; toxin; carpenter; fire; argentine; pharaoh ant.
XX
OS Bacillus thuringiensis.
XX
XX EP1065275-A1.
XX
XX 03-JAN-2001.
XX
XX 22-MAY-1992; 2000EP-00114196.
XX
XX 22-MAY-1991; 91US-00703997.
XX
XX 25-NOV-1991; 91US-00797645.
XX
XX 22-MAY-1992; 92EP-00913802.
XX
XX (MYCO ) MYCOGEN CORP.
XX
XX Payne JM, Kennedy MK, Randall JB, Meler H, Vick HJ,
XX
XX WPI; 1992-400664/49.
XX
XX Controlling hymenopteran insect pests - comprises contacting insect with
XX
XX new Bacillus thuringiensis and their mutants, useful for killing partic.
XX
XX pharaoh ants.
XX
XX Example 2; Page 16; 55pp; English.
XX
XX PS The present invention relates to toxins from Bacillus thuringiensis (see
XX
XX CC AAF23793-AAF23797 and AAB59881-AAB59885). The toxins have activity
XX
XX CC against hymenopteran pests e.g. carpenter, fire, argentine and pharaoh
XX
XX CC ants. The toxins can therefore be used to produce formicidal compositions
XX
XX CC for controlling ants, which are a better alternative to chemical
XX
XX CC insecticides. The present sequence is an internal peptide from one toxin
XX
XX CC (63B) identified in the present invention
XX
XX SQ Sequence 15 AA;

Query Match 41.8%; Score 28; DB 2; Length 15;
Best Local Similarity 66.7%; Pred. No. 8.4e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DEKNSPECT 9
DB 6 DEKLSFQLI 14

RESULT 52
AAR63075
ID AAR63075 standard; peptide; 15 AA.
XX
XX AAR63075;
XX
XX AC 16-OCT-2003 (revised)
XX
XX DT 25-MAR-2003 (revised)
XX
XX DT 12-AUG-1995 (first entry)
XX
XX DE B.t. PS63B toxin internal peptide.
XX
XX KW Delta-endotoxin; crystal protein; biological control agent; Calliphorida;
XX
XX KW screw-worm; sheep blowfly; Lucilia; Phormia; Calliphora; insecticide;
XX
XX KW pesticide; B.t.
XX
XX OS Bacillus thuringiensis; isolate PS63B.
XX
XX PN WO9502694-A2.
XX
XX PD 26-JAN-1995.
XX
XX PF 13-JUL-1994; 94MO-US007902.
XX
XX PR 15-JUL-1993; 93US-00093199.
XX

```

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PA (MYCO ) MYCOGEN CORP.
XX
XX PI Hickle LA, Payne J;
XX
XX DR WPI; 1995-067338/09.
XX
XX PT Method for controlling Calliphoridae pests - specifically utilises
XX
XX PT Bacillus thuringiensis isolates or toxins.
XX
XX PS Example 2; Page 15; 50pp; English.
XX
XX CC N-terminal sequences of proteins from parasporal inclusion bodies of
XX
XX CC Bacillus thuringiensis (B.t.) isolates PS8603, PS63B, PS52A1 and PS33F2,
XX
XX CC and an internal peptide of the 63B protein, are given in AAR63071-75, and
XX
XX CC were used to design probes and primers (AA081159-77) for the isolation
XX
XX CC and cloning of B.t. genes encoding delta-endotoxins, used to control e.g.
XX
XX CC screw-worm and sheep blowfly. (Updated on 25-MAR-2003 to correct PN
XX
XX CC field.) (Updated on 16-OCT-2003 to standardise OS field)
XX
XX SQ Sequence 15 AA;

Query Match 41.8%; Score 28; DB 2; Length 15;
Best Local Similarity 66.7%; Pred. No. 8.4e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DEKNSPECT 9
DB 6 DEKLSFQLI 14

RESULT 53
AAW13880
ID AAW13880 standard; protein; 15 AA.
XX
XX AC AAW13880;
XX
XX AC 17-OCT-2003 (revised)
XX
XX DT 25-MAR-2003 (revised)
XX
XX DT 14-MAY-1997 (first entry)
XX
XX DE N-terminal peptide of protein 63B(2).
XX
XX KW Toxin; ant; Bacillus thuringiensis; hymenopteran pest; pharaoh ant;
XX
XX KW biological control; Monomorium pharaonis; delta-endotoxin; Lepidoptera;
XX
XX KW insect; N-terminal peptide.
XX
XX OS Bacillus thuringiensis; isolate PS63B.
XX
XX PN US5596071-A.
XX
XX PD 21-JAN-1997.
XX
XX PF 24-NOV-1993; 93US-00158232.
XX
XX PR 22-MAY-1991; 91US-00703977.
XX
XX PR 25-NOV-1991; 91US-00797645.
XX
XX PR 22-MAY-1992; 92US-00887980.
XX
XX PA (MYCO ) MYCOGEN CORP.
XX
XX PI Vick HJ, Meler H, Payne JM, Schwab GE, Fu J, Foncerra L;
XX
XX PI Kennedy MK, Schnef H, Randall JB;
XX
XX DR WPI; 1997-107615/10.
XX
XX PT Bacillus thuringiensis toxin - active against hymenopteran pests.
XX
XX PS Example 2; Col 19; 64pp; English.
XX
XX CC AAW13873-W13881 represent N-terminal peptides for the proteins of the
XX
XX CC invention (see AAW13872, and AAW13884-W13887). The peptides were all
XX
XX CC isolated from different Bacillus thuringiensis (B.t.) isolates. B.t. is a
XX
XX CC gram-positive, spore forming, soil bacterium, characterised by parasporal

```

CC crystalline protein inclusions. These proteins can be highly toxic to  
 CC pests, and have been used to produce insect resistant plants. The  
 CC previously isolated B. t. delta-endotoxins were mainly active against  
 CC lepidopteran insects, however the proteins of the invention are active  
 CC against hymenopteran insects. The sequences represented by AAW13888 and  
 CC AAW13871 represent the generic formulae for the toxins of the invention.  
 CC As the toxins of the invention are active against hymenopteran pests,  
 CC they can be used for the biological control of ants, particularly pharaoh  
 CC ants (Monomorium pharaonis). (Updated on 25-MAR-2003 to correct PR  
 CC field.) (Updated on 17-OCT-2003 to standardise OS field)

XX Sequence 15 AA;

Query Match 41.8%; Score 28; DB 2; Length 15;  
 Best Local Similarity 66.7%; Pred. No. 8.4e+02;  
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DEKNSPECT 9  
 DB 6 DEKLSFOLI 14

RESULT 54  
 ID AAW73115 standard; protein; 15 AA.

XX AAW73115;

DT 06-JUN-1999 (first entry)

DE B. t. toxin protein N-terminal fragment.

XX B. t. toxin; hymenopteran pest; pesticide; ant; insecticide;  
 KM paraeporal crystalline protein inclusion.

XX Bacillus thuringiensis.

PN US5824792-A.

PD 20-OCT-1998.

PF 06-MAR-1996; 96US-00611928.

PR 22-MAY-1991; 91US-00703977.

PR 25-NOV-1991; 91US-00797645.

PR 22-MAY-1992; 92US-00887980.

PR 24-NOV-1993; 93US-00158232.

XX (MYCO ) MYCOGEN CORP.

XX Payne JM, Meier H, Fonceerrada L, Schwab GE, Fu J, Vick HJ;

PI Kennedy MK, Schnepf HE, Randall JB;

DR WPI; 1998-582628/49.

XX Bacillus thuringiensis toxin proteins - useful for insecticidal activity

PT against hymenopteran pests i.e. ants.

PS Example 2; Col 19; 65pp; English.

XX This sequence is a fragment of a Bacillus thuringiensis (B. t.) toxin of

CC the invention. The toxins are lethal to a hymenopteran pest. The DNA

CC sequences are useful for the recombinant production of B. t. toxins. These

CC toxins in turn are useful as pesticides against hymenopteran (ant) pests,

CC especially fire, carpenter, Argentine and pharaoh ants. The toxins are

CC paraeporal crystalline protein inclusions that are highly specific toxins

CC to pests. The toxins are highly specific against ants, rather than e.g.

CC toxic chemicals used as insecticides which can be harmful to humans and

CC the environment in general

XX Sequence 15 AA;

Query Match 41.8%; Score 28; DB 2; Length 15;

Best Local Similarity 66.7%; Pred. No. 8.4e+02;  
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DEKNSPECT 9  
 DB 6 DEKLSFOLI 14

RESULT 55  
 ID AAB13902 standard; peptide; 15 AA.

XX AAB13902;

DT 13-NOV-2000 (first entry)

DE Internal peptide of Bacillus thuringiensis 63B protein.

XX Hymenopteran; ant; pest control; 86Q3a; 17a; 17b; 33P2; 63B.

XX Bacillus thuringiensis.

OS US6077937-A.

PN 20-JUN-2000.

PF 16-OCT-1998; 98US-00173891.

PR 22-MAY-1991; 91US-00703977.

PR 25-NOV-1991; 91US-00797645.

PR 22-MAY-1992; 92US-00887980.

PR 24-NOV-1993; 93US-00158232.

PR 06-MAR-1996; 96US-00611928.

XX (MYCO ) MYCOGEN CORP.

XX Meier H, Kennedy MK, Schwab GE, Fu J, Payne JM, Vick HJ;

PI Fonceerrada L, Schnepf HE, Randall JB;

DR WPI; 2000-450980/39.

XX N-PSDB; AAA65095.

XX New Bacillus thuringiensis toxins with activity against hymenopteran

PT pests such as fire ants and carpenter ants, conform to a specific generic

PT formula and have a specific amino acid sequence.

XX Example 2; Col 20; 67pp; English.

XX The present invention relates to novel Bacillus thuringiensis toxins with

CC hymenopteran activity. Preparations containing protein from Bacillus

CC thuringiensis were tested for toxicity to ants. The N-terminal amino

CC acids of toxic proteins were then sequenced. The present sequence is an

CC internal peptide of the 65B protein. These sequences were used to design

CC genes. The toxic proteins can be used to control pests such as fire ants,

CC carpenter ants, Argentine ants and pharaoh ants. The proteins can also be

CC used for producing transgenic plants that are resistant to attack by

CC ants. The proteins are a safe and effective biological control agent

CC against ant pests

XX Sequence 15 AA;

Query Match 41.8%; Score 28; DB 3; Length 15;

Best Local Similarity 66.7%; Pred. No. 8.4e+02;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DEKNSPECT 9

DB 6 DEKLSFOLI 14

RESULT 56

AAU10365

```

ID AAU10365 standard; peptide; 15 AA.
XX
XX AAU10365;
AC
XX 14-FEB-2002 (first entry)
DT
XX Bacillus thuringiensis delta-endotoxin PS63B, internal sequence.
DE
XX Bacillus thuringiensis.
XX
XX EP1143004-A2.
XX
XX 10-OCT-2001.
XX
XX 04-JUN-1991; 2001BP-00102789.
XX
XX 11-JUN-1990; 90US-00535810.
XX
XX 24-JUL-1990; 90US-00557246.
XX
XX 27-JUL-1990; 90US-00558738.
XX
XX 10-AUG-1990; 90US-00565544.
XX
XX 14-MAR-1991; 91US-00669126.
XX
XX 27-MAR-1991; 91US-00675772.
XX
XX 03-MAY-1991; 91US-00693018.
XX
XX 04-JUN-1991; 91BP-00305047.
XX
XX (MYCO ) MYCOGEN CORP.
XX
XX Narva KE, Payne JM, Schwab GR, Hickie LA, Galasan T, Sick AJ;
PI MPI; 2002-043040/06.
XX
XX Bacillus thuringiensis isolate encoding a toxin active against nematodes.
XX
XX Claim 2; Page 47; 47pp; English.
XX
XX The invention relates to a Bacillus thuringiensis isolate (I) active
CC against nematodes, selected from strains PS167P, PS158D5, PS169E,
CC PS177F1, PS177G, PS204G4, and PS204G6. (I) comprises a toxin encoded by
CC (II). Contacting nematodes with (I), where the DNA (II) has been
CC transformed into a plant or other host cell, may be used to control
CC nematodes. In addition, administering a toxin, from a wild-type Bacillus
CC thuringiensis DNA, to a host harbouring a fluke, or directly to a fluke
CC may also be useful for controlling flukes. The present sequence
CC represents an internal amino acid sequence of B. thuringiensis PS63B, a
CC nematode-active delta-endotoxin as described in the invention
XX
XX
SQ Sequence 15 AA;
Query Match 41.8%; Score 28; DB 5; Length 15;
Best Local Similarity 66.7%; Pred. No. 8.4e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 DEKNSPECTI 9
Db 6 DEKLSFOLI 14
RESULT 57
ABR30097
ID ABR30097 standard; peptide; 15 AA.
XX
XX ABR30097;
AC
XX 19-MAY-2003 (first entry)
DT
XX Human cancer-related protein 74P3B3 HLA peptide #2941.
XX
XX Human; cytostatic; vaccine; cancer; immune response; HLA;
XX human leukocyte antigen.
XX

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OS Homo sapiens.
XX
XX WO200283921-A2.
XX
XX 24-OCT-2002.
XX
XX 10-APR-2002; 2002WO-US011654.
XX
XX 10-APR-2001; 2001US-0282739P.
XX
XX 10-APR-2001; 2001US-0283112P.
XX
XX 25-APR-2001; 2001US-028630P.
XX
XX (AGEN-) AGENSYS INC.
XX
XX Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
PI Morrison K, Morrison RK, Raitano AB;
XX
XX MPI; 2003-075555/07.
XX
XX New composition comprising a substance that modulates the structure of
XX proteins and polynucleotides, useful for therapeutic, prognostic and
XX diagnostic reagents for eliciting cellular or humoral immune response in
XX cancer patients.
XX
XX Claim 13; Page 468; 1021pp; English.
XX
XX The present invention relates to novel human cancer-related genes and
XX proteins (AB278120-AB278168 and ABR01789-ABR01861). The genes and
XX proteins are useful for eliciting a humoral or cellular immune response.
XX The genes are useful as probes and primers for the amplification and/or
XX detection of genes, mRNAs or their fragments, as reagents for the
XX diagnosis and/or prognosis of cancer, as coding sequences capable of
XX directing the expression of the protein, as tools for modulating or
XX inhibiting the expression of genes and/or translation of transcripts, and
XX as therapeutic agents. The proteins and peptides are useful as
XX therapeutic, prognostic and diagnostic reagents for cancer. The present
XX sequence is a human leukocyte antigen (HLA) peptide, used in an example
XX from the invention
XX
XX
SQ Sequence 15 AA;
Query Match 41.8%; Score 28; DB 6; Length 15;
Best Local Similarity 58.3%; Pred. No. 8.4e+02;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 1 DEKNSPECTICP 12
Db 2 DELISFEHVGVP 13
RESULT 58
ABR30031
ID ABR30031 standard; peptide; 15 AA.
XX
XX ABR30031;
AC
XX 19-MAY-2003 (first entry)
DT
XX Human cancer-related protein 74P3B3 HLA peptide #2875.
XX
XX Human; cytostatic; vaccine; cancer; immune response; HLA;
XX human leukocyte antigen.
XX
XX Homo sapiens.
XX
XX WO200283921-A2.
XX
XX 24-OCT-2002.
XX
XX 10-APR-2002; 2002WO-US011654.
XX
XX 10-APR-2001; 2001US-0282739P.
XX
XX 10-APR-2001; 2001US-0283112P.
XX

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PR 25-APR-2001, 2001US-0286630P.  
XX (AGEN-) AGENSYS INC.  
XX  
PI Jakobovits A, Challita-Bid PM, Paris M, Ge W, Hubert RS;  
PI Morrison K, Morrison RK, Raitano AB;  
XX  
DR WPI, 2003-075555/07.  
XX  
PT New composition comprising a substance that modulates the structure of  
PT proteins and polynucleotides, useful for therapeutic, prognostic and  
PT diagnostic reagents for eliciting cellular or humoral immune response in  
PT cancer patients.  
XX  
PS Claim 13, Page 467, 1021pp; English.  
XX  
CC The present invention relates to novel human cancer-related genes and  
CC proteins (AB278120-AB278168 and ABR01789-ABR01861). The genes and  
CC proteins are useful for eliciting a humoral or cellular immune response.  
CC The genes are useful as probes and primers for the amplification and/or  
CC detection of genes, mRNAs or their fragments, as reagents for the  
CC diagnosis and/or prognosis of cancer, as coding sequences capable of  
CC directing the expression of the protein, as tools for modulating or  
CC inhibiting the expression of genes and/or translation of transcripts, and  
CC as therapeutic agents. The proteins and peptides are useful as  
CC therapeutic, prognostic and diagnostic reagents for cancer. The present  
CC sequence is a human leukocyte antigen (HLA) peptide, used in an example  
CC from the invention  
XX  
SQ Sequence 15 AA;  
XX  
Query Match 41.8%; Score 28; DB 6; Length 15;  
Best Local Similarity 58.3%; Pred. No. 8.4e+02;  
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
QY 1 DENRSECTIGP 12  
||| |  
2 DELISFEHVGP 13  
Db  
RESULT 59  
ABR30127  
ID ABR30127 standard; peptide; 15 AA.  
XX  
AC ABR30127;  
XX  
DT 19-MAY-2003 (first entry)  
XX  
DE Human cancer-related protein 74P3B3 HLA peptide #2971.  
XX  
KW Human; cytostatic; vaccine; cancer; immune response; HLA;  
KW human leukocyte antigen.  
XX  
OS Homo sapiens.  
XX  
PN MO200283921-A2.  
XX  
PD 24-OCT-2002.  
XX  
PF 10-APR-2002, 2002MO-US011654.  
XX  
PR 10-APR-2001, 2001US-0282739P.  
PR 10-APR-2001, 2001US-0283112P.  
PR 25-APR-2001, 2001US-0286630P.  
XX  
PA (AGEN-) AGENSYS INC.  
XX  
PI Jakobovits A, Challita-Bid PM, Paris M, Ge W, Hubert RS;  
PI Morrison K, Morrison RK, Raitano AB;  
XX  
DR WPI, 2003-075555/07.  
XX  
PT New composition comprising a substance that modulates the structure of

PT proteins and polynucleotides, useful for therapeutic, prognostic and  
PT diagnostic reagents for eliciting cellular or humoral immune response in  
PT cancer patients.  
XX  
PS Claim 13, Page 469, 1021pp; English.  
XX  
CC The present invention relates to novel human cancer-related genes and  
CC proteins (AB278120-AB278168 and ABR01789-ABR01861). The genes and  
CC proteins are useful for eliciting a humoral or cellular immune response.  
CC The genes are useful as probes and primers for the amplification and/or  
CC detection of genes, mRNAs or their fragments, as reagents for the  
CC diagnosis and/or prognosis of cancer, as coding sequences capable of  
CC directing the expression of the protein, as tools for modulating or  
CC inhibiting the expression of genes and/or translation of transcripts, and  
CC as therapeutic agents. The proteins and peptides are useful as  
CC therapeutic, prognostic and diagnostic reagents for cancer. The present  
CC sequence is a human leukocyte antigen (HLA) peptide, used in an example  
CC from the invention  
XX  
SQ Sequence 15 AA;  
XX  
Query Match 41.8%; Score 28; DB 6; Length 15;  
Best Local Similarity 58.3%; Pred. No. 8.4e+02;  
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
QY 1 DENRSECTIGP 12  
||| |  
2 DELISFEHVGP 13  
Db  
RESULT 60  
ABR30078  
ID ABR30078 standard; peptide; 15 AA.  
XX  
AC ABR30078;  
XX  
DT 19-MAY-2003 (first entry)  
XX  
DE Human cancer-related protein 74P3B3 HLA peptide #2922.  
XX  
KW Human; cytostatic; vaccine; cancer; immune response; HLA;  
KW human leukocyte antigen.  
XX  
OS Homo sapiens.  
XX  
PN MO200283921-A2.  
XX  
PD 24-OCT-2002.  
XX  
PF 10-APR-2002, 2002MO-US011654.  
XX  
PR 10-APR-2001, 2001US-0282739P.  
PR 10-APR-2001, 2001US-0283112P.  
PR 25-APR-2001, 2001US-0286630P.  
XX  
PA (AGEN-) AGENSYS INC.  
XX  
PI Jakobovits A, Challita-Bid PM, Paris M, Ge W, Hubert RS;  
PI Morrison K, Morrison RK, Raitano AB;  
XX  
DR WPI, 2003-075555/07.  
XX  
PT New composition comprising a substance that modulates the structure of  
PT proteins and polynucleotides, useful for therapeutic, prognostic and  
PT diagnostic reagents for eliciting cellular or humoral immune response in  
PT cancer patients.  
XX  
PS Claim 13, Page 468, 1021pp; English.  
XX  
CC The present invention relates to novel human cancer-related genes and  
CC proteins (AB278120-AB278168 and ABR01789-ABR01861). The genes and  
CC proteins are useful for eliciting a humoral or cellular immune response.  
CC The genes are useful as probes and primers for the amplification and/or

CC detection of genes, mRNAs or their fragments, as reagents for the  
CC diagnosis and/or prognosis of cancer, as coding sequences capable of  
CC directing the expression of the protein, as tools for modulating or  
CC inhibiting the expression of genes and/or translation of transcripts, and  
CC as therapeutic agents. The proteins and peptides are useful as  
CC therapeutic, prognostic and diagnostic reagents for cancer. The present  
CC sequence is a human leukocyte antigen (HLA) peptide, used in an example  
CC from the invention  
XX  
SQ Sequence 15 AA;  
  
Query Match 41.8%; Score 28; DB 6; Length 15;  
Best Local Similarity 58.3%; Pred. No. 8.4e+02;  
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
  
QY 1 DEKNSFECITLGP 12  
DB 1 DELISFEEHVG 12  
  
RESULT 61  
ABR29975  
ID ABR29975 standard; peptide, 15 AA.  
XX ABR29975;  
AC  
XX  
XX 19-MAY-2003 (first entry)  
DT  
XX  
DE Human cancer-related protein 74P3B3 HLA peptide #2819.  
XX  
XX Human, cytosolic; vaccine; cancer; immune response; HLA;  
KW human leukocyte antigen.  
XX  
OS Homo sapiens.  
XX  
XX WO200283921-A2.  
PN  
XX  
PD 24-OCT-2002.  
XX  
XX 10-APR-2002; 2002WO-US011654.  
PP  
XX 10-APR-2001; 2001US-0282739P.  
PR 10-APR-2001; 2001US-0283112P.  
PR 25-APR-2001; 2001US-0286630P.  
XX  
XX (AGEN-) AGENSYS INC.  
PA  
XX  
XX Jakobovits A, Chailita-Eld PM, Faris M, Ge W, Hubert RS;  
PI Morrison K, Morrison RK, Raitano AB;  
XX  
XX MPI; 2003-075555/07.  
DR  
XX  
XX New composition comprising a substance that modulates the structure of  
PT proteins and polynucleotides, useful for therapeutic, prognostic and  
PT diagnostic reagents for eliciting cellular or humoral immune response in  
PT cancer patients.  
XX  
XX Claim 13; Page 466; 1021pp; English.  
PS  
XX The present invention relates to novel human cancer-related genes and  
CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and  
CC proteins are useful for eliciting a humoral or cellular immune response.  
CC The genes are useful as probes and primers for the amplification and/or  
CC detection of genes, mRNAs or their fragments, as reagents for the  
CC diagnosis and/or prognosis of cancer, as coding sequences capable of  
CC directing the expression of the protein, as tools for modulating or  
CC inhibiting the expression of genes and/or translation of transcripts, and  
CC as therapeutic agents. The proteins and peptides are useful as  
CC therapeutic, prognostic and diagnostic reagents for cancer. The present  
CC sequence is a human leukocyte antigen (HLA) peptide, used in an example  
CC from the invention  
XX  
SQ Sequence 15 AA;

Query Match 41.8%; Score 28; DB 6; Length 15;  
Best Local Similarity 58.3%; Pred. No. 8.4e+02;  
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
  
QY 1 DEKNSFECITLGP 12  
DB 1 DELISFEEHVG 12  
  
RESULT 62  
ABR30106  
ID ABR30106 standard; peptide, 15 AA.  
XX  
XX ABR30106;  
AC  
XX  
XX 19-MAY-2003 (first entry)  
DT  
XX  
DE Human cancer-related protein 74P3B3 HLA peptide #2950.  
XX  
XX Human, cytosolic; vaccine; cancer; immune response; HLA;  
KW human leukocyte antigen.  
XX  
XX Homo sapiens.  
XX  
XX WO200283921-A2.  
PN  
XX  
PD 24-OCT-2002.  
XX  
XX 10-APR-2002; 2002WO-US011654.  
PP  
XX  
XX 10-APR-2001; 2001US-0282739P.  
PR 10-APR-2001; 2001US-0283112P.  
PR 25-APR-2001; 2001US-0286630P.  
XX  
XX (AGEN-) AGENSYS INC.  
PA  
XX  
XX Jakobovits A, Chailita-Eld PM, Faris M, Ge W, Hubert RS;  
PI Morrison K, Morrison RK, Raitano AB;  
XX  
XX MPI; 2003-075555/07.  
DR  
XX  
XX New composition comprising a substance that modulates the structure of  
PT proteins and polynucleotides, useful for therapeutic, prognostic and  
PT diagnostic reagents for eliciting cellular or humoral immune response in  
PT cancer patients.  
XX  
XX Claim 13; Page 468; 1021pp; English.  
PS  
XX The present invention relates to novel human cancer-related genes and  
CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and  
CC proteins are useful for eliciting a humoral or cellular immune response.  
CC The genes are useful as probes and primers for the amplification and/or  
CC detection of genes, mRNAs or their fragments, as reagents for the  
CC diagnosis and/or prognosis of cancer, as coding sequences capable of  
CC directing the expression of the protein, as tools for modulating or  
CC inhibiting the expression of genes and/or translation of transcripts, and  
CC as therapeutic agents. The proteins and peptides are useful as  
CC therapeutic, prognostic and diagnostic reagents for cancer. The present  
CC sequence is a human leukocyte antigen (HLA) peptide, used in an example  
CC from the invention  
XX  
SQ Sequence 15 AA;  
  
Query Match 41.8%; Score 28; DB 6; Length 15;  
Best Local Similarity 58.3%; Pred. No. 8.4e+02;  
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
  
QY 1 DEKNSFECITLGP 12  
DB 1 DELISFEEHVG 12

RESULT 63  
 ABR30059 ID ABR30059 standard; peptide; 15 AA.  
 XX AC ABR30059;  
 XX OS  
 XX DN 19-MAY-2003 (first entry)  
 XX DE Human cancer-related protein 74P3B3 HLA peptide #2903.  
 XX KM Human; cytostatic; vaccine; cancer; immune response; HLA;  
 XX KW human leukocyte antigen.  
 XX OS Homo sapiens.  
 XX PA WO200283921-A2.  
 XX PN 24-OCT-2002.  
 XX PD 10-APR-2002; 2002WO-US011654.  
 XX PF 10-APR-2001; 2001US-0282739P.  
 XX PR 10-APR-2001; 2001US-0283112P.  
 XX PR 25-APR-2001; 2001US-0286630P.  
 XX PS (AGEN-) AGENSYS INC.  
 XX PI Jakobovits A, Chailita-Bid PM, Paris M, Ge W, Hubert RS,  
 PI Morrison K, Morrison RK, Raitano AB;  
 XX DR WPI; 2003-07555/07.  
 XX PT New composition comprising a substance that modulates the structure of  
 PT proteins and polynucleotides, useful for therapeutic, prognostic and  
 PT diagnostic reagents for eliciting cellular or humoral immune response in  
 PT cancer patients.  
 XX PS Claim 13; Page 467; 1021pp; English.  
 XX CC The present invention relates to novel human cancer-related genes and  
 CC proteins (AB278120-AB278168 and ABR01789-ABR01861). The genes and  
 CC proteins are useful for eliciting a humoral or cellular immune response.  
 CC The genes are useful as probes and primers for the amplification and/or  
 CC detection of genes, mRNAs or their fragments, as reagents for the  
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of  
 CC directing the expression of the protein, as tools for modulating or  
 CC inhibiting the expression of genes and/or translation of transcripts, and  
 CC as therapeutic agents. The proteins and peptides are useful as  
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present  
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example  
 CC from the invention  
 XX SQ Sequence 15 AA;  
 XX DB

Query Match 41.8%; Score 28; DB 6; Length 15;  
 Best Local Similarity 58.3%; Pred. NO. 8.4e+02;  
 Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 DENRSEFCIGP 12  
 |||||  
 1 DELISFEBHVG 12  
 DB

RESULT 64  
 ABR91283 ID ABR91283 standard; peptide; 15 AA.  
 XX AC ABR91283;  
 XX OS  
 XX DN 10-SEP-2003 (first entry)  
 XX DT P. papataasi salivary polypeptide immunogenic peptide SEQ ID NO:117.  
 XX DE

KM Phlebotomus papataasi; salivary polypeptide; antigenic; immunogenic;  
 KW protozoacide; immunostimulant; vaccine; immune response; Leishmaniasis.  
 XX OS  
 XX OS Phlebotomus papataasi.  
 XX OS Synthetic.  
 XX PN WO2002102324-A2.  
 XX PD 27-DEC-2002.  
 XX PF 18-JUN-2002; 2002WO-US019663.  
 XX PR 19-JUN-2001; 2001US-0299391P.  
 XX PS (USSH ) US DBPT HEALTH & HUMAN SERVICES.  
 XX PI Valenzuela JG, Belkaid Y, Kamhawi S, Sacks D, Ribeiro JMC;  
 XX DR WPI; 2003-157000/15.  
 XX PT Novel isolated salivary polypeptide of Phlebotomus papataasi, useful for  
 PT producing an immune response in a subject or for preventing Leishmaniasis  
 PT in a subject.  
 XX PS Claim 10; Page 95; 279pp; English.  
 XX CC The present invention describes an isolated salivary polypeptide (I), of  
 CC Phlebotomus papataasi. Also described: (1) an isolated nucleic acid (II)  
 CC encoding (I); (2) an isolated fragment (III) of (II), where the fragment  
 CC encodes the polypeptide fragment specific for a polypeptide such as  
 CC Phlebotomus papataasi salivary polypeptide (PSP) 12, PSP14, PSP15,  
 CC PSP30, PSP32, PSP36, PSP42 or PSP44; (3) an isolated antigenic or  
 CC immunogenic fragment (IV) of (I); (4) a nucleic acid (V) that hybridises  
 CC under stringent conditions to (II); (5) a vector (VI) comprising (II) or  
 CC (III); and (6) a composition (VII) comprising (I) or its fragment, (IV)  
 CC or (VI), and a pharmaceutically acceptable carrier. (I) has protozoacide  
 CC and immunostimulant activities, and can be used in vaccines. (VII) is  
 CC useful for producing an immune response in a subject or for preventing  
 CC Leishmaniasis in a subject. (II) is also useful for preventing  
 CC Leishmaniasis in a subject. (VII) is useful as a vaccine. ACC79987 to  
 CC ACC79999 and ABR91176 to ABR92046 represent sequences used in the  
 CC exemplification of the present invention  
 XX SQ Sequence 15 AA;  
 XX DB

Query Match 41.8%; Score 28; DB 6; Length 15;  
 Best Local Similarity 100.0%; Pred. NO. 8.4e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 6 FPCIL 10  
 |||||  
 5 FPCIL 9  
 DB

RESULT 65  
 ABR91282 ID ABR91282 standard; peptide; 15 AA.  
 XX AC ABR91282;  
 XX OS  
 XX DN 10-SEP-2003 (first entry)  
 XX DT P. papataasi salivary polypeptide immunogenic peptide SEQ ID NO:116.  
 XX DE  
 XX KW Phlebotomus papataasi; salivary polypeptide; antigenic; immunogenic;  
 KW protozoacide; immunostimulant; vaccine; immune response; Leishmaniasis.  
 XX OS  
 XX OS Phlebotomus papataasi.  
 XX OS Synthetic.  
 XX PN WO2002102324-A2.  
 XX PD 27-DEC-2002.  
 XX PT

```

XX 18-JUN-2002; 2002WO-US019663.
XX
XX 19-JUN-2001; 2001US-0299391P.
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Valenzuela JG, Belkaid Y, Kamhawi S, Sacke D, Ribeiro JMC;
XX WPI; 2003-157000/15.
XX
XX Novel isolated salivary polypeptide of Phlebotomus papatasi, useful for
XX producing an immune response in a subject or for preventing Leishmaniasis
XX in a subject.
XX
XX Claim 10; Page 95; 279pp; English.
XX
XX The present invention describes an isolated salivary polypeptide (I), of
XX Phlebotomus papatasi. Also described: (1) an isolated nucleic acid (II)
XX encoding (I); (2) an isolated fragment (III) of (II), where the fragment
XX encodes the polypeptide fragment specific for a polypeptide such as
XX Phlebotomus papatasi salivary polypeptide (PSP) 12, PSP14, PSP15,
XX PSP30, PSP32, PSP36, PSP42 or PSP44; (3) an isolated antigenic or
XX immunogenic fragment (IV) of (I); (4) a nucleic acid (V) that hybridizes
XX under stringent conditions to (II); (5) a vector (VI) comprising (II) or
XX (III); and (6) a composition (VII) comprising (I) or its fragment, (IV)
XX or (VI), and a pharmaceutically acceptable carrier. (I) has protozoacide
XX and immunostimulant activities, and can be used in vaccines. (VII) is
XX useful for producing an immune response in a subject or for preventing
XX Leishmaniasis in a subject. (II) is also useful for preventing
XX Leishmaniasis in a subject. (VII) is useful as a vaccine. ACC79987 to
XX exemplification of the present invention
XX
SQ Sequence 15 AA;

Query Match          41.8%; Score 28; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 8.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 FPCIL 10
   |||||
DB 7 FPCIL 11

RESULT 66
ADX08687          41.8%; Score 28; DB 6; Length 15;
ID ADX08687 standard; peptide; 15 AA.
XX
XX ADX08687;
XX
XX 21-APR-2005 (first entry)
XX
XX HLA class II restricted epitope (derived from fusion protein) peptide 13.
XX
XX vaccine; infection; viral infections; virucide; bacterial infection;
XX antibacterial; yeast infection; fungicide; fungal infection;
XX protozoal infection; protozoacide; cancer; cytostatic; melanoma;
XX lung tumor; colon tumor; breast tumor; leukemia; autoimmune disease;
XX multiple sclerosis; neuroprotective; rheumatoid arthritis; antiarthritic;
XX antirheumatic; systemic lupus erythematosus; antiinflammatory;
XX dermatological; immunosuppressive.
XX
XX Unidentified.
XX
XX WO2005011730-A1.
XX
XX 10-FEB-2005.
XX
XX 30-JUL-2004; 2004WO-GB003285.
XX
XX 01-AUG-2003; 2003GB-00018096.
XX

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PA (UNLO ) QUEEN MARY & WESTFIELD COLLEGE.
XX
XX Wang P, Li S;
XX
XX WPI; 2005-152360/16.
XX
XX New vaccine composition comprises inverted microsomes from animal cells
XX with an externally disposed peptide antigen and a protein of the Major
XX Histocompatibility Complex (MHC), useful for treating or preventing, e.g.
XX cancer.
XX
XX Disclosure; Page 61; 83pp; English.
XX
XX The invention comprises a vaccine composition that consists of isolated
XX inverted microsomes from an animal cell (or its membrane fragments), in
XX association with an externally disposed peptide antigen and a protein of
XX the MHC. The vaccine composition of the invention is useful for the
XX prophylaxis or treatment of: infection (e.g. viral, bacterial, yeast,
XX fungal or protozoal), cancer (e.g. melanoma, lung adenocarcinoma, colon
XX cancer, breast cancer or leukemia), autoimmune disease (e.g. multiple
XX sclerosis, rheumatoid arthritis or systemic lupus erythematosus). The
XX present amino acid sequence represents an HLA class II restricted epitope
XX derived from a fusion protein.
XX
SQ Sequence 15 AA;

Query Match          41.8%; Score 28; DB 9; Length 15;
Best Local Similarity 100.0%; Pred. No. 8.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 ECIIG 11
   |||||
DB 6 ECIIG 10

RESULT 67
AAW81961
ID AAW81961 standard; peptide; 16 AA.
XX
XX AAW81961;
XX
XX 05-FEB-1999 (first entry)
XX
XX Rat ENDO-I protein fragment.
XX
XX ENDO; endometriosis; reproductive age; peritoneal fluid; secreted;
XX stromal cell; tissue inhibitor; metalloproteinases-1; TIMP-1.
XX
XX Ratcus sp.
XX
XX US5843673-A.
XX
XX 01-DEC-1998.
XX
XX 07-JUN-1995; 95US-00474696.
XX
XX 25-OCT-1994; 94US-00328451.
XX
XX (UMOR ) UNTV MISSOURI.
XX
XX Sharpe-Timms KL;
XX
XX WPI; 1999-044572/04.
XX
XX Diagnosis of endometriosis - based on reduced levels of tissue inhibitor
XX of metalloproteinases-1 or related protein.
XX
XX Example 3; Col 23-24; 17pp; English.
XX
XX This sequence is a fragment of the rat ENDO-I protein used in a method to
XX screen for endometriosis in a woman of reproductive age. The method
XX involves determining if a protein is present in a peritoneal fluid or
XX serum sample at a level below that of normal controls. The protein has a

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RESULT 70  
ADU92006  
ID ADU92006 standard; peptide; 17 AA.  
XX  
AC ADU92006;  
XX  
DT 10-FEB-2005 (first entry)  
XX  
DE EPO-R agonist SEQ ID NO 147.  
XX  
KM erythropoietin receptor; EPO-R; erythropoietin; renal failure;  
KM autoimmune disease; cystic fibrosis; anemia; inflammation;  
KM spinal cord injury; aging; neurological disease; nephrotropic;  
KM anti-anemic; immunosuppressive; CNS-Gen.; neuroprotective;  
KM respiratory-Gen.; anti-inflammatory; vulnerrary; nootropic; cyostatic;  
KM hemostatic; cyclic.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Modified-site 1 /note="Acetylated residue"  
FT Disulfide-bond 4..13  
FT Modified-site 17 /note="C-terminal amide"  
XX  
PN MO2004101611-A2.  
XX  
PD 25-NOV-2004.  
XX  
PF 12-MAY-2004; 2004WO-US014886.  
XX  
PR 12-MAY-2003; 2003US-0470245P.  
XX  
PA (AFPR-) APFPMAX INC.  
XX  
PI Yin K, Holmes C, Lalonde G, Balu P, Schatz PJ, Tumely D,  
PI WPI; 2005-039329/04.  
XX  
PT New peptide comprising specified sequence of amino acid is erythropoietin  
PT receptor agonist useful for treating e.g. anemia, beta-thalassemia, renal  
PT disorders.  
XX  
PS Disclosure; SEQ ID NO 147; 83pp; English.  
XX  
CC This invention describes a novel peptide which is an erythropoietin  
CC receptor (EPO-R) activator. The peptide forms a dimer comprising a  
CC linking moiety connecting two peptide chains composed of ADU91861. The N-  
CC terminal of the peptide is acetylated. The EPO-R activator further  
CC comprises at least one water soluble polymer, preferably polyethylene  
CC glycol (PEG) covalently bound to the peptide and a spacer moiety. The  
CC products of the invention are used for treating disorders associated with  
CC deficiency of erythropoietin or low or defective red blood cell  
CC population, end stage renal failure or dialysis, anemia associated with  
CC AIDS, autoimmune disease or malignancy, beta-thalassemia, cystic  
CC fibrosis, early anemia of prematurity, anemia associated with chronic  
CC inflammatory disease, spinal cord injury, acute blood loss, aging and  
CC neoplastic disease states accompanied by abnormal erythropoiesis. The  
CC peptide compounds are potent agonists of erythropoietin receptor and have  
CC nephrotropic, anti-anemic, immunosuppressive, CNS-Gen., neuroprotective,  
CC respiratory-Gen., anti-inflammatory, vulnerrary, nootropic, cyostatic and  
CC hemostatic activity. This sequence represents a peptide which acts as an  
CC erythropoietin receptor (EPO-R) agonist.  
XX  
SQ Sequence 17 AA;

Query Match 41.8%; Score 28; DB 9; Length 17;  
Best Local Similarity 50.0%; Pred. No. 9.5e+02;  
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 5 SPECTIGP 12  
|::|:|

Db 1 SWDCRIGP 8  
RESULT 71  
AA26517  
ID AA26517 standard; peptide; 18 AA.  
XX  
AC AA26517;  
XX  
DT 06-SEP-1999 (first entry)  
XX  
DE Erythropoietin receptor (EPO-R) binding peptide.  
XX  
KM Erythropoietin; EPO; receptor; EPO deficiency; renal failure; AIDS;  
KM dialysis; anaemia; autoimmune disease; chronic inflammatory disease;  
KM malignancy; beta-thalassemia; cystic fibrosis; prematurity; blood loss;  
KM spinal cord injury; aging; neoplastic disease; erythropoiesis; EPO-R.  
XX  
OS Synthetic.  
XX  
PN MO9640749-A1.  
XX  
PD 19-DEC-1996.  
XX  
PF 07-JUN-1996; 96WO-US009810.  
XX  
PR 07-JUN-1995; 95US-00484631.  
XX  
PR 07-JUN-1995; 95US-00484635.  
XX  
PA (JOHU ) JOHNSON & JOHNSON CORP.  
PA (AFPR-) APFPMAX TECHNOLOGIES NV.  
XX  
PI Wrighton NC, Dower WJ, Chang RS, Kashyap AK, Joliffe LK;  
PI Johnson D, Mulcahy L;  
XX  
DR WPI; 1997-052225/05.  
XX  
PT Erythropoietin receptor binding peptide - useful for treating disorders  
PT characterised by deficiency of EPO, or low or defective red blood cell  
PT population.  
XX  
PS Disclosure; Page 25; 95pp; English.  
XX  
CC The invention describes a peptide of 10-40 amino acid residues which  
CC binds to erythropoietin (EPO) receptor and which includes the amino acid  
CC sequence Cys-Xaa1-Xaa2-Gly-Pro-Xaa3-Thr-Tyr-Xaa4-Cys, where Xaa1 = Arg,  
CC His, Leu or Tyr, Xaa2 = Met, Phe or Ile, Xaa3 = 1 of the 20 genetically  
CC coded L-amino acids, and Xaa4 = Asp, Glu, Ile, Leu or Val. Optionally,  
CC the peptide may be cyclised or dimerised. The peptide can be used to  
CC treat a patient having a disorder characterised by a deficiency of EPO or  
CC a low or defective red blood cell population. It can be used to treat end  
CC stage renal failure or dialysis; anaemia associated with AIDS, autoimmune  
CC disease, chronic inflammatory diseases or malignancy; beta-thalassemia;  
CC cystic fibrosis; early anaemia of prematurity; spinal cord injury; acute  
CC blood loss; aging; and neoplastic disease states accompanied by abnormal  
CC erythropoiesis. The peptides can also be used as reagents for detecting  
CC EPO receptors on living cells, in biological fluids, in tissue  
CC homogenates, etc. Sequences AA26512-548 are representative peptides  
CC falling within the above peptide motif and isolated during the affinity  
CC selection process  
XX  
SQ Sequence 18 AA;

Query Match 41.8%; Score 28; DB 2; Length 18;  
Best Local Similarity 36.4%; Pred. No. 1e+03;  
Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 EKNSPECTIGP 12  
|:|:|:|  
Db 1 ERRPYKCRFGP 11

RESULT 72

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AAW67525
ID AAW67525 standard, peptide, 18 AA.
XX
XX AAW67525,
XX
XX 02-MAR-1999 (first entry)
XX
XX IGF-1/IGFBP inhibitory peptide 23B3.7.
DE
KW Inhibition, interaction, insulin-like growth factor, IGF, receptor;
KW binding protein, serum, tissue, insulin; plasma, growth hormone; glucose;
XX secretion, blood, hyperglycaemia, obesity.
XX
XX Synthetic.
OS
XX WO9845427-A2.
XX
XX 15-OCT-1998.
XX
XX 31-MAR-1998; 98WO-US006514.
XX
XX 04-APR-1997; 97US-00825852.
XX
XX (GETH ) GENENTECH INC.
XX
XX Clark RG, Lowman HB, Robinson ICAF,
PI
XX WPI, 1998-583196/49.
XX
XX Inhibitors of interaction between insulin-like growth factor - useful
PT for, e.g. treating or preventing hyperglycaemia, obesity and neurological
PT disorders, and are optionally formulated with thiazolidinone.
XX
XX Example 7; Page 57; 133pp; English.
XX
XX The invention relates to the isolation of compounds, especially peptides,
XX ther: (a) inhibit interaction between an insulin-like growth factor (IGF),
XX with any one of its binding proteins (IGFBP), and (b) do not bind to a
XX human IGF receptor (hIGFR), e.g. see AAW67476-W67491 and AAW67503-W67565.
XX The peptides are produced synthetically or are isolated from peptide
XX libraries where the encoding sequence is generated so that the resulting
XX peptide produced retains its structure in solution. This sequence
XX represents a peptide isolated from a 98 display peptide library which
XX binds the IGF-1 binding protein IGFBP-3. The compounds are used to
XX increase serum and tissue levels of active IGF-1, preferably also to
XX reduce insulin and plasma growth hormone (GH) secretion, and blood
XX glucose levels, without direct stimulation of secretion or release of
XX endogenous GH. Particularly the compounds are used to treat or prevent
XX hyperglycaemia, obesity-related disorders, neurological, cardiac,
XX anabolic, renal and immunological diseases
XX
XX Sequence 18 AA,
SQ
Query Match 41.8%; Score 28; DB 2; Length 18;
Best Local Similarity 83.3%; Pred. No.1e+03;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0
Oy 7 ECIIIGP 12
Db 4 ECIEGP 9
RESULT 73
AAW67523
ID AAW67523 standard, peptide, 18 AA.
XX
XX AAW67523,
XX
XX 02-MAR-1999 (first entry)
XX
XX IGF-1/IGFBP inhibitory peptide 23B3.4.
DE
XX Inhibition, interaction, insulin-like growth factor, IGF, receptor;
XX

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KW binding protein; serum; tissue; insulin; plasma; growth hormone; glucose;
KW secretion; blood; hyperglycaemia; obesity.
XX Synthetic.
OS MO9845427-A2.
XX PN
XX WO9845427-A2.
XX PD
XX 15-OCT-1998.
XX PF
XX 31-MAR-1998; 98WO-US006514.
XX PR
XX 04-APR-1997; 97US-00825852.
XX PA
XX (GETH ) GENENTECH INC.
XX PI
XX Clark RG, Lowman HB, Robinson ICAF,
XX WPI, 1998-583196/49.
XX DR
XX PT
XX Inhibitors of interaction between insulin-like growth factor - useful
PT for, e.g. treating or preventing hyperglycaemia, obesity and neurological
PS disorders, and are optionally formulated with thiazolidinone.
XX PS
XX Example 7; Page 57; 133pp; English.
CC The invention relates to the isolation of compounds, especially peptides,
CC that: (a) inhibit interaction between an insulin-like growth factor (IGF)
CC with any one of its binding proteins (IGFBP), and (b) do not bind to a
CC human IGF receptor (hIGR), e.g. see AAW67476-W67491 and AAW67503-W67565.
CC The peptides are produced synthetically or are isolated from peptide
CC libraries where the encoding sequence is generated so that the resulting
CC peptide produced retains its structure in solution. This sequence
CC represents a peptide isolated from a 98 display peptide library which
CC binds the IGF-1 binding protein IGFBP-3. The compounds are used to
CC increase serum and tissue levels of active IGF-I, preferably also to
CC reduce insulin and plasma growth hormone (GH) secretion, and blood
CC glucose levels, without direct stimulation of secretion or release of
CC endogenous GH. Particularly the compounds are used to treat or prevent
CC hyperglycaemia, obesity-related disorders, neurological, cardiac,
CC anabolic, renal and immunological diseases
XX SQ
XX Sequence 18 AA;
Query Match 41.8%; Score 28; DB 2; Length 18;
Beat Local Similarity 66.7%; Pred. No. 1e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0
QY 7 ECIIIGP 12
Db 4 ECVWGP 9
RESULT 74
ID ABB38888 standard; peptide; 18 AA.
XX ABB38888;
AC ABB38888;
DT 04-FEB-2002 (first entry)
DX Peptide #6394 encoded by human foetal liver single exon probe.
XX Human; foetal liver; gene expression; single exon nucleic acid probe.
XX Homo sapiens.
XX MO200157277-A2.
XX 09-AUG-2001.
XX 30-JAN-2001; 2001WO-US000669.
XX 04-FEB-2000; 2000US-0180312P.

```

PR 26-MAY-2000; 2000US-0207456P.  
PR 30-JUN-2000; 2000US-00608408.  
PR 03-AUG-2000; 2000US-00632366.  
PR 21-SEP-2000; 2000US-0234687P.  
PR 27-SEP-2000; 2000US-0236359P.  
PR 04-OCT-2000; 2000GB-00024263.  
XX  
XX (MOLE-) MOLECULAR DYNAMICS INC.  
XX  
XX Penn SG, Hanzel DK, Chen W, Rank DR;  
XX  
XX WPI; 2001-483447/52.  
XX  
XX Human genome-derived single exon nucleic acid probes useful for analyzing  
PT gene expression in human fetal liver.  
XX  
XX Claim 27; SEQ ID NO 31523; 639pp + Sequence Listing; English.  
XX  
XX The invention relates to a single exon nucleic acid probe for measuring  
CC human gene expression in a sample derived from human foetal liver. The  
CC single exon nucleic acid probes may be used for predicting, measuring and  
CC displaying gene expression in samples derived from human fetal liver. The  
CC present sequence is a peptide encoded by a single exon nucleic acid probe  
CC of the invention. Note: The sequence data for this patent did not form  
CC part of the printed specification, but was obtained in electronic format  
CC directly from WIPO at fcp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 18 AA;

Query Match 41.8%; Score 28; DB 4; Length 18;  
Best Local Similarity 62.5%; Pred. No. 1e+03;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 5 SPECILGP 12  
||:||||  
Db 2 SFQGLGP 9

RESULT 75  
AAM32369  
ID AAM32369 standard; protein; 18 AA.  
XX  
XX AAM32369;

DT 17-OCT-2001 (first entry)

DE Peptide #6406 encoded by probe for measuring placental gene expression.

KW Probe; microarray; human; placenta; antenatal diagnosis;  
KW genetic disorder.

OS Homo sapiens.

PN WO200157272-A2.

PD 09-AUG-2001.

PF 30-JAN-2001; 2001WO-US0000663.

PR 04-FEB-2000; 2000US-0180312P.

PR 26-MAY-2000; 2000US-0207456P.

PR 30-JUN-2000; 2000US-00608408.

PR 03-AUG-2000; 2000US-00632366.

PR 21-SEP-2000; 2000US-0234687P.

PR 27-SEP-2000; 2000US-0236359P.

PR 04-OCT-2000; 2000GB-00024263.  
XX  
XX (MOLE-) MOLECULAR DYNAMICS INC.  
XX  
XX Penn SG, Hanzel DK, Chen W, Rank DR;  
XX  
XX WPI; 2001-488897/53.  
XX

PT Human genome-derived single exon nucleic acid probes useful for analyzing  
PT gene expression in human placenta.  
XX  
XX Claim 27; SEQ ID NO 32638; 654pp; English.

XX  
XX The present invention relates to single exon nucleic acid probes (SENP;  
CC see AAI31315-AAI57546). The present sequence is a peptide encoded by one  
CC such probe. The probes are useful for producing a microarray for  
CC predicting, measuring and displaying gene expression in samples derived  
CC from human placenta. The probes are useful for antenatal diagnosis of  
CC human genetic disorders  
XX  
XX

SQ Sequence 18 AA;

Query Match 41.8%; Score 28; DB 4; Length 18;  
Best Local Similarity 62.5%; Pred. No. 1e+03;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 5 SPECILGP 12  
||:||||  
Db 2 SFQGLGP 9

RESULT 76  
AAM72107  
ID AAM72107 standard; protein; 18 AA.  
XX  
XX AAM72107;

DT 06-NOV-2001 (first entry)

DE Human bone marrow expressed probe encoded protein SEQ ID NO: 32413.

KW Human; bone marrow expressed exon; gene expression analysis; probe;  
KW microarray; cancer; leukaemia; lymphoma; myeloma.

OS Homo sapiens.

PN WO200157276-A2.

PD 09-AUG-2001.

PF 30-JAN-2001; 2001WO-US0000668.

PR 04-FEB-2000; 2000US-0180312P.

PR 26-MAY-2000; 2000US-0207456P.

PR 30-JUN-2000; 2000US-00608408.

PR 03-AUG-2000; 2000US-00632366.

PR 21-SEP-2000; 2000US-0234687P.

PR 27-SEP-2000; 2000US-0236359P.

PR 04-OCT-2000; 2000GB-00024263.  
XX  
XX (MOLE-) MOLECULAR DYNAMICS INC.  
XX  
XX Penn SG, Hanzel DK, Chen W, Rank DR;  
XX  
XX WPI; 2001-488900/53.  
XX

PT Human genome-derived single exon nucleic acid probes useful for analyzing  
PT gene expression in human bone marrow.  
XX  
XX Example 4; SEQ ID NO 32413; 658pp + Sequence Listing; English.

XX  
XX The present invention provides a number of single exon nucleic acid  
CC probes which are derived from genomic sequences expressed in the human  
CC bone marrow. They can be used to measure gene expression in bone marrow  
CC samples, which may enable the improved diagnosis and treatment of cancers  
CC such as lymphoma, leukemia and myeloma. The present sequence is a  
CC protein encoded by one of the probes of the invention  
XX  
XX

SQ Sequence 18 AA;

Query Match 41.8%; Score 28; DB 4; Length 18;



Best Local Similarity 62.5%; Pred. No. 1e+03; Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 SFECLIGP 12  
||:||||  
Db 2 SFGGLIGP 9

## RESULT 77

AAMS9539 standard; protein; 18 AA.

XX AAMS9539;

XX 05-NOV-2001 (first entry)

XX Human brain expressed single exon probe encoded protein SEQ ID NO: 31644.

XX Human; brain expressed exon; gene expression analysis; probe; microarray;

XX Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer.

XX Homo sapiens.

XX MO200157275-A2.

XX 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US000667.

XX 04-FEB-2000; 2000US-0180312P.

XX 26-MAY-2000; 2000US-0207456P.

XX 30-JUN-2000; 2000US-00608408.

XX 03-AUG-2000; 2000US-00632366.

XX 21-SEP-2000; 2000US-0234687P.

XX 27-SEP-2000; 2000US-0236359P.

XX 04-OCT-2000; 2000GB-00024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR,

XX WPI; 2001-483446/52.

XX Single exon nucleic acid probes for analyzing gene expression in human

XX brains.

XX Example 4; SEQ ID NO 31644; 650bp + Sequence Listing; English.

XX The present invention provides a number of single exon nucleic acid

XX probes which are derived from genomic sequences expressed in the human

XX brain. They can be used to measure gene expression in brain cell samples,

XX which may enable the diagnosis and improved treatment of nervous system

XX diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,

XX epilepsy and cancers. The present sequence is a protein encoded by one of

XX the probes of the invention

XX Sequence 18 AA;

XX

XX

XX

DT 25-FEB-2003 (first entry)

XX Human liver peptide, SEQ ID NO 32441.

XX Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia;

XX hypercholesterolaemia; coronary heart disease.

XX Homo sapiens.

XX MO200157273-A2.

XX 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US000664.

XX 04-FEB-2000; 2000US-0180312P.

XX 26-MAY-2000; 2000US-0207456P.

XX 30-JUN-2000; 2000US-00608408.

XX 03-AUG-2000; 2000US-00632366.

XX 21-SEP-2000; 2000US-0234687P.

XX 27-SEP-2000; 2000US-0236359P.

XX 04-OCT-2000; 2000GB-00024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR,

XX WPI; 2001-48898/53.

XX Human genome-derived single exon nucleic acid probes useful for analyzing

XX gene expression in human adult liver.

XX Claim 27; SEQ ID NO 32441; 658bp; English.

XX The invention relates to a single exon nucleic acid probe (SENP) (I) for

XX measuring human gene expression in a sample derived from human adult

XX liver, comprising one of 13109 defined nucleotide sequences given in the

XX specification (or complements/ fragments). The probe hybridizes at high

XX stringency to a nucleic acid molecule expressed in the human adult liver.

XX (I) may be used for predicting, measuring and displaying gene expression

XX in samples derived from human adult liver. The genes identified may be

XX involved in genetic liver diseases such as cirrhosis,

XX hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is

XX associated with coronary heart disease. ABG47346-ABG5930 represent human

XX liver single exon encoded peptides of the invention. Note: The sequence

XX information for this patent does not appear in the printed specification

XX but was obtained in electronic format directly from WIPO at

XX ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 18 AA;

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

KW immunological disorder; kidney regeneration; degenerative disorder;  
 KW hypoxia; wound healing; cardiac regeneration; cancer; angiogenesis;  
 KW metabolic stress; growth hormone deficiency; diabetes; short stature;  
 KW osteoporosis; obesity.  
 XX Synthetic.  
 XX US6251865-B1.  
 XX PN  
 XX PD 26-JUN-2001.  
 XX PF 31-MAR-1998; 98US-00052888.  
 XX PR 04-APR-1997; 97US-00825852.  
 XX PA (GETH ) GENENTECH INC.  
 XX PI Clark RG, Lowman HB, Robinson ICAF;  
 XX DR WPI; 2001-520042/57.  
 XX PT Isolated peptides used to increase serum and tissue levels of insulin-  
 PT like growth factor in those with hyperglycemic, obesity-related,  
 PT neurological, cardiac, anabolic, renal or immunological disorders.  
 XX PS Example 7; Col 57; 108pp; English.  
 XX CC The present sequence represents a synthetic peptide, which binds to an  
 CC insulin-like growth factor (IGF)-1 binding protein. The specification  
 CC describes IGF agonists. IGF agonist peptides are used to increase serum  
 CC and tissue levels of IGF-1 in mammals with hyperglycemic, obesity-  
 CC related, neurological, cardiac, anabolic, renal or immunological  
 CC disorders. They may also be used to increase whole body, bone and muscle  
 CC growth rate in normal and hypopituitary animals, to protect body weight  
 CC and nitrogen loss during catabolic states, kidney regeneration, to treat  
 CC peripheral and central nervous system (CNS) degenerative disorders and  
 CC promote neuroprotection or repair following CNS damage or injury, to  
 CC treat hypoxia, to promote wound healing, for cardiac regeneration, to  
 CC reverse cancer cachexia, to inhibit angiogenesis, to regenerate the  
 CC gastrointestinal tract, to stimulate mammary function, to counteract IGF-  
 CC 1-dependent actions of growth hormone such as metabolic stress, age-  
 CC related decline in growth hormone activity and adult growth hormone  
 CC deficiency, to treat maturity onset diabetes and/or to treat specific IGF  
 CC deficiency. They may also be used to treat growth-hormone resistant short  
 CC stature, growth hormone insensitivity syndrome, osteoporosis and  
 CC catabolic states, and reduce obesity  
 XX SQ Sequence 18 AA;  
 XX  
 XX Query Match 41.8%; Score 28; DB 4; Length 18;  
 XX Best Local Similarity 66.7%; Pred. No. 1e+03;  
 XX Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 OY 7 ECILGP 12  
 XX |||  
 XX 4 ECVWGP 9  
 DB  
 XX  
 XX RESULT 80  
 XX AAG63762  
 XX ID AAG63762 standard; peptide; 18 AA.  
 XX AC AAG63762;  
 XX DT 29-OCT-2001 (first entry)  
 XX  
 XX Synthetic peptide which binds to IGF-1 binding protein IGFBP-3.  
 DB Insulin-like growth factor; IGF; IGF-1; IGF binding protein; IGFBP-3;  
 KW hyperglycemic disorder; obesity-related disorder; neurological disorder;  
 KW cardiac disorder; anabolic disorder; renal disorder; neuroprotection;  
 KW immunological disorder; kidney regeneration; degenerative disorder;  
 KW hypoxia; wound healing; cardiac regeneration; cancer; angiogenesis;

KW metabolic stress; growth hormone deficiency; diabetes; short stature;  
 KW osteoporosis; obesity.  
 XX Synthetic.  
 XX US6251865-B1.  
 XX PN  
 XX PD 26-JUN-2001.  
 XX PF 31-MAR-1998; 98US-00052888.  
 XX PR 04-APR-1997; 97US-00825852.  
 XX PA (GETH ) GENENTECH INC.  
 XX PI Clark RG, Lowman HB, Robinson ICAF;  
 XX DR WPI; 2001-520042/57.  
 XX PT Isolated peptides used to increase serum and tissue levels of insulin-  
 PT like growth factor in those with hyperglycemic, obesity-related,  
 PT neurological, cardiac, anabolic, renal or immunological disorders.  
 XX PS Example 7; Col 57; 108pp; English.  
 XX CC The present sequence represents a synthetic peptide, which binds to an  
 CC insulin-like growth factor (IGF)-1 binding protein. The specification  
 CC describes IGF agonists. IGF agonist peptides are used to increase serum  
 CC and tissue levels of IGF-1 in mammals with hyperglycemic, obesity-  
 CC related, neurological, cardiac, anabolic, renal or immunological  
 CC disorders. They may also be used to increase whole body, bone and muscle  
 CC growth rate in normal and hypopituitary animals, to protect body weight  
 CC and nitrogen loss during catabolic states, kidney regeneration, to treat  
 CC peripheral and central nervous system (CNS) degenerative disorders and  
 CC promote neuroprotection or repair following CNS damage or injury, to  
 CC treat hypoxia, to promote wound healing, for cardiac regeneration, to  
 CC reverse cancer cachexia, to inhibit angiogenesis, to regenerate the  
 CC gastrointestinal tract, to stimulate mammary function, to counteract IGF-  
 CC 1-dependent actions of growth hormone such as metabolic stress, age-  
 CC related decline in growth hormone activity and adult growth hormone  
 CC deficiency, to treat maturity onset diabetes and/or to treat specific IGF  
 CC deficiency. They may also be used to treat growth-hormone resistant short  
 CC stature, growth hormone insensitivity syndrome, osteoporosis and  
 CC catabolic states, and reduce obesity  
 XX SQ Sequence 18 AA;  
 XX  
 XX Query Match 41.8%; Score 28; DB 4; Length 18;  
 XX Best Local Similarity 83.3%; Pred. No. 1e+03;  
 XX Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 OY 7 ECILGP 12  
 XX |||  
 XX 4 ECTRGP 9  
 DB  
 XX  
 XX RESULT 81  
 XX ABG41921  
 XX ID ABG41921 standard; peptide; 18 AA.  
 XX AC ABG41921;  
 XX DT 19-AUG-2002 (first entry)  
 XX  
 XX Human peptide encoded by genome-derived single exon probe SEQ ID 31586.  
 DB Human; single exon probe; asthma; lung cancer; COPD; ILD;  
 KW chronic obstructive pulmonary disease; interstitial lung disease;  
 KW familial idiopathic pulmonary fibrosis; neurofibromatosis;  
 KW tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;  
 KW Hereditary spherocytosis; sarcoidosis; pulmonary haemosiderosis;  
 KW pulmonary histiocytosis; lymphangioleiomyomatosis; Karsenger syndrome;  
 KW pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;

KW primary ciliary dyskinesia; pulmonary hypertension;  
 KM hyaline membrane disease.  
 XX Homo sapiens.  
 OS  
 PN WO200186003-A2.  
 XX  
 PD 15-NOV-2001.  
 XX  
 PF 30-JAN-2001; 2001WO-US000665.  
 XX  
 PR 04-FEB-2000; 2000US-0180312P.  
 PR 26-MAY-2000; 2000US-0207456P.  
 PR 30-JUN-2000; 2000US-00608408.  
 PR 03-AUG-2000; 2000US-00632366.  
 PR 21-SEP-2000; 2000US-0234687P.  
 PR 27-SEP-2000; 2000US-0236359P.  
 PR 04-OCT-2000; 2000GB-00024263.  
 XX  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 XX  
 PI Penn SG, Hanzel DK, Chen W, Rank DR;  
 XX  
 DR WPI; 2002-114183/15.  
 XX  
 PT Spatially-addressable set of single exon nucleic acid probes, used to  
 PT measure gene expression in human lung samples.  
 XX  
 PS Claim 27, SEQ ID NO 31586; 634bp; English.  
 XX  
 CC The invention relates to a spatially-addressable set of single exon  
 CC nucleic acid probes for measuring gene expression in a sample derived  
 CC from human lung comprising single exon nucleic acid probes having one of  
 CC 12614 nucleic acid sequences mentioned in the specification, or their  
 CC complements or the 12387 open reading frames derived from the 12614  
 CC probes. Also included are a microarray comprising the novel set of probes  
 CC; the novel set of probes which hybridize at high stringency to a nucleic  
 CC acid expressed in the human lung; measuring gene expression in a sample  
 CC derived from human lung, comprising (a) contacting the array with a  
 CC collection of detectably labeled nucleic acids derived from human lung  
 CC mRNA; and (b) measuring the label detectably bound to each probe of the  
 CC array; identifying exons in a eukaryotic genome, comprising (a)  
 CC algorithmically predicting at least one exon from genomic sequences of  
 CC the eukaryote; and (b) detecting specific hybridization of detectably  
 CC labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,  
 CC having a fragment identical to the predicted exon, the probe is included  
 CC in the above mentioned microarray; assigning exons to a single gene,  
 CC comprising (a) identifying exons from genomic sequence by the method  
 CC above and (b) measuring the expression of each of the exons in several  
 CC tissues and/or cell types using hybridization to a single exon  
 CC microarray having a probe with the exon, where a common pattern of  
 CC expression of the exons in the tissues and/or cell types indicates that  
 CC the exons should be assigned to a single gene; a peptide comprising one  
 CC of 12011 sequences, mentioned in the specification, or encoded by the  
 CC probes/open reading frames (ORF). The probes are used for gene expression  
 CC analysis and for identifying exons in a gene, particularly using human  
 CC lung derived mRNA and for the study of lung diseases such as asthma, lung  
 CC cancer, chronic obstructive pulmonary disease (COPD), interstitial lung  
 CC disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis,  
 CC tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-  
 CC Judd syndrome, sarcoidosis, pulmonary haemangiomas, pulmonary  
 CC histiocytosis, lymphangioleiomyomatosis, pulmonary alveolar proteinosis,  
 CC Karsenger syndrome, fibrocystic pulmonary dysplasia, primary ciliary  
 CC dyskinesia, pulmonary hypertension and hyaline membrane disease. The  
 CC present sequence is a peptide/protein encoded by a single exon probe of  
 CC the invention. Note: The sequence data for this patent did not form part  
 CC of the printed specification, but was obtained in electronic format  
 CC directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 18 AA;

Query Match 41.8%; Score 28; DB 5; Length 18;  
 Best Local Similarity 62.5%; Pred. No. 1e+03;

Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 Qy 5 SPECILGP 12  
 Db 2 SFQGLGP 9  
 RESULT 82  
 ABB57684  
 ID ABB57684 standard; peptide; 18 AA.  
 XX  
 AC ABB57684;  
 XX  
 DT 18-MAR-2002 (first entry)  
 XX  
 DE IGFBP-3 binding peptide #33.  
 XX  
 KM Antirheumatic; antiarthritis; osteopathic; cartilage disorder;  
 KM Insulin-like growth factor; IGF; binding protein; IGFBP;  
 KM rheumatoid arthritis; osteoarthritis.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200187323-A2.  
 XX  
 PD 22-NOV-2001.  
 XX  
 PF 16-MAY-2001; 2001WO-US015904.  
 XX  
 PR 16-MAY-2000; 2000US-0204490P.  
 PR 15-NOV-2000; 2000US-0248985P.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Dubague Y, Filvaroff EH, Lowman HB;  
 XX  
 DR WPI; 2002-082942/11.  
 XX  
 CC Treating cartilage disorders including cartilage damage by injury or  
 CC PT degenerative cartilaginous disorders, by contacting cartilage with  
 CC PT insulin-like growth factor analog with altered affinity for IGF-binding  
 CC PT proteins.  
 XX  
 PS Example 1; Page 44; 136bp; English.  
 XX  
 CC The present invention relates to a method for treating cartilage  
 CC disorders. The method comprises contacting cartilage with an active agent  
 CC such as insulin-like growth factor (IGF-1) analog with a binding affinity  
 CC preference for IGF binding protein-3 (IGFBP-3) over IGFBP-1, an IGF-1  
 CC analog with a binding affinity preference for IGFBP-1 over IGFBP-3, or a  
 CC IGFBP displacer peptide that prevents the interaction of IGF with an  
 CC IGFBP and does not bind to human IGF receptor. The method is useful for  
 CC treating cartilage disorders (CD), including degenerative CD, articular  
 CC CD such as rheumatoid arthritis and osteoarthritis. The present sequence  
 CC was used to illustrate the invention  
 XX  
 SQ Sequence 18 AA;

Query Match 41.8%; Score 28; DB 5; Length 18;  
 Best Local Similarity 83.3%; Pred. No. 1e+03;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Qy 7 ECIIGP 12  
 Db 4 ECIIGP 9  
 RESULT 83  
 ABB57681  
 ID ABB57681 standard; peptide; 18 AA.  
 XX  
 AC ABB57681;  
 XX

DT	18-MAR-2002	(first entry)	
XX	IGFBP-3 binding peptide #30.		
DE	Antirheumatic; antiarthritic; osteopathic; cartilage disorder;		
KW	insulin-like growth factor; IGF, binding protein, IGFBP,		
KM	rheumatoid arthritis; osteoarthritis.		
XX			
OS	Synthetic.		
XX			
PM	WO200187323-A2.		
XX			
PD	22-NOV-2001.		
XX			
PF	16-MAY-2001; 2001WO-US015904.		
XX			
PR	16-MAY-2000; 2000US-0204490P.		
PR	15-NOV-2000; 2000US-0248985P.		
PA	(GETH ) GENENTECH INC.		
PI	Dubaquie Y, Flivartoff EH, Lowman HB;		
XX	WPI, 2002-082942/11.		
XX			
PT	Treating cartilage disorders including cartilage damage by injury or		
PT	degenerative cartilaginous disorders, by contacting cartilage with		
PT	insulin-like growth factor analog with altered affinity for IGF-binding		
PT	proteins.		
XX			
PS	Example 1, Page 44, 136pp, English.		
XX			
CC	The present invention relates to a method for treating cartilage		
CC	disorders. The method comprises contacting cartilage with an active agent		
CC	such as insulin-like growth factor (IGF-1) analog with a binding affinity		
CC	preference for IGF binding protein-3 (IGFBP-3) over IGFBP-1, an IGF-1		
CC	analog with a binding affinity preference for IGFBP-1 over IGFBP-3, or a		
CC	IGFBP displacer peptide that prevents the interaction of IGF with an		
CC	IGFBP and does not bind to human IGF receptor. The method is useful for		
CC	treating cartilage disorders (CD), including degenerative CD, articular		
CC	CD such as rheumatoid arthritis and osteoarthritis. The present sequence		
CC	was used to illustrate the invention		
XX			
SQ	Sequence 18 AA;		
Query Match	41.8%; Score 28; DB 5; Length 18;		
Best Local Similarity	66.7%; Pred. No. 16+03;		
Matches	4; Conservative 1; Mismatches 1; Indels 0; Gaps 0		
QY	7 ECILGP 12		
	:		
DB	4 ECWGP 9		
RESULT 84			
ID	ADA03290 standard; peptide, 18 AA.		
AC	ADA03290;		
XX			
DT	06-NOV-2003 (first entry)		
XX			
DE	Angiotensin converting enzyme 2 binding peptide #88.		
XX			
KM	hypotensive; cardiac; cerebroprotective; antihypertensive; analgesic;		
KM	antiinflammatory; nephroprotective; hypertensive; vasotropic; cytosolic;		
KM	antiallergic; antiparkinsonian;		
KM	neurotic; antineumatic; antirheumatic; antispasmodic; tranquilizer;		
KM	vulnerable; antidiabetic; dermatological; immunosuppressive; hepatotropic;		
KM	anti-HIV; antibacterial; angiotensin converting enzyme; ACE-2;		
KM	angiotensin converting enzyme; ACE-2; hypertension;		
KM	congestive heart failure; stroke; left ventricular failure;		
KM	atherosclerotic heart disease; stenosis; pain; inflammatory reaction;		

KM	hitamine; vasoconstriction; epitope; aldosterone; cell proliferation;
KM	renal disorder; acute glomerulonephritis; immunophenotyping;
KM	cardiac myocyte; Bowman's capsule; hypotension; ischemia; asthma; allergy;
KM	multiple sclerosis; cancer; Parkinson's disease; Alzheimer's disease;
KM	rheumatoid arthritis; gout; trauma; dermatitis; diabetes mellitus;
KM	Sjogren's syndrome; Addison's disease; hepatitis; Crohn's disease;
KM	sarcoidosis; AIDS; sepsis.
XX	
OS	Synthetic.
XX	
PN	WO200298448-A1.
XX	
PD	12-DEC-2002.
XX	
PP	03-JUN-2002; 2002WO-US017199.
XX	
PR	04-JUN-2001; 2001US-0294976P.
XX	
PA	(HUMA-) HUMAN GENOME SCI INC.
XX	
P1	Parry TJ, Rosen CA, Albert VR, Sanyal I, Huang L, Wescott CR,
XX	Sekut L;
DR	WPI; 2003-140552/13.
XX	
PT	Novel angiotensin converting enzyme-2 binding polypeptide useful for
PT	treating, preventing or ameliorating hypertension, congestive heart
PT	failure, stroke, left ventricular failure and atherosclerotic heart
XX	disease.
XX	
PS	Example 1; Page 179; 246pp; English.
XX	
CC	The invention relates to novel isolated angiotensin converting enzyme
CC	(ACE)-2 binding polypeptides (I), which are useful for treating,
CC	preventing or ameliorating hypertension, congestive heart failure,
CC	stroke, left ventricular failure and atherosclerotic heart disease in an
CC	animal. The peptides are useful for detecting, isolating, or purifying
CC	ACE-2 proteins or ACE-2 like polypeptides in solutions, mixtures, or
CC	biological samples; for inhibiting or reducing stenosis, pain,
CC	inflammatory reactions, abnormal histamine release, vasoconstriction,
CC	diseases or disorders related to vasoconstriction, and diseases and/or
CC	disorders associated with aberrant action of ACE-2; to detect, isolate,
CC	or remove ACE-2 target proteins in solutions, and also to identify
CC	epitopes of ACE-2; to detect, diagnose, prognose, or monitor
CC	cardiovascular diseases, and disorders associated with aberrant
CC	aldosterone activity, or cell proliferation; for preventing and treating
CC	renal disorders, e.g., acute glomerulonephritis, and diseases associated
CC	with it; to assay protein levels in a biological sample, for
CC	immunophenotyping of cell lines and biological samples by their ACE-2
CC	expression, and for identifying cells, such as cardiac myocytes,
CC	endothelial and epithelial cells of Bowman's capsule. The peptides are
CC	especially useful for treating, preventing, or ameliorating diseases or
CC	disorders associated with hypotension, ischemia, asthma, allergy, multiple
CC	sclerosis, cancers, Parkinson's and Alzheimer's diseases, rheumatoid
CC	arthritis, gout, trauma, dermatitis, diabetes mellitus, Sjogren's
CC	syndrome, Addison's disease, chronic active hepatitis, Crohn's disease,
CC	sarcoidosis, AIDS, and sepsis. In an example of the invention, ACE-2
CC	binding peptides were isolated from a number of peptide display
CC	libraries. Evaluation of the peptide sequences revealed a series of
CC	peptide families. This sequence represents a specific example of one of
CC	the ACE-2 binding peptides of the invention
XX	
SO	Sequence 18 AA;
XX	
QY	Query Match 41.8%; Score 28; DB 6; Length 18;
DB	Best Local Similarity 71.4%; Pred. NO. 1e+03;
	Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0.
	6 FECTLIP 12
	2 PCDWGP 8

RESULT 85  
ABR56660 standard; peptide; 18 AA.  
XX  
AC ABR56660;  
XX  
DT 30-JUL-2003 (first entry)  
XX  
DE Angiotensin converting enzyme 2 (ACE-2) binding peptide SEQ ID NO:88.  
XX  
KW Human; angiotensin converting enzyme 2; ACE-2 binding; ACE-2;  
KM vasoconstriction; low blood pressure; angiotensin II; angiotensin;  
XX hypertensive; vasotropic; vaccine; hypotension; shock; syncope.  
XX  
OS Homo sapiens.  
XX  
PN WO200298906-A1.  
XX  
PD 12-DEC-2002.  
XX  
PF 03-JUN-2002; 2002WO-US017213.  
XX  
PR 04-JUN-2001; 2001US-0295004P.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
PI Parry TJ;  
XX  
DR WPI; 2003-140586/13.  
XX  
PT Increasing vasoconstriction or ameliorating a disorder resulting from low  
PT blood pressure, e.g. hypotension, shock or syncope, comprises  
PT administering an angiotensin II in combination with angiotensin 1-9 to an  
PT individual.  
XX  
PS Example 1; Page 9; 237p; English.  
XX  
CC The present invention describes a method for increasing vasoconstriction  
CC or ameliorating a disorder resulting from low blood pressure, which  
CC comprises administering to an individual an amount of angiotensin II in  
CC combination with angiotensin 1-9. Angiotensin has hypertensive and  
CC vasotropic activities, and can be used in vaccines. The method is useful  
CC for increasing vasoconstriction or ameliorating a disorder resulting from  
CC low blood pressure, such as hypotension, shock or syncope. ABR56663 to  
CC ABR5708 represent angiotensin converting enzyme 2 (ACE-2) binding  
CC peptides, ABR5709 to ABR56725 and ACC79021 to ACC79025 represent  
CC sequences used in the exemplification of the present invention. Human ACE  
CC -2 is located to chromosome X, more specifically to Xp22. N.B. ABR56563  
CC to ABR56572 represent SEQ ID NO:1 to 10 and should be the same as  
CC ABR56573 to ABR56582, but the Z's given at the beginning and end of the  
CC peptides in the disclosure have been expanded to Glx in the Sequence  
CC Listing and in this case the Z's do not represent Gln or Glu (see pages 4  
CC to 7). SEQ ID NO:40 to 116 in the Sequence Listing (see also pages 7 to  
CC 10) have been specified as SEQ ID NO:20 to 116 in Example 1 (see pages  
CC 174 to 177)  
XX  
SQ Sequence 18 AA;  
XX  
Query Match 41.8%; Score 28; DB 6; Length 18;  
Best Local Similarity 71.4%; Pred. No. 1e+03;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 6 PECTIGP 12  
DB 2 PECTMGP 8  
XX  
RESULT 86  
ADD84843  
ID ADD84843 standard; peptide; 18 AA.  
XX  
AC ADD84843;  
XX

DT 29-JAN-2004 (first entry)  
XX  
XX Synthetic peptide #50.  
XX  
KW Insulin-like growth factor I; IGF-I; growth hormone;  
KM growth hormone releasing peptide; growth hormone binding protein; IGF;  
KM growth hormone secretagogue; growth hormone binding protein; IGF;  
KM IGF binding protein; insulin; plasma insulin secretion;  
KM blood glucose level; hyperglycaemic disorder; obesity-related disorder;  
KM neurological disorder; cardiac disorder; anabolic disorder;  
XX renal disorder; immunological disorder; anorectic; neuroprotective;  
XX cardiac; nephrotropic; immunomodulator; antidiabetic.  
XX  
OS Synthetic.  
XX  
PN US6632794-B1.  
XX  
PD 14-OCT-2003.  
XX  
PF 28-NOV-2000; 2000US-00723547.  
XX  
PR 04-MAR-1997; 97US-00825852.  
PR 31-MAR-1998; 98US-00052888.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Clark RG, Lowman HB, Robinson ICAF;  
XX  
DR WPI; 2003-810559/76.  
XX  
PT Increasing serum and tissue levels of biologically active insulin-like  
PT growth factor (IGF)-I in a mammal for treating e.g. renal disorder, by  
PT administering IGF peptide.  
XX  
PS Example 7; SEQ ID NO 67; 117p; English.  
XX  
CC The invention relates to a method for increasing serum and tissue levels  
CC of biologically active insulin-like growth factor I (IGF-I) in a mammal  
CC comprising administering a growth hormone, a growth hormone releasing  
CC peptide, a growth hormone releasing hormone, a growth hormone  
CC secretagogue, a growth hormone in combination with growth hormone binding  
CC protein, an IGF, an IGF in combination with an IGF binding protein, an  
CC IGF binding protein, insulin or a hypoglycaemic agent. The invention also  
CC relates to a method of reducing plasma insulin secretion and blood  
CC glucose levels in a mammal. The method is useful for increasing serum and  
CC tissue levels of biologically active IGF-I in a mammal for treating  
CC hyperglycaemic, obesity-related, neurological, cardiac, anabolic, renal  
CC or immunological disorders. This sequence represents a peptide used in  
CC the method of the invention.  
XX  
SQ Sequence 18 AA;  
XX  
Query Match 41.8%; Score 28; DB 7; Length 18;  
Best Local Similarity 66.7%; Pred. No. 1e+03;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 7 ECTIGP 12  
DB 4 ECTMGP 9  
XX  
RESULT 87  
ADD84845  
ID ADD84845 standard; peptide; 18 AA.  
XX  
AC ADD84845;  
XX  
DT 29-JAN-2004 (first entry)  
XX  
DE Synthetic peptide #52.  
XX  
KW Insulin-like growth factor I; IGF-I; growth hormone;  
KM growth hormone releasing peptide; growth hormone releasing hormone;

KW growth hormone secretagogue; growth hormone binding protein; IGF;  
 KW IGF binding protein; insulin; plasma insulin secretion;  
 KW blood glucose level; hyperglycaemic disorder; obesity-related disorder;  
 KW neurological disorder; cardiac disorder; anabolic disorder;  
 KW renal disorder; immunological disorder; anorectic; neuroprotective;  
 KW cardiac; nephrotoxic; immunomodulator; antidiabetic.  
 OS Synthetic.  
 XX  
 XX US6632794-B1.  
 PN  
 XX  
 PD 14-OCT-2003.  
 XX  
 PF 28-NOV-2000; 2000US-00723547.  
 XX  
 PR 04-APR-1997; 97US-00825852.  
 PR 31-MAR-1998; 98US-00052888.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Clark RG, Lowman HB, Robinson ICAF;  
 XX  
 DR WPI; 2003-810559/76.  
 XX  
 PT Increasing serum and tissue levels of biologically active insulin-like  
 PT growth factor (IGF)-I in a mammal for treating e.g. renal disorder, by  
 PT administering IGF peptide.  
 XX  
 PS Example 7, SEQ ID NO 69, 117pp; English.  
 XX  
 CC The invention relates to a method for increasing serum and tissue levels  
 CC of biologically active insulin-like growth factor I (IGF-I) in a mammal  
 CC comprising administering a growth hormone, a growth hormone releasing  
 CC peptide, a growth hormone releasing hormone, a growth hormone  
 CC secretagogue, a growth hormone in combination with growth hormone binding  
 CC protein, an IGF, an IGF in combination with an IGF binding protein, an  
 CC IGF binding protein, insulin or a hypoglycaemic agent. The invention also  
 CC relates to a method of reducing plasma insulin secretion and blood  
 CC glucose levels in a mammal. The method is useful for increasing serum and  
 CC tissue levels of biologically active IGF-I in a mammal for treating  
 CC hyperglycaemic, obesity-related, neurological, cardiac, anabolic, renal  
 CC or immunological disorders. This sequence represents a peptide used in  
 CC the method of the invention.  
 CC  
 SQ Sequence 18 AA;  
 QY  
 DB 7 ECLIGP 12  
 DB 4 ECLIGP 9  
 RESULT 88  
 ADH48156  
 ID ADH48156 standard; peptide; 18 AA.  
 AC ADH48156;  
 XX  
 DT 25-MAR-2004 (first entry)  
 XX  
 DE IGFBP-3 binding peptide #21.  
 XX  
 KW IGF-I serum level; IGF-I tissue level; insulin-like growth factor; IGF-I;  
 KW hyperglycaemic disorder; obesity-related disorder; neurological disorder;  
 KW cardiac disorder; anabolic disorder; renal disorder;  
 KW immunological disorder; IGFBP-3.  
 XX  
 OS Synthetic.  
 OS  
 XX US6635619-B1.

XX  
 PD 21-OCT-2003.  
 XX  
 PF 28-NOV-2000; 2000US-00724127.  
 XX  
 PR 04-APR-1997; 97US-00825852.  
 PR 31-MAR-1998; 98US-00052888.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Clark RG, Lowman HB, Robinson ICAF;  
 XX  
 DR WPI; 2003-810559/76.  
 XX  
 PT Increasing serum and tissue levels of biologically active insulin-like  
 PT growth factor (IGF)-I in a mammal for treating e.g., renal disorder by  
 PT administering IGF peptide.  
 XX  
 PS Example 7, SEQ ID NO 67, 117pp; English.  
 XX  
 CC The invention relates to a method of increasing serum and tissue levels  
 CC of biologically active insulin-like growth factor (IGF)-I in a mammal.  
 CC The method is useful for increasing serum and tissue levels of  
 CC biologically active IGF-I in a mammal for treating hyperglycaemic,  
 CC obesity-related, neurological, cardiac, anabolic, renal or immunological  
 CC disorder. The present sequence represents the amino acid sequence of an  
 CC IGFBP-3 binding peptide.  
 CC  
 SQ Sequence 18 AA;  
 QY  
 DB 7 ECLIGP 12  
 DB 4 ECLWGP 9  
 RESULT 89  
 ADH48158  
 ID ADH48158 standard; peptide; 18 AA.  
 AC ADH48158;  
 XX  
 DT 25-MAR-2004 (first entry)  
 XX  
 DE IGFBP-3 binding peptide #23.  
 XX  
 KW IGF-I serum level; IGF-I tissue level; insulin-like growth factor; IGF-I;  
 KW hyperglycaemic disorder; obesity-related disorder; neurological disorder;  
 KW cardiac disorder; anabolic disorder; renal disorder;  
 KW immunological disorder; IGFBP-3.  
 XX  
 OS Synthetic.  
 OS  
 XX US6635619-B1.  
 PN  
 PD 21-OCT-2003.  
 XX  
 PF 28-NOV-2000; 2000US-00724127.  
 XX  
 PR 04-APR-1997; 97US-00825852.  
 PR 31-MAR-1998; 98US-00052888.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Clark RG, Lowman HB, Robinson ICAF;  
 XX  
 DR WPI; 2003-810559/76.  
 XX  
 PT Increasing serum and tissue levels of biologically active insulin-like  
 PT growth factor (IGF)-I in a mammal for treating e.g., renal disorder by

PT administering IGF peptide.  
 XX  
 PS Example 7, SEQ ID NO 69, 117pp; English.  
 XX  
 CC The invention relates to a method of increasing serum and tissue levels  
 CC of biologically active insulin-like growth factor (IGF-I in a mammal.  
 CC The method is useful for increasing serum and tissue levels of  
 CC biologically active IGF-I in a mammal for treating hyperglycaemic,  
 CC obesity-related, neurological, cardiac, anabolic, renal or immunological  
 CC disorder. The present sequence represents the amino acid sequence of an  
 CC IGFbp-3 binding peptide.  
 XX  
 SQ Sequence 18 AA;  
 XX  
 QY Query Match 41.8%; Score 28; DB 7; Length 18;  
 Best Local Similarity 83.3%; Pred. No. 1e+03;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 XX  
 Db 4 ECIIGP 12  
 4 ECIIGP 9  
 XX  
 RESULT 90  
 ADF47647  
 ID ADF47647 standard; peptide; 18 AA.  
 XX  
 AC ADF47647;  
 XX  
 DT 12-FEB-2004 (first entry)  
 XX  
 DE Insulin-like growth factor (IGF) inhibitory peptide #48.  
 XX  
 KW Insulin-like growth factor; IGF; inhibitory peptide; IGF binding protein;  
 KW hyperglycaemic disorder; diabetes; hyperlipidaemia;  
 KW obesity-related disease; neurological disorder; multiple sclerosis;  
 KW Alzheimer's disease; schizophrenia; depression; cardiac disorder;  
 KW congestive heart failure; renal disorder; chronic renal failure;  
 KW glomerulonephritis; glomerulosclerosis; interstitial nephritis;  
 KW immunological disorder; immunodeficiency; anabolic disorder;  
 KW osteoporosis.  
 XX  
 OS Synthetic.  
 XX  
 PN US6608031-B1.  
 XX  
 PD 19-AUG-2003.  
 XX  
 PF 28-NOV-2000; 2000US-00723890.  
 XX  
 PR 04-APR-1997; 97US-00825852.  
 PR 31-MAR-1998; 98US-00052888.  
 XX  
 PA (GETH ) GENENTECH INC.  
 PI Clark RG, Lowman HB, Robinson ICAF;  
 PT  
 PT WPI; 2004-030477/03.  
 XX  
 DR New insulin-like growth factor agonist peptides, useful for treating or  
 PT preventing hyperglycaemic disorders such as diabetes or hyperlipidaemia,  
 PT obesity-related diseases, or neurological disorders such as multiple  
 PT sclerosis.  
 XX  
 PS Example 7, SEQ ID NO 67, 117pp; English.  
 XX  
 CC The invention relates to an insulin-like growth factor (IGF) inhibitory  
 CC peptide which inhibits the interaction of an IGF with one or more of its  
 CC binding proteins. The peptides of the invention are useful for increasing  
 CC serum and tissue levels of active insulin-like growth factor in a mammal,  
 CC and for treating or preventing hyperglycaemic disorders such as diabetes,  
 CC hyperlipidaemia, obesity-related diseases, neurological disorders such as  
 CC multiple sclerosis, Alzheimer's disease, schizophrenia or depression.

CC cardiac disorders such as congestive heart failure, renal disorders such  
 CC as end-stage chronic renal failure, glomerulonephritis,  
 CC glomerulosclerosis or interstitial nephritis and immunological disorders  
 CC such as immunodeficiencies, anabolic disorders or osteoporosis. This  
 CC sequence represents an inhibitory peptide of the invention.  
 XX  
 SQ Sequence 18 AA;  
 XX  
 QY Query Match 41.8%; Score 28; DB 8; Length 18;  
 Best Local Similarity 66.7%; Pred. No. 1e+03;  
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 XX  
 Db 4 ECIIGP 12  
 4 ECIIGP 9  
 XX  
 RESULT 91  
 ADF47649  
 ID ADF47649 standard; peptide; 18 AA.  
 XX  
 AC ADF47649;  
 XX  
 DT 12-FEB-2004 (first entry)  
 XX  
 DE Insulin-like growth factor (IGF) inhibitory peptide #50.  
 XX  
 KW Insulin-like growth factor; IGF; inhibitory peptide; IGF binding protein;  
 KW hyperglycaemic disorder; diabetes; hyperlipidaemia;  
 KW obesity-related disease; neurological disorder; multiple sclerosis;  
 KW Alzheimer's disease; schizophrenia; depression; cardiac disorder;  
 KW congestive heart failure; renal disorder; chronic renal failure;  
 KW glomerulonephritis; glomerulosclerosis; interstitial nephritis;  
 KW immunological disorder; immunodeficiency; anabolic disorder;  
 KW osteoporosis.  
 XX  
 OS Synthetic.  
 XX  
 PN US6608031-B1.  
 XX  
 PD 19-AUG-2003.  
 XX  
 PF 28-NOV-2000; 2000US-00723890.  
 XX  
 PR 04-APR-1997; 97US-00825852.  
 PR 31-MAR-1998; 98US-00052888.  
 XX  
 PA (GETH ) GENENTECH INC.  
 PI Clark RG, Lowman HB, Robinson ICAF;  
 PT  
 PT WPI; 2004-030477/03.  
 XX  
 DR New insulin-like growth factor agonist peptides, useful for treating or  
 PT preventing hyperglycaemic disorders such as diabetes or hyperlipidaemia,  
 PT obesity-related diseases, or neurological disorders such as multiple  
 PT sclerosis.  
 XX  
 PS Example 7, SEQ ID NO 69; 117pp; English.  
 XX  
 CC The invention relates to an insulin-like growth factor (IGF) inhibitory  
 CC peptide which inhibits the interaction of an IGF with one or more of its  
 CC binding proteins. The peptides of the invention are useful for increasing  
 CC serum and tissue levels of active insulin-like growth factor in a mammal,  
 CC and for treating or preventing hyperglycaemic disorders such as diabetes,  
 CC hyperlipidaemia, obesity-related diseases, neurological disorders such as  
 CC multiple sclerosis, Alzheimer's disease, schizophrenia or depression,  
 CC cardiac disorders such as congestive heart failure, renal disorders such  
 CC as end-stage chronic renal failure, glomerulonephritis,  
 CC glomerulosclerosis or interstitial nephritis and immunological disorders  
 CC such as immunodeficiencies, anabolic disorders or osteoporosis. This  
 CC sequence represents an inhibitory peptide of the invention.

SQ Sequence 18 AA;

Query Match 41.8%; Score 28; DB 8; Length 18;

Best Local Similarity 83.3%; Pred. No. 1e+03;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 ECTIGP 12

DB 4 ECTIGP 9

RESULT 92

ADG39595

ID ADG39595 standard; peptide; 18 AA.

XX ADG39595;

DT 26-FEB-2004 (first entry)

DE IGFBP-3 binding peptide seq id 69.

XX insulin-like growth factor binding protein; IGFBP;

KW insulin-like growth factor; IGF binding site; IGFBP antibody;

KW solid-phase carrier; IGF receptor; IGFBP-3; IGF-I.

XX Synthetic.

XX US6645775-B1.

XX 11-NOV-2003.

PF 28-NOV-2000; 2000US-00723931.

XX 04-APR-1997; 97US-00825852.

PR 31-MAR-1998; 98US-00052888.

XX (GETH ) GENENTECH INC.

PI Clark RG, Lowman HB, Robinson ICAF;

DR WPI; 2004-050510/05.

PT fluid, by contacting the fluid with antibody that binds epitopes and  
PT peptide concentration to saturate insulin-like growth factor binding  
PT sites.

PS Example 7; SEQ ID NO 69; 116pp; English.

XX The invention describes a method of determining an amount of insulin-like  
CC growth factor binding protein (IGFBP) that binds a peptide in a  
CC biological fluid. Measuring the amount of insulin-like growth factor  
CC binding protein that binds a peptide in a biological fluid involves  
CC contacting the fluid with a first antibody attached to a solid-phase  
CC carrier and a concentration of the peptide for a time to saturate all IGF  
CC binding sites on the IGFBP to form a saturated complex. The first  
CC antibody binds epitopes on the IGFBP so that in the presence of the  
CC antibody the IGF binding sites remain on the IGFBP for binding the  
CC peptide thus forming a complex between the first antibody and the IGFBP.  
CC The unbound peptide is removed and the saturated complex is contacted  
CC with a labeled second antibody, which binds epitopes on the peptide that  
CC are available for binding when the peptide is bound to the IGFBP. The  
CC unbound second antibody is removed and the amount of labeled second bound  
CC is analysed as a measure of the amount of IGFBP in the biological sample.  
CC The method is useful for determining IGFBP that binds a peptide in a  
CC biological fluid. The method provides antibody attached to a solid-phase  
CC carrier and a peptide concentration that inhibits interaction of the IGF  
CC with IGFBPs and does not bind to human IGF receptor. This is the amino  
CC acid sequence of a peptide that binds IGFBP-3 blocking binding of IGFBP-3  
CC to IGF-I.

XX Sequence 18 AA;

SQ

Query Match 41.8%; Score 28; DB 8; Length 18;

Best Local Similarity 83.3%; Pred. No. 1e+03;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 ECTIGP 12

DB 4 ECTIGP 9

RESULT 93

ADG39593

ID ADG39593 standard; peptide; 18 AA.

XX ADG39593;

DT 26-FEB-2004 (first entry)

DE IGFBP-3 binding peptide seq id 67.

XX insulin-like growth factor binding protein; IGFBP;

KW insulin-like growth factor; IGF binding site; IGFBP antibody;

KW solid-phase carrier; IGF receptor; IGFBP-3; IGF-I.

XX Synthetic.

XX US6645775-B1.

XX 11-NOV-2003.

PF 28-NOV-2000; 2000US-00723931.

XX 04-APR-1997; 97US-00825852.

PR 31-MAR-1998; 98US-00052888.

XX (GETH ) GENENTECH INC.

PI Clark RG, Lowman HB, Robinson ICAF;

DR WPI; 2004-050510/05.

PT fluid, by contacting the fluid with antibody that binds epitopes and  
PT peptide concentration to saturate insulin-like growth factor binding  
PT sites.

PS Example 7; SEQ ID NO 67; 116pp; English.

XX The invention describes a method of determining an amount of insulin-like  
CC growth factor binding protein (IGFBP) that binds a peptide in a  
CC biological fluid. Measuring the amount of insulin-like growth factor  
CC binding protein that binds a peptide in a biological fluid involves  
CC contacting the fluid with a first antibody attached to a solid-phase  
CC carrier and a concentration of the peptide for a time to saturate all IGF  
CC binding sites on the IGFBP to form a saturated complex. The first  
CC antibody binds epitopes on the IGFBP so that in the presence of the  
CC antibody the IGF binding sites remain on the IGFBP for binding the  
CC peptide thus forming a complex between the first antibody and the IGFBP.  
CC The unbound peptide is removed and the saturated complex is contacted  
CC with a labeled second antibody, which binds epitopes on the peptide that  
CC are available for binding when the peptide is bound to the IGFBP. The  
CC unbound second antibody is removed and the amount of labeled second bound  
CC is analysed as a measure of the amount of IGFBP in the biological sample.  
CC The method is useful for determining IGFBP that binds a peptide in a  
CC biological fluid. The method provides antibody attached to a solid-phase  
CC carrier and a peptide concentration that inhibits interaction of the IGF  
CC with IGFBPs and does not bind to human IGF receptor. This is the amino  
CC acid sequence of a peptide that binds IGFBP-3 blocking binding of IGFBP-3  
CC to IGF-I.

XX Sequence 18 AA;

SQ

Query Match 41.8%; Score 28; DB 8; Length 18;

Best Local Similarity 66.7%; Pred. No. 1e+03;



Matches 4, Conservative 1, Mismatches 1, Indels 0, Gaps 0;

QY 7 ECLIGP 12  
 ||: ||  
 DB 4 ECWGP 9

RESULT 94  
 ADI62076  
 ID ADI62076 standard; peptide; 18 AA.  
 XX  
 AC ADI62076;  
 OS Synthetic.  
 XX  
 DT 15-APR-2004 (first entry)  
 XX  
 DE IGFBP-3 binding peptide from g8 display #21.  
 XX  
 KW Insulin-like growth factor; IGF; thiazolidinedione;  
 KW hyperglycaemic disorders; renal disorders; acute renal insufficiency;  
 KW chronic renal insufficiency; pyelonephritis; Turner's syndrome;  
 KW Laron's syndrome; congestive heart failure; neuromuscular disorders;  
 KW multiple sclerosis; trauma; infection; HIV; IGF-1; IGFBP-1;  
 KW protein co-ordinate data.  
 XX  
 OS Synthetic.  
 XX  
 PN US6677305-B1.  
 XX  
 PD 13-JAN-2004.  
 XX  
 PF 28-NOV-2000; 2000US-00723873.  
 XX  
 PR 04-APR-1997; 97US-00825852.  
 XX  
 PR 31-MAR-1998; 98US-00052888.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Clark RG, Lowman HB, Robinson ICAF;  
 XX  
 DR WPI; 2004-153869/15.  
 XX  
 PS Sterile pharmaceutical composition comprising insulin-like growth factor  
 PT and thiazolidinedione, useful for treating hyperglycemic disorders, renal  
 PT disorders, pyelonephritis, Turner's syndrome, Laron's syndrome.  
 XX  
 PS Example 7; SEQ ID NO 67; 116pp; English.  
 XX  
 CC The invention relates to a sterile pharmaceutical composition comprising  
 CC an insulin-like growth factor (IGF) and a thiazolidinedione. The  
 CC pharmaceutical composition is useful for treating hyperglycaemic  
 CC disorders, renal disorders such as acute and chronic renal insufficiency,  
 CC pyelonephritis, Turner's syndrome, Laron's syndrome, congestive heart  
 CC failure, neuromuscular disorders, multiple sclerosis, trauma, infections  
 CC such as HIV, etc. The present sequence is used in the exemplification of  
 CC the present invention.  
 XX  
 SQ Sequence 18 AA;

Query Match 41.8%; Score 28; DB 8; Length 18;  
 Best Local Similarity 66.7%; Pred. No. 1e+03;  
 Matches 4, Conservative 1, Mismatches 1, Indels 0, Gaps 0;

QY 7 ECLIGP 12  
 ||: ||  
 DB 4 ECWGP 9

RESULT 95  
 ADI62078  
 ID ADI62078 standard; peptide; 18 AA.  
 XX  
 AC ADI62078;  
 OS Synthetic.

DT 15-APR-2004 (first entry)  
 XX  
 DE IGFBP-3 binding peptide from g8 display #23.  
 XX  
 KW Insulin-like growth factor; IGF; thiazolidinedione;  
 KW hyperglycaemic disorders; renal disorders; acute renal insufficiency;  
 KW chronic renal insufficiency; pyelonephritis; Turner's syndrome;  
 KW Laron's syndrome; congestive heart failure; neuromuscular disorders;  
 KW multiple sclerosis; trauma; infection; HIV; IGF-1; IGFBP-1;  
 KW protein co-ordinate data.  
 XX  
 OS Synthetic.  
 XX  
 PN US6677305-B1.  
 XX  
 PD 13-JAN-2004.  
 XX  
 PF 28-NOV-2000; 2000US-00723873.  
 XX  
 PR 04-APR-1997; 97US-00825852.  
 XX  
 PR 31-MAR-1998; 98US-00052888.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Clark RG, Lowman HB, Robinson ICAF;  
 XX  
 DR WPI; 2004-153869/15.  
 XX  
 PS Sterile pharmaceutical composition comprising insulin-like growth factor  
 PT and thiazolidinedione, useful for treating hyperglycemic disorders, renal  
 PT disorders, pyelonephritis, Turner's syndrome, Laron's syndrome.  
 XX  
 PS Example 7; SEQ ID NO 69; 116pp; English.  
 XX  
 CC The invention relates to a sterile pharmaceutical composition comprising  
 CC an insulin-like growth factor (IGF) and a thiazolidinedione. The  
 CC pharmaceutical composition is useful for treating hyperglycaemic  
 CC disorders, renal disorders such as acute and chronic renal insufficiency,  
 CC pyelonephritis, Turner's syndrome, Laron's syndrome, congestive heart  
 CC failure, neuromuscular disorders, multiple sclerosis, trauma, infections  
 CC such as HIV, etc. The present sequence is used in the exemplification of  
 CC the present invention.  
 XX  
 SQ Sequence 18 AA;

Query Match 41.8%; Score 28; DB 8; Length 18;  
 Best Local Similarity 83.3%; Pred. No. 1e+03;  
 Matches 5, Conservative 0, Mismatches 1, Indels 0, Gaps 0;

QY 7 ECLIGP 12  
 ||| ||  
 DB 4 ECLIGP 9

RESULT 96  
 ADI57587  
 ID ADI57587 standard; peptide; 18 AA.  
 XX  
 AC ADI57587;  
 OS Synthetic.

DT 15-APR-2004 (first entry)  
 XX  
 DE Inhibitor of bonding of IGF-I to IGFBP-3, BP3-23B3.4.  
 XX  
 KW Insulin-like growth factor-I; IGF-I; IGF binding protein; IGFBP3;  
 KW agonist; hyperglycaemia; obesity; neurological disorder;  
 KW cardiac disorder; congestive heart failure; renal disorder;  
 KW immunological disorder; anabolic disorder; protein co-ordinate data.  
 XX  
 OS Synthetic.  
 XX  
 PN US6683053-B1.

```

PD 27-JAN-2004.
XX PF 28-NOV-2000; 2000US-00723913.
XX PR 04-APR-1997; 97US-00825852.
XX PR 31-MAR-1998; 98US-00052888.
XX PA (GETH ) GENENTECH INC.
XX PI Clark RG, Lowman HB, Robinson ICAF;
XX DR WPI; 2004-118578/12.
XX PT New insulin-like growth factor binding protein, for preparing a
XX PT composition for treating e.g. obesity-related, neurological, cardiac,
XX PT renal or immunological disorders.
XX PS Example 7; SEQ ID NO 67; 117pp; English.
XX
XX CC The invention relates to a peptide which inhibits the binding of insulin-
XX CC like growth factor-1 (IGF-1) to IGF binding protein (IGFBP) but does not
XX CC inhibit binding of IGF-1 to its receptor, comprising the peptides
XX CC appearing as AD157608, AD157618-AD157620. Also included are a composition
XX CC comprising the peptide in a carrier, a kit comprising a container
XX CC containing the composition and instructions directing the user to utilize
XX CC the composition. The composition is further comprises a growth hormone, a
XX CC growth hormone releasing peptide, a growth hormone releasing hormone, a
XX CC growth hormone secretagogue, an insulin-like growth factor (IGF), an IGF
XX CC in combination with an IGF binding protein, an IGF binding protein, a
XX CC growth hormone in combination with growth hormone binding protein, a
XX CC insulin or hypoglycaemic agent. The peptide is useful as IGF agonist for
XX CC preparing a composition for treating e.g. hypoglycaemic, obesity-
XX CC related, neurological, cardiac (e.g. congestive heart failure), renal or
XX CC immunological disorders. The present sequence inhibits binding of IGF-1
XX CC to IGFBP-3.
XX
SQ Sequence 18 AA;
XX
Query Match 41.8%; Score 28; DB 8; Length 18;
Best Local Similarity 66.7%; Pred. No.1e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0
OY 7 ECIIGP 12
||: ||
4 ECVWGP 9
DB
RESULT 97
AD157589
ID AD157589 standard; peptide; 18 AA.
XX AC AD157589;
XX
DT 15-APR-2004 (first entry)
XX
DE Inhibitor of bonding of IGF-1 to IGFBP-3, BP3-23B3.7.
XX
KW Insulin-like growth factor-1; IGF-1; IGF binding protein; IGFBP3;
KW agonist; hypoglycaemia; obesity; neurological disorder;
KW cardiac disorder; congestive heart failure; renal disorder;
KW immunological disorder; anabolic disorder; protein co-ordinate data.
XX OS Synthetic.
XX PN US6683053-B1.
XX PD 27-JAN-2004.
XX PF 28-NOV-2000; 2000US-00723913.
XX PR 04-APR-1997; 97US-00825852.
XX PR 31-MAR-1998; 98US-00052888.
XX

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PA (GETH ) GENENTECH INC.
PX
PI Clark RG, Lowman HB, Robinson ICAF,
DR WPI; 2004-118578/12.
XX
XX New insulin-like growth factor binding protein, for preparing a
PT composition for treating e.g. obesity-related, neurological, cardiac,
PT renal or immunological disorders.
XX
XX Example 7; SEQ ID NO 69; 117pp; English.
XX
CC The invention relates to a peptide which inhibits the binding of insulin-
CC like growth factor-1 (IGF-1) to IGF binding protein (IGFBP) but does not
CC inhibit binding of IGF-1 to its receptor, comprising the peptides
CC appearing as AD157608, AD157616-AD157620. Also included are a composition
CC comprising the peptide in a carrier, a kit comprising a container
CC containing the composition and instructions directing the user to utilize
CC the composition. The composition is further comprises a growth hormone, a
CC growth hormone releasing peptide, a growth hormone releasing hormone, a
CC growth hormone secretagogue, an insulin-like growth factor (IGF), an IGF
CC in combination with an IGF binding protein, an IGF binding protein, a
CC growth hormone in combination with growth hormone binding protein,
CC insulin or hypoglycaemic agent. The peptide is useful as IGF agonist for
CC preparing a composition for treating e.g. hyperglycaemic, obesity-
CC related, neurological, cardiac (e.g. congestive heart failure), renal or
CC immunological disorders. The present sequence inhibits binding of IGF-1
CC to IGFBP-3.
XX
SQ Sequence 18 AA;
XX
Query Match 41.8%; Score 28; DB 8; Length 18;
Best Local Similarity 83.3%; Pred. No. 1e+03;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 7 ECICGP 12
DB 4 ECICGP 9
XX
RESULT 98
AD157480
ID AD157480 standard; peptide; 18 AA.
XX
AC AD157480;
XX
DT 22-APR-2004 (first entry)
XX
DE Inhibitor of bonding of IGF-1 to IGFBP-3, BP3-23b3.4.
XX
XX Insulin-like growth factor-1; IGF-1; IGF binding protein; IGFBP3;
KW agonist; hyperglycaemia; obesity; neurological disorder;
KW cardiac disorder; congestive heart failure; renal disorder;
KW immunological disorder; anabolic disorder; protein co-ordinate data.
XX
OS Synthetic.
XX
XX US6680298-B1.
XX
XX 20-JAN-2004.
XX
XX 28-NOV-2000; 2000US-00724114.
XX
XX 04-APR-1997; 97US-00825852.
XX
XX 31-MAR-1998; 98US-00052888.
XX
XX (GETH ) GENENTECH INC.
XX
XX Clark RG, Lowman HB, Robinson ICAF;
XX
XX WPI; 2004-141375/14.
XX
XX Increasing serum and tissue levels of insulin-like growth factor-1 in

```

PT humans, useful for treating diabetes, comprises administering an amount  
 PT of a peptide that e.g. reduces plasma insulin secretion or blood glucose  
 PT levels.  
 XX  
 XX Example 7, SEQ ID NO 67, 121pp, English.  
 XX  
 CC The invention relates to a peptide which inhibits the binding of insulin-  
 CC like growth factor-1 (IGF-1) to IGF binding protein (IGFBP) but does not  
 CC inhibit binding of IGF-1 to its receptor, comprising the peptides  
 CC appearing as AD157501, AD157509-AD157513. Also included are a composition  
 CC comprising the peptide in a carrier, a kit comprising a container  
 CC containing the composition and instructions directing the user to utilize  
 CC the composition. The composition is further comprises a growth hormone, a  
 CC growth hormone releasing peptide, a growth hormone releasing hormone, a  
 CC growth hormone secretagogue, an insulin-like growth factor (IGF), an IGF  
 CC in combination with an IGF binding protein, an IGF binding protein, a  
 CC growth hormone in combination with growth hormone binding protein,  
 CC insulin or hypoglycaemic agent. The peptide is useful as IGF agonist for  
 CC preparing a composition for treating e.g. hyperglycaemic, obesity-  
 CC related, neurological, cardiac (e.g. congestive heart failure), renal or  
 CC immunological disorders. The present sequence inhibits binding of IGF-1  
 CC to IGFBP-3.  
 CC  
 XX  
 XX Sequence 18 AA;  
 S0  
 Query Match 41.8%; Score 28; DB 8; Length 18;  
 Best Local Similarity 66.7%; Pred. NO. 1e+03;  
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 7 ECTIGP 12  
 ID AD157482  
 DB 4 ECTWGP 9  
 AD157482 standard; peptide; 18 AA.  
 AD157482;  
 22-APR-2004 (first entry)  
 Inhibitor of bonding of IGF-1 to IGFBP-3, BP3-23B3.7.  
 Insulin-like growth factor-1; IGF-1; IGF binding protein; IGFBP3;  
 agonist; hyperglycaemia; obesity; neurological disorder;  
 cardiac disorder; congestive heart failure; renal disorder;  
 immunological disorder; anabolic disorder; protein co-ordinate data.  
 OS  
 XX Synthetic.  
 XX US6680298-B1.  
 XX  
 XX 20-JAN-2004.  
 XX  
 XX 28-NOV-2000; 2000US-00724114.  
 XX  
 XX 04-APR-1997; 97US-00825852.  
 XX  
 XX 31-MAR-1998; 98US-00052888.  
 XX  
 XX (GENTH ) GENENTECH INC.  
 XX  
 XX Clark RG, Lowman HB, Robinson ICAF,  
 XX  
 XX WPI; 2004-141375/14.  
 XX  
 PT Increasing serum and tissue levels of insulin-like growth factor-1 in  
 PT humans, useful for treating diabetes, comprises administering an amount  
 PT of a peptide that e.g. reduces plasma insulin secretion or blood glucose  
 PT levels.  
 XX  
 XX Example 7, SEQ ID NO 69, 121pp, English.

CC The invention relates to a peptide which inhibits the binding of insulin-  
 CC like growth factor-1 (IGF-1) to IGF binding protein (IGFBP) but does not  
 CC inhibit binding of IGF-1 to its receptor, comprising the peptides  
 CC appearing as AD157501, AD157509-AD157513. Also included are a composition  
 CC comprising the peptide in a carrier, a kit comprising a container  
 CC containing the composition and instructions directing the user to utilize  
 CC the composition. The composition is further comprises a growth hormone, a  
 CC growth hormone releasing peptide, a growth hormone releasing hormone, a  
 CC growth hormone secretagogue, an insulin-like growth factor (IGF), an IGF  
 CC in combination with an IGF binding protein, an IGF binding protein, a  
 CC growth hormone in combination with growth hormone binding protein,  
 CC insulin or hypoglycaemic agent. The peptide is useful as IGF agonist for  
 CC preparing a composition for treating e.g. hyperglycaemic, obesity-  
 CC related, neurological, cardiac (e.g. congestive heart failure), renal or  
 CC immunological disorders. The present sequence inhibits binding of IGF-1  
 CC to IGFBP-3.  
 CC  
 XX  
 XX Sequence 18 AA;  
 S0  
 Query Match 41.8%; Score 28; DB 8; Length 18;  
 Best Local Similarity 83.3%; Pred. NO. 1e+03;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 7 ECTIGP 12  
 ID ADJ56638  
 DB 4 ECTIGP 9  
 ADJ56638 standard; peptide; 18 AA.  
 ADJ56638;  
 06-MAY-2004 (first entry)  
 Inhibitor of bonding of IGF-1 to IGFBP-3, BP3-23B3.7.  
 Insulin-like growth factor-1; IGF-1; IGF binding protein; IGFBP3;  
 agonist; hyperglycaemia; obesity; neurological disorder;  
 cardiac disorder; congestive heart failure; renal disorder;  
 immunological disorder; anabolic disorder; protein co-ordinate data.  
 OS  
 XX Synthetic.  
 XX US6693079-B1.  
 XX  
 XX 17-FEB-2004.  
 XX  
 XX 28-NOV-2000; 2000US-00724157.  
 XX  
 XX 04-APR-1997; 97US-00825852.  
 XX  
 XX 31-MAR-1998; 98US-00052888.  
 XX  
 XX (GENTH ) GENENTECH INC.  
 XX  
 XX Clark RG, Lowman HB, Robinson ICAF,  
 XX  
 XX WPI; 2004-223910/21.  
 XX  
 PT New peptide that binds an IGF binding protein, useful for preparing a  
 PT composition for treating various diseases, e.g., cardiac or renal  
 PT disorders.  
 XX  
 XX Example 7, SEQ ID NO 69, 117pp, English.  
 XX  
 CC The invention relates to a peptide which inhibits the binding of insulin-  
 CC like growth factor-1 (IGF-1) to IGF binding protein (IGFBP) but does not  
 CC inhibit binding of IGF-1 to its receptor, comprising the peptides  
 CC appearing as ADJ56652 and ADJ56586. Also included are a composition  
 CC comprising the peptide in a carrier, a kit comprising a container  
 CC containing the composition and instructions directing the user to utilize  
 CC the composition. The composition is further comprises a growth hormone, a

CC growth hormone releasing peptide, a growth hormone releasing hormone, a  
CC growth hormone secretagogue, an insulin-like growth factor (IGF), an IGF  
CC in combination with an IGF binding protein, an IGF binding protein, a  
CC growth hormone in combination with growth hormone binding protein, a  
CC insulin or hypoglycaemic agent. The peptide is useful as IGF agonist for  
CC preparing a composition for treating e.g. hyperglycaemic, obesity-  
CC related, neurological, cardiac (e.g. congestive heart failure), renal or  
CC immunological disorders. The present sequence inhibits binding of IGF-1  
to IGFBP-3.

XX  
SQ Sequence 18 AA;

Query Match 41.8%; Score 28; DB 8; Length 18;

Best Local Similarity 83.3%; Pred. No. 1e+03;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 ECIIIGP 12

DB 4 ECIEGP 9

Search completed: January 20, 2006, 19:05:20  
Job time : 48.3462 secs

GenCore version 5.1.6  
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OM protein - protein search, using SW model

Run on: January 20, 2006, 18:58:05 ; Search time 12.5769 Seconds  
(without alignments)  
78.863 Million cell updates/sec

Title: US-09-662-293-5

Perfect score: 67

Sequence: 1 DENNSPFCILGP 12

Scoring table: BLOSUM62

Searched: Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 223517

Minimum DB seq length: 0  
Maximum DB seq length: 20

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 100 summaries

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4: /cgn2\_6/prodata/1/1aa/8 COMB.pep:\*  
5: /cgn2\_6/prodata/1/1aa/9 COMB.pep:\*  
6: /cgn2\_6/prodata/1/1aa/backfile1.pep:\*

Prod. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	34	50.7	20	1	US-08-484-635-187
3	34	50.7	20	1	US-08-484-631-187
4	34	50.7	20	1	US-08-827-570-187
5	32	47.8	15	1	US-08-179-481-17
6	32	47.8	15	1	US-08-484-635-135
7	32	47.8	15	1	US-08-484-631-135
8	32	47.8	15	1	US-08-827-570-135
9	31	46.3	9	6	5204326-137
10	30	44.8	16	1	US-08-092-817-6
11	30	44.8	16	1	US-08-485-128-6
12	30	44.8	16	2	US-09-824-637-6
13	30	44.8	20	1	US-08-484-135-43
14	30	44.8	20	1	US-08-484-635-27
15	30	44.8	20	1	US-08-484-631-27
16	30	44.8	20	1	US-08-827-570-27
17	30	44.8	20	2	US-09-449-064A-47
18	29	43.3	19	1	US-08-484-635-136
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23	29	43.3	20	1	US-08-484-135-79
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84	29	43.3	20	1	US-08-827-570-96
85	29	43.3	20	1	US-08-827-570-97
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88	29	43.3	20	1	US-08-827-570-100
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92	29	43.3	20	1	US-08-827-570-104
93	29	43.3	20	1	US-08-827-570-105
94	29	43.3	20	1	US-08-827-570-106
95	29	43.3	20	1	US-08-827-570-107
96	29	43.3	20	1	US-08-827-570-108
97	29	43.3	20	1	US-08-827-570-109
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99	29	43.3	20	1	US-08-827-570-111
100	29	43.3	20	1	US-08-827-570-112

## ALIGNMENTS

## RESULT 1

US-09-292-225-5  
Sequence 5, Application US/09292225  
Patent No. 6455686  
GENERAL INFORMATION:  
APPLICANT: McCall, Catherine A.  
APPLICANT: Hunter, Shirley Wu  
APPLICANT: Weber, Eric R.  
TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS  
TITLE OF INVENTION: AND USES THEREOF  
FILE REFERENCE: AT-2-C3  
CURRENT APPLICATION NUMBER: US/09/292,225  
CURRENT FILING DATE: 1999-04-15  
EARLIER APPLICATION NUMBER: 60/098,909  
EARLIER FILING DATE: 1998-09-02  
EARLIER APPLICATION NUMBER: 60/085,295  
EARLIER FILING DATE: 1998-05-13  
EARLIER APPLICATION NUMBER: 60/098,565  
EARLIER FILING DATE: 1998-04-17  
EARLIER APPLICATION NUMBER: 09/062,013  
EARLIER FILING DATE: 1998-04-17  
NUMBER OF SEQ ID NOS: 49  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 5  
LENGTH: 12  
TYPE: PRT  
ORGANISM: Dermatophagoides farinae  
US-09-292-225-5

Query Match Best Local Similarity 100.0%; Score 67; DB 2; Length 12;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEKNSFECILGP 12  
Db 1 DEKNSFECILGP 12

## RESULT 2

US-08-484-635-187  
Sequence 187, Application US/08484635  
Patent No. 5773569  
GENERAL INFORMATION:  
APPLICANT: Wrighton, Nicholas C.  
APPLICANT: Dower, William J.  
APPLICANT: Chang, Ray S.  
APPLICANT: Kashyap, Arun K.  
APPLICANT: Jolliffe, Linda K.  
APPLICANT: Johnson, Dana  
APPLICANT: Mulcahy, Linda  
TITLE OF INVENTION: Compounds and Peptides That Bind to the  
TITLE OF INVENTION: Erythropoietin Receptor  
NUMBER OF SEQUENCES: 259  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew  
STREET: One Market Plaza, Stewart Street Tower  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105-1492  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/484,635  
FILING DATE: 07-JUN-1995

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/155,940

FILING DATE: 19-NOV-1993

ATTORNEY/AGENT INFORMATION:

NAME: Garrett-Wackowski, Eugenia

REGISTRATION NUMBER: 37,330

REFERENCE/DOCKET NUMBER: 16528A-43-1-1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 543-9600

TELEFAX: (415) 543-5043

INFORMATION FOR SEQ ID NO: 187:

SEQUENCE CHARACTERISTICS:

LENGTH: 20 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: peptide

Query Match Best Local Similarity 50.7%; Score 34; DB 1; Length 20;

Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 3 KNSFECILGP 12  
Db 2 KNNYRCQGRF 11

## RESULT 3

US-08-484-631-187  
Sequence 187, Application US/08484631  
Patent No. 5830851  
GENERAL INFORMATION:  
APPLICANT: Wrighton, Nicholas C.  
APPLICANT: Dower, William J.  
APPLICANT: Chang, Ray S.  
APPLICANT: Kashyap, Arun K.  
APPLICANT: Jolliffe, Linda K.  
APPLICANT: Johnson, Dana  
APPLICANT: Mulcahy, Linda  
TITLE OF INVENTION: Compounds and Peptides That Bind to the  
TITLE OF INVENTION: Erythropoietin Receptor  
NUMBER OF SEQUENCES: 259  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew  
STREET: One Market Plaza, Stewart Street Tower  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105-1492  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/484,631  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/155,940  
FILING DATE: 19-NOV-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Garrett-Wackowski, Eugenia  
REGISTRATION NUMBER: 37,330  
REFERENCE/DOCKET NUMBER: 16528A-43-1-2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 543-9600  
TELEFAX: (415) 543-5043  
INFORMATION FOR SEQ ID NO: 187:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids

TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-484-631-187

Query Match 50.7%; Score 34; DB 1; Length 20;  
Best Local Similarity 50.0%; Pred. No. 21;  
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 KNSPECTLGP 12  
|:|:|  
DB 2 KNNVRCQFGP 11

RESULT 4  
US-08-827-570-187  
Sequence 187, Application US/08827570  
Patent No. 5986047  
GENERAL INFORMATION:  
APPLICANT: Wrighton, Nicholas C.  
APPLICANT: Dower, William J.  
APPLICANT: Chang, Ray S.  
APPLICANT: Kashyap, Arun K.  
APPLICANT: Jolliffe, Linda K.  
APPLICANT: Johnson, Dana  
APPLICANT: Mulcahy, Linda  
TITLE OF INVENTION: Compounds and Peptides That Bind to the  
TITLE OF INVENTION: Erythropoietin Receptor  
NUMBER OF SEQUENCES: 259  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew  
STREET: One Market Plaza, Stewart Street Tower  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105-1492  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/827,570  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/484,635  
FILING DATE: 07-JUN-1995  
APPLICATION NUMBER: US 08/155,940  
FILING DATE: 19-NOV-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Garrett-Wackowski, Eugenia  
REGISTRATION NUMBER: 37,330  
REFERENCE/DOCKET NUMBER: 16528A-43-1-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 543-9600  
TELEFAX: (415) 543-5043  
INFORMATION FOR SEQ ID NO: 187:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-827-570-187

Query Match 50.7%; Score 34; DB 1; Length 20;  
Best Local Similarity 50.0%; Pred. No. 21;  
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 KNSPECTLGP 12  
|:|:|

DB 2 KNNVRCQFGP 11

RESULT 5  
US-08-179-481-17  
Sequence 17, Application US/08179481  
Patent No. 5624816  
GENERAL INFORMATION:  
APPLICANT: CARAWAY, KENNETH L.  
APPLICANT: CAROTHERS CARAWAY, CORALIE A.  
APPLICANT: FREIGEN, NEVIS L.  
TITLE OF INVENTION: ONCOGENE PRODUCT LIGAND  
NUMBER OF SEQUENCES: 125  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CUSHMAN, DARBY & CUSHMAN  
STREET: 1100 NEW YORK AVENUE, N.W.  
CITY: WASHINGTON  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005-3918  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/179,481  
FILING DATE: 28-DEC-1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/922,521  
FILING DATE: 30-JUL-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: KOKULIS, PAUL N.  
REGISTRATION NUMBER: 16,773  
REFERENCE/DOCKET NUMBER: 200702/UM92-08CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 861-3000  
TELEFAX: (202) 822-0944  
TELLEX: 6714627 CUSH  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-179-481-17

Query Match 47.8%; Score 32; DB 1; Length 15;  
Best Local Similarity 62.5%; Pred. No. 36;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 DKNSPEC 8  
|:|:|  
DB 2 DDINSYEC 9

RESULT 6  
US-08-484-635-135  
Sequence 135, Application US/08484635  
Patent No. 5773569  
GENERAL INFORMATION:  
APPLICANT: Wrighton, Nicholas C.  
APPLICANT: Dower, William J.  
APPLICANT: Chang, Ray S.  
APPLICANT: Kashyap, Arun K.  
APPLICANT: Jolliffe, Linda K.  
APPLICANT: Johnson, Dana  
APPLICANT: Mulcahy, Linda  
TITLE OF INVENTION: Compounds and Peptides That Bind to the  
TITLE OF INVENTION: Erythropoietin Receptor  
NUMBER OF SEQUENCES: 259

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew  
STREET: One Market Plaza, Stewart Street Tower  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105-1492  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/484,635  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/155,940  
FILING DATE: 19-NOV-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Garrett-Wackowski, Eugenia  
REGISTRATION NUMBER: 37,330  
REFERENCE/DOCKET NUMBER: 16528A-43-1-1  
TELEPHONE: (415) 543-9600  
TELEFAX: (415) 543-5043  
INFORMATION FOR SEQ ID NO: 135:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-484-635-135

Query Match 47.8%; Score 32; DB 1; Length 19;  
Best Local Similarity 40.0%; Pred. No. 45;  
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 KNSFCTIGP 12  
DB 2 KTKYKCYWGP 11

RESULT 7  
US-08-484-631-135  
Sequence 135, Application US/08484631  
Patent No. 5830851  
GENERAL INFORMATION:  
APPLICANT: Wrighton, Nicholas C.  
APPLICANT: Dower, William J.  
APPLICANT: Chang, Ray S.  
APPLICANT: Kashyap, Arun K.  
APPLICANT: Jolliffe, Linda K.  
APPLICANT: Johnson, Dana  
APPLICANT: Mulcahy, Linda  
TITLE OF INVENTION: Compounds and Peptides That Bind to the  
TITLE OF INVENTION: Erythropoietin Receptor  
NUMBER OF SEQUENCES: 259  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew  
STREET: One Market Plaza, Stewart Street Tower  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105-1492  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/484,631

FILING DATE: 07-JUN-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/155,940  
FILING DATE: 19-NOV-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Garrett-Wackowski, Eugenia  
REGISTRATION NUMBER: 37,330  
REFERENCE/DOCKET NUMBER: 16528A-43-1-2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 543-9600  
TELEFAX: (415) 543-5043  
INFORMATION FOR SEQ ID NO: 135:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-484-631-135

Query Match 47.8%; Score 32; DB 1; Length 19;  
Best Local Similarity 40.0%; Pred. No. 45;  
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 KNSFCTIGP 12  
DB 2 KTKYKCYWGP 11

RESULT 8  
US-08-827-570-135  
Sequence 135, Application US/08827570  
Patent No. 5986047  
GENERAL INFORMATION:  
APPLICANT: Wrighton, Nicholas C.  
APPLICANT: Dower, William J.  
APPLICANT: Chang, Ray S.  
APPLICANT: Kashyap, Arun K.  
APPLICANT: Jolliffe, Linda K.  
APPLICANT: Johnson, Dana  
APPLICANT: Mulcahy, Linda  
TITLE OF INVENTION: Compounds and Peptides That Bind to the  
TITLE OF INVENTION: Erythropoietin Receptor  
NUMBER OF SEQUENCES: 259  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew  
STREET: One Market Plaza, Stewart Street Tower  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105-1492  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/827,570  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/484,635  
FILING DATE: 07-JUN-1995  
APPLICATION NUMBER: US 08/155,940  
FILING DATE: 19-NOV-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Garrett-Wackowski, Eugenia  
REGISTRATION NUMBER: 37,330  
REFERENCE/DOCKET NUMBER: 16528A-43-1-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 543-9600  
TELEFAX: (415) 543-5043



/ INFORMATION FOR SEQ ID NO: 135:  
/ SEQUENCE CHARACTERISTICS:  
/ LENGTH: 19 amino acids  
/ TYPE: amino acid  
/ STRANDEDNESS:  
/ TOPOLOGY: linear  
/ MOLECULE TYPE: peptide  
/ US-08-827-570-135

Query Match 47.8%; Score 32; DB 1; Length 19;  
Best Local Similarity 40.0%; Pred. No. 45;  
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 3 KNSPFCILGP 12  
Db 2 KTKYKCTMGP 11

RESULT 9  
5204326-127  
/ Patent No. 5204326  
/ APPLICANT: FUJII, SETSURO,YAMAMOTO, YOSHIMITO,SHIMIZU, FUMIO  
/ INAI, MASATOSHI,KINOSHITA, NAOSUMI,NAKAMURA, SHIZUO,HIROASHI,  
/ MITSURU, SAKAMOTO, TAKASHI,TSUTSUMI, KAZUHIKO,SHIRASAKA, TETSUHIKO  
/ TITLE OF INVENTION: POLYPEPTIDE DERIVATIVES AND CALCIUM  
/ METABOLISM IMPROVING AGENT  
/ NUMBER OF SEQUENCES: 147  
/ CURRENT APPLICATION DATA:  
/ APPLICANT: RUBINSTEIN, Menachem  
/ FILING DATE: 14-MAR-1990  
/ SEQ ID NO:127:  
/ LENGTH: 9  
/ 5204326-127

Query Match 46.3%; Score 31; DB 6; Length 9;  
Best Local Similarity 62.5%; Pred. No. 4.6e+05;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 4 NSPFCILG 11  
Db 2 NSLTCVIG 9

RESULT 10  
US-08-092-817-6  
/ Sequence 6, Application US/08092817  
/ Patent No. 5496926  
/ GENERAL INFORMATION:  
/ APPLICANT: RUBINSTEIN, Menachem  
/ APPLICANT: NOVICK, Daniela  
/ APPLICANT: TAL, Nathan  
/ TITLE OF INVENTION: SOLUBLE LDL RECEPTOR, ITS PRODUCTION AND  
/ TITLE OF INVENTION: USE  
/ NUMBER OF SEQUENCES: 6  
/ CORRESPONDENCE ADDRESS:  
/ ADDRESSEE: BROWDY AND NEIMARK  
/ STREET: 419 Seventh Street, Suite 300  
/ CITY: Washington  
/ STATE: D.C.  
/ COUNTRY: USA  
/ ZIP: 20004  
/ COMPUTER READABLE FORM:  
/ MEDIUM TYPE: floppy disk  
/ COMPUTER: IBM PC compatible  
/ OPERATING SYSTEM: PC-DOS/MS-DOS  
/ SOFTWARE: Patentin Release #1.0, Version #1.25  
/ CURRENT APPLICATION DATA:  
/ APPLICATION NUMBER: US/08/092.817  
/ FILING DATE: 19-JUL-1993  
/ CLASSIFICATION: 435  
/ PRIOR APPLICATION DATA:  
/ APPLICATION NUMBER: IL 100696  
/ FILING DATE: 19-JAN-1992

/ PRIOR APPLICATION DATA:  
/ APPLICATION NUMBER: IL 102915  
/ FILING DATE: 23-AUG-1992  
/ ATTORNEY/AGENT INFORMATION:  
/ NAME: TOWNSEND, G. Kevin  
/ REGISTRATION NUMBER: 34,033  
/ REFERENCE/DOCKET NUMBER: RUBINSTEIN-5A  
/ TELECOMMUNICATION INFORMATION:  
/ TELEPHONE: 202-628-5197  
/ TELEFAX: 202-737-3528  
/ TELLEX: 248633

/ INFORMATION FOR SEQ ID NO: 6:  
/ SEQUENCE CHARACTERISTICS:  
/ LENGTH: 16 amino acids  
/ TYPE: amino acid  
/ STRANDEDNESS: single  
/ TOPOLOGY: linear  
/ MOLECULE TYPE: peptide  
/ US-08-092-817-6

Query Match 44.8%; Score 30; DB 1; Length 16;  
Best Local Similarity 57.1%; Pred. No. 86;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 EKNSPFC 8  
Db 4 ERNEPFC 10

RESULT 11  
US-08-485-128-6  
/ Sequence 6, Application US/08485128  
/ Patent No. 6365713  
/ GENERAL INFORMATION:  
/ APPLICANT: RUBINSTEIN, Menachem  
/ APPLICANT: NOVICK, Daniela  
/ APPLICANT: TAL, Nathan  
/ TITLE OF INVENTION: SOLUBLE LDL RECEPTOR, ITS PRODUCTION AND  
/ TITLE OF INVENTION: USE  
/ NUMBER OF SEQUENCES: 6  
/ CORRESPONDENCE ADDRESS:  
/ ADDRESSEE: BROWDY AND NEIMARK  
/ STREET: 419 Seventh Street, Suite 300  
/ CITY: Washington  
/ STATE: D.C.  
/ COUNTRY: USA  
/ ZIP: 20004  
/ COMPUTER READABLE FORM:  
/ MEDIUM TYPE: floppy disk  
/ COMPUTER: IBM PC compatible  
/ OPERATING SYSTEM: PC-DOS/MS-DOS  
/ SOFTWARE: Patentin Release #1.0, Version #1.25  
/ CURRENT APPLICATION DATA:  
/ APPLICATION NUMBER: US/08/485.128  
/ FILING DATE: 07-JUN-1995  
/ CLASSIFICATION: 530  
/ PRIOR APPLICATION DATA:  
/ APPLICATION NUMBER: US 08/092,817  
/ FILING DATE: 19-JUL-1993  
/ APPLICATION NUMBER: IL 100696  
/ FILING DATE: 19-JAN-1992  
/ PRIOR APPLICATION DATA:  
/ APPLICATION NUMBER: IL 102915  
/ FILING DATE: 23-AUG-1992  
/ ATTORNEY/AGENT INFORMATION:  
/ NAME: TOWNSEND, G. Kevin  
/ REGISTRATION NUMBER: 34,033  
/ REFERENCE/DOCKET NUMBER: RUBINSTEIN-5A  
/ TELECOMMUNICATION INFORMATION:  
/ TELEPHONE: 202-628-5197  
/ TELEFAX: 202-737-3528  
/ TELLEX: 248633  
/ INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:  
LENGTH: 16 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-485-128-6

Query Match 44.8%; Score 30; DB 2; Length 16;  
Best Local Similarity 57.1%; Pred. No. 86;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 EKNSEFC 8  
Db 4 ERNRFQC 10

RESULT 12  
US-09-824-637-6  
Sequence 6, Application US/09824637  
Patent No. 6703222  
GENERAL INFORMATION:  
APPLICANT: RUBINSTEIN, Menachem  
APPLICANT: NOVICK, Daniela  
APPLICANT: TAL, Nachan  
APPLICANT: Fischer, Dina  
TITLE OF INVENTION: SOLUBLE LDL RECEPTOR, ITS PRODUCTION AND USE  
FILE REFERENCE: RUBINSTEIN-5D  
CURRENT APPLICATION NUMBER: US/09/824,637  
CURRENT FILING DATE: 2001-04-04  
PRIOR APPLICATION NUMBER: US 08/485,128  
PRIOR FILING DATE: 1995-06-07  
PRIOR APPLICATION NUMBER: US 08/092,817  
PRIOR FILING DATE: 1993-07-19  
PRIOR APPLICATION NUMBER: IL 100696  
PRIOR FILING DATE: 1992-01-19  
PRIOR APPLICATION NUMBER: IL 102915  
PRIOR FILING DATE: 1992-08-23  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 6  
LENGTH: 16  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-824-637-6

Query Match 44.8%; Score 30; DB 2; Length 16;  
Best Local Similarity 57.1%; Pred. No. 86;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 EKNSEFC 8  
Db 4 ERNRFQC 10

RESULT 13  
US-08-484-135-43  
Sequence 43, Application US/08484135  
Patent No. 5767078  
GENERAL INFORMATION:  
APPLICANT: Johnson, Dana L  
APPLICANT: ZIVLIN, Robert A  
TITLE OF INVENTION: AGONIST PEPTIDE DIMERS  
NUMBER OF SEQUENCES: 93  
CORRESPONDENCE ADDRESS:  
ADDRESSES: Frank S. Digiglio  
STREET: 400 Garden City Plaza  
CITY: Garden City  
STATE: New York  
COUNTRY: U.S.A..  
ZIP: 11530  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/484,135  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Digiglio, Frank S  
REGISTRATION NUMBER: 31,346  
REFERENCE/DOCKET NUMBER: 9594  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (516) 742-4343  
TELEFAX: (516) 742-4366  
INFORMATION FOR SEQ ID NO: 43:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-484-135-43

Query Match 44.8%; Score 30; DB 1; Length 20;  
Best Local Similarity 42.9%; Pred. No. 1.1e+02;  
Matches 3; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 6 PCLTIGP 12  
Db 4 YKCLMGF 10

RESULT 14  
US-08-484-635-27  
Sequence 27, Application US/08484635  
Patent No. 5773569  
GENERAL INFORMATION:  
APPLICANT: Wrighton, Nicholas C.  
APPLICANT: Dower, William J.  
APPLICANT: Chang, Ray S.  
APPLICANT: Kashyap, Arun K.  
APPLICANT: Jolliffe, Linda K.  
APPLICANT: Johnson, Dana  
APPLICANT: Mulcahy, Linda  
TITLE OF INVENTION: Compounds and Peptides That Bind to the  
NUMBER OF SEQUENCES: 259  
CORRESPONDENCE ADDRESS:  
ADDRESSES: Townsend and Townsend and Crew  
STREET: One Market Plaza, Stewart Street Tower  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105-1492  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/484,635  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/155,940  
FILING DATE: 19-NOV-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Garrett-Wackowski, Eugenia  
REGISTRATION NUMBER: 37,330  
REFERENCE/DOCKET NUMBER: 16528A-43-1-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 543-9600  
TELEFAX: (415) 543-5043

INFORMATION FOR SEQ ID NO: 27:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-484-631-27

Query Match 44.8%; Score 30; DB 1; Length 20;  
Best Local Similarity 42.9%; Pred. No. 1.1e+02;  
Matches 3; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 6 FECTIGP 12  
DB 4 YKCLMGP 10

RESULT 15  
US-08-484-631-27  
Sequence 27, Application US/08484631  
Patent No. 5830851  
GENERAL INFORMATION:  
APPLICANT: Wighton, Nicholas C.  
APPLICANT: Dower, William J.  
APPLICANT: Chang, Ray S.  
APPLICANT: Kaahya, Arun K.  
APPLICANT: Jolliffe, Linda K.  
APPLICANT: Johnson, Dana  
APPLICANT: Mulcahy, Linda  
TITLE OF INVENTION: Compounds and Peptides That Bind to the  
TITLE OF INVENTION: Erythropoietin Receptor  
NUMBER OF SEQUENCES: 259  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Townsend and Townsend and Crew  
STREET: One Market Plaza, Stewart Street Tower  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105-1492  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/484,631  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/155,940  
FILING DATE: 19-NOV-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Garrett-Mackowski, Eugenia  
REGISTRATION NUMBER: 37,330  
REFERENCE/DOCKET NUMBER: 16528A-43-1-2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 543-9600  
TELEFAX: (415) 543-5043  
INFORMATION FOR SEQ ID NO: 27:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-484-631-27

Query Match 44.8%; Score 30; DB 1; Length 20;  
Best Local Similarity 42.9%; Pred. No. 1.1e+02;  
Matches 3; Conservative 4; Mismatches 0; Indels 0; Gaps 0;  
QY 6 FECTIGP 12

DB 4 YKCLMGP 10

RESULT 16  
US-08-827-570-27  
Sequence 27, Application US/08827570  
Patent No. 5986047  
GENERAL INFORMATION:  
APPLICANT: Wighton, Nicholas C.  
APPLICANT: Dower, William J.  
APPLICANT: Chang, Ray S.  
APPLICANT: Kaahya, Arun K.  
APPLICANT: Jolliffe, Linda K.  
APPLICANT: Johnson, Dana  
APPLICANT: Mulcahy, Linda  
TITLE OF INVENTION: Compounds and Peptides That Bind to the  
TITLE OF INVENTION: Erythropoietin Receptor  
NUMBER OF SEQUENCES: 259  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Townsend and Townsend and Crew  
STREET: One Market Plaza, Stewart Street Tower  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105-1492  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/827,570  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/484,635  
FILING DATE: 07-JUN-1995  
APPLICATION NUMBER: US 08/155,940  
FILING DATE: 19-NOV-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Garrett-Mackowski, Eugenia  
REGISTRATION NUMBER: 37,330  
REFERENCE/DOCKET NUMBER: 16528A-43-1-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 543-9600  
TELEFAX: (415) 543-5043  
INFORMATION FOR SEQ ID NO: 27:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-827-570-27

Query Match 44.8%; Score 30; DB 1; Length 20;  
Best Local Similarity 42.9%; Pred. No. 1.1e+02;  
Matches 3; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 6 FECTIGP 12  
DB 4 YKCLMGP 10

RESULT 17  
US-09-449-064A-47  
Sequence 47, Application US/09449064A  
Patent No. 6703480  
GENERAL INFORMATION:  
APPLICANT: BALU, PALANI  
TITLE OF INVENTION: NOVEL PEPTIDE DIMERS AS AGONISTS OF THE ERYTHROPOIETIN  
TITLE OF INVENTION: (EPO) RECEPTOR, AND ASSOCIATED METHODS OF SYNTHESIS AND

;; TITLE OF INVENTION: USE  
;; FILE REFERENCE: 0300-0005  
;; CURRENT APPLICATION NUMBER: US/09/449,064A  
;; CURRENT FILING DATE: 1999-11-24  
;; NUMBER OF SEQ ID NOS: 93  
;; SOFTWARE: Patentin Ver. 2.1  
;; SEQ ID NO: 47  
;; LENGTH: 20  
;; TYPE: PRT  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
;; OTHER INFORMATION: Peptide  
;; NAME/KEY: MOD RES  
;; LOCATION: (13)  
;; OTHER INFORMATION: 1-Nal  
US-09-449-064A-47

Query Match 44.8%; Score 30; DB 2; Length 20;  
Best Local Similarity 42.9%; Pred. No. 1.1e+02;  
Matches 3; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 6 FECTICGP 12  
DB 4 YKCLMGP 10

RESULT 18  
US-08-484-635-136  
;; Sequence 136, Application US/08484635  
;; Patent No. 5773569  
;; GENERAL INFORMATION:  
;; APPLICANT: Wrighton, Nicholas C.  
;; APPLICANT: Dower, William J.  
;; APPLICANT: Chang, Ray S.  
;; APPLICANT: Kashyap, Arun K.  
;; APPLICANT: Jolliffe, Linda K.  
;; APPLICANT: Johnson, Dana  
;; APPLICANT: Mulcahy, Linda  
;; TITLE OF INVENTION: Compounds and Peptides That Bind to the  
;; TITLE OF INVENTION: Erythropoietin Receptor  
;; NUMBER OF SEQUENCES: 259  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Townsend and Townsend and Crew  
;; STREET: One Market Plaza, Stewart Street Tower  
;; CITY: San Francisco  
;; STATE: California  
;; COUNTRY: USA  
;; ZIP: 94105-1492  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patentin Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/484,635  
;; FILING DATE: 07-JUN-1995  
;; CLASSIFICATION: 514  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/155,940  
;; FILING DATE: 19-NOV-1993  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Garrett-Wackowski, Eugenia  
;; REGISTRATION NUMBER: 37,330  
;; REFERENCE/DOCKET NUMBER: 16528A-43-1-1  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (415) 543-9600  
;; TELEFAX: (415) 543-5043  
;; INFORMATION FOR SEQ ID NO: 136:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 19 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS:

;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
US-08-484-635-136

Query Match 43.3%; Score 29; DB 1; Length 19;  
Best Local Similarity 40.0%; Pred. No. 1.5e+02;  
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 3 KNSFCTICGP 12  
DB 2 KTKYRCBNGP 11

RESULT 19  
US-08-484-631-136  
;; Sequence 136, Application US/08484631  
;; Patent No. 5830851  
;; GENERAL INFORMATION:  
;; APPLICANT: Wrighton, Nicholas C.  
;; APPLICANT: Dower, William J.  
;; APPLICANT: Chang, Ray S.  
;; APPLICANT: Kashyap, Arun K.  
;; APPLICANT: Jolliffe, Linda K.  
;; APPLICANT: Johnson, Dana  
;; APPLICANT: Mulcahy, Linda  
;; TITLE OF INVENTION: Compounds and Peptides That Bind to the  
;; TITLE OF INVENTION: Erythropoietin Receptor  
;; NUMBER OF SEQUENCES: 259  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Townsend and Townsend and Crew  
;; STREET: One Market Plaza, Stewart Street Tower  
;; CITY: San Francisco  
;; STATE: California  
;; COUNTRY: USA  
;; ZIP: 94105-1492  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patentin Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/484,631  
;; FILING DATE: 07-JUN-1995  
;; CLASSIFICATION: 514  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/155,940  
;; FILING DATE: 19-NOV-1993  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Garrett-Wackowski, Eugenia  
;; REGISTRATION NUMBER: 37,330  
;; REFERENCE/DOCKET NUMBER: 16528A-43-1-2  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (415) 543-9600  
;; TELEFAX: (415) 543-5043  
;; INFORMATION FOR SEQ ID NO: 136:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 19 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS:  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
US-08-484-631-136

Query Match 43.3%; Score 29; DB 1; Length 19;  
Best Local Similarity 40.0%; Pred. No. 1.5e+02;  
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 3 KNSFCTICGP 12  
DB 2 KTKYRCBNGP 11

RESULT 20

US-08-827-570-136  
; Sequence 136, Application US/08827570  
; Patent No. 5986047  
; GENERAL INFORMATION:  
; APPLICANT: WRIGHTON, Nicholas C.  
; APPLICANT: DOWER, William J.  
; APPLICANT: Chang, Ray S.  
; APPLICANT: Kashyap, Arun K.  
; APPLICANT: Jolliffe, Linda K.  
; APPLICANT: Johnson, Dana  
; APPLICANT: Mulcahy, Linda  
; TITLE OF INVENTION: Compounds and Peptides That Bind to the  
; TITLE OF INVENTION: Erythropoietin Receptor  
; NUMBER OF SEQUENCES: 259  
; CORRESPONDENCE ADDRESS:  
; ADDRESSER: Townsend and Townsend and Crew  
; STREET: One Market Plaza, Stewart Street Tower  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94105-1492  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/827,570  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/484,635  
; FILING DATE: 07-JUN-1995  
; APPLICATION NUMBER: US 08/155,940  
; FILING DATE: 19-NOV-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Garrett-Mackowski, Eugenia  
; REGISTRATION NUMBER: 37,330  
; REFERENCE/DOCKET NUMBER: 16528A-43-1-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 543-9600  
; TELEFAX: (415) 543-5043  
; INFORMATION FOR SEQ ID NO: 136:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 19 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-827-570-136

Query Match 43.3%; Score 29; DB 1; Length 19;  
Best Local Similarity 40.0%; Pred. No. 1.5e+02;  
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 3 KNSFCLGP 12  
DB 2 KTKRCWGP 11

RESULT 21  
US-08-484-135-44  
; Sequence 44, Application US/08484135  
; Patent No. 5767078  
; GENERAL INFORMATION:  
; APPLICANT: Johnson, Dana L  
; APPLICANT: Zivlin, Robert A  
; TITLE OF INVENTION: AGONIST PEPTIDE DIMERS  
; NUMBER OF SEQUENCES: 93  
; CORRESPONDENCE ADDRESS:  
; ADDRESSER: Frank S. DiGioglio  
; STREET: 400 Garden City Plaza  
; CITY: Garden City

STATE: New York  
COUNTRY: U.S.A.  
ZIP: 11530  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/484,135  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: DiGioglio, Frank S  
; REGISTRATION NUMBER: 31,346  
; REFERENCE/DOCKET NUMBER: 9594  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (516) 742-4343  
; TELEFAX: (516) 742-4366  
; INFORMATION FOR SEQ ID NO: 44:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 20 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-484-135-44

Query Match 43.3%; Score 29; DB 1; Length 20;  
Best Local Similarity 42.9%; Pred. No. 1.6e+02;  
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 6 FPCILGP 12  
DB 4 YSCIMGP 10

RESULT 22  
US-08-484-135-53  
; Sequence 53, Application US/08484135  
; Patent No. 5767078  
; GENERAL INFORMATION:  
; APPLICANT: Johnson, Dana L  
; APPLICANT: Zivlin, Robert A  
; TITLE OF INVENTION: AGONIST PEPTIDE DIMERS  
; NUMBER OF SEQUENCES: 93  
; CORRESPONDENCE ADDRESS:  
; ADDRESSER: Frank S. DiGioglio  
; STREET: 400 Garden City Plaza  
; CITY: Garden City  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 11530  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/484,135  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: DiGioglio, Frank S  
; REGISTRATION NUMBER: 31,346  
; REFERENCE/DOCKET NUMBER: 9594  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (516) 742-4343  
; TELEFAX: (516) 742-4366  
; INFORMATION FOR SEQ ID NO: 53:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 20 amino acids  
; TYPE: amino acid

STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-484-135-53

Query Match 43.3%; Score 29; DB 1; Length 20;  
Best Local Similarity 57.1%; Pred. No. 1.6e+02;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 6 FECTIGP 12  
: : : :  
Db 4 YECRMGP 10

RESULT 23  
US-08-484-135-79  
Sequence 79, Application US/08484135  
Patent No. 5767078  
GENERAL INFORMATION:  
APPLICANT: Johnson, Dana L  
APPLICANT: Zayin, Robert A  
TITLE OF INVENTION: AGONIST PEPTIDE DIMERS  
NUMBER OF SEQUENCES: 93  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Frank S. Digiglio  
STREET: 400 Garden City Plaza  
CITY: Garden City  
STATE: New York  
COUNTRY: U.S.A..  
ZIP: 11530  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/484,135  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Digiglio, Frank S  
REGISTRATION NUMBER: 31,346  
REFERENCE/DOCKET NUMBER: 9534  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (516) 742-4343  
TELEFAX: (516) 742-4366  
INFORMATION FOR SEQ ID NO: 79:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-484-135-79

Query Match 43.3%; Score 29; DB 1; Length 20;  
Best Local Similarity 42.9%; Pred. No. 1.6e+02;  
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 6 FECTIGP 12  
: : : :  
Db 4 YECRMGP 10

RESULT 24  
US-08-484-635-41  
Sequence 41, Application US/08484635  
Patent No. 5773569  
GENERAL INFORMATION:  
APPLICANT: Wrighton, Nicholas C.  
APPLICANT: Dower, William J.  
APPLICANT: Chang, Ray S.  
APPLICANT: Kashyap, Arun K.

APPLICANT: Jolliffe, Linda K.  
APPLICANT: Johnson, Dana  
APPLICANT: Mulcahy, Linda  
TITLE OF INVENTION: Compounds and Peptides That Bind to the  
TITLE OF INVENTION: Erythropoietin Receptor  
NUMBER OF SEQUENCES: 259  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew  
STREET: One Market Plaza, Steuart Street Tower  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105-1492  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/484,635  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/155,940  
FILING DATE: 19-NOV-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Garrett-Mackowaki, Eugenia  
REGISTRATION NUMBER: 37,330  
REFERENCE/DOCKET NUMBER: 16528A-43-1-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 543-9600  
TELEFAX: (415) 543-5043  
INFORMATION FOR SEQ ID NO: 41:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-484-635-41

Query Match 43.3%; Score 29; DB 1; Length 20;  
Best Local Similarity 57.1%; Pred. No. 1.6e+02;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 6 FECTIGP 12  
: : : :  
Db 4 YECRMGP 10

RESULT 25  
US-08-484-635-42  
Sequence 42, Application US/08484635  
Patent No. 5773569  
GENERAL INFORMATION:  
APPLICANT: Wrighton, Nicholas C.  
APPLICANT: Dower, William J.  
APPLICANT: Chang, Ray S.  
APPLICANT: Kashyap, Arun K.  
APPLICANT: Johnson, Dana  
APPLICANT: Jolliffe, Linda K.  
APPLICANT: Mulcahy, Linda  
TITLE OF INVENTION: Compounds and Peptides That Bind to the  
TITLE OF INVENTION: Erythropoietin Receptor  
NUMBER OF SEQUENCES: 259  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew  
STREET: One Market Plaza, Steuart Street Tower  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105-1492  
COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/484,635  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/155,940  
FILING DATE: 19-NOV-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Garrett-Wackowski, Eugenia  
REGISTRATION NUMBER: 37,330  
REFERENCE/DOCKET NUMBER: 16528A-43-1-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 543-9600  
TELEFAX: (415) 543-5043  
INFORMATION FOR SEQ ID NO: 42:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-484-635-42

Query Match 43.3%; Score 29; DB 1; Length 20;  
Best Local Similarity 42.9%; Pred. No. 1.6e+02;  
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 6 FRCILGP 12  
:|:|:  
DB 4 YSCILGP 10

RESULT 26  
US-08-484-635-218  
Sequence 218, Application US/08484635  
Patent No. 5773569  
GENERAL INFORMATION:  
APPLICANT: Wrighton, Nicholas C.  
APPLICANT: Chang, Ray S.  
APPLICANT: Dower, William J.  
APPLICANT: Kashyap, Arun K.  
APPLICANT: Jolliffe, Linda K.  
APPLICANT: Johnson, Dana  
APPLICANT: Mulcahy, Linda  
TITLE OF INVENTION: Compounds and Peptides That Bind to the  
TITLE OF INVENTION: Erythropoietin Receptor  
NUMBER OF SEQUENCES: 259  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Townsend and Townsend and Crew  
STREET: One Market Plaza, Stewart Street Tower  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105-1492  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/484,635  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/155,940  
FILING DATE: 19-NOV-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Garrett-Wackowski, Eugenia  
REGISTRATION NUMBER: 37,330

REFERENCE/DOCKET NUMBER: 16528A-43-1-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 543-9600  
TELEFAX: (415) 543-5043  
INFORMATION FOR SEQ ID NO: 218:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-484-635-218

Query Match 43.3%; Score 29; DB 1; Length 20;  
Best Local Similarity 42.9%; Pred. No. 1.6e+02;  
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 6 FRCILGP 12  
:|:|:  
DB 4 YSCILGP 10

RESULT 27  
US-08-484-631-41  
Sequence 41, Application US/08484631  
Patent No. 5830851  
GENERAL INFORMATION:  
APPLICANT: Wrighton, Nicholas C.  
APPLICANT: Dower, William J.  
APPLICANT: Chang, Ray S.  
APPLICANT: Kashyap, Arun K.  
APPLICANT: Jolliffe, Linda K.  
APPLICANT: Johnson, Dana  
APPLICANT: Mulcahy, Linda  
TITLE OF INVENTION: Compounds and Peptides That Bind to the  
TITLE OF INVENTION: Erythropoietin Receptor  
NUMBER OF SEQUENCES: 259  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Townsend and Townsend and Crew  
STREET: One Market Plaza, Stewart Street Tower  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105-1492  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/484,631  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/155,940  
FILING DATE: 19-NOV-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Garrett-Wackowski, Eugenia  
REGISTRATION NUMBER: 37,330  
REFERENCE/DOCKET NUMBER: 16528A-43-1-2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 543-9600  
TELEFAX: (415) 543-5043  
INFORMATION FOR SEQ ID NO: 41:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-484-631-41

Query Match 43.3%; Score 29; DB 1; Length 20;

Best Local Similarity 57.1%; Pred. No. 1.6e+02;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 6 FECTIGP 12  
: ||: ||  
Db 4 YSCLMGP 10

## RESULT 28

US-08-484-631-42  
; Sequence 42, Application US/08484631  
; Patent No. 5830851  
; GENERAL INFORMATION:  
; APPLICANT: Wrighton, Nicholas C.  
; APPLICANT: Dower, William J.  
; APPLICANT: Chang, Ray S.  
; APPLICANT: Kashyap, Arun K.  
; APPLICANT: Jolliffe, Linda K.  
; APPLICANT: Johnson, Dana  
; APPLICANT: Mulcahy, Linda  
; TITLE OF INVENTION: Compounds and Peptides That Bind to the  
; TITLE OF INVENTION: Erythropoietin Receptor  
; NUMBER OF SEQUENCES: 259  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew  
; STREET: One Market Plaza, Stewart Street Tower  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94105-1492  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/484,631  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/155,940  
; FILING DATE: 19-NOV-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Garrett-Wackowek1, Eugenia  
; REGISTRATION/DOCKET NUMBER: 37,330  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 543-5043  
; TELEFAX: (415) 543-9600  
; INFORMATION FOR SEQ ID NO: 42:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 20 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-484-631-42

Query Match 43.3%; Score 29; DB 1; Length 20;  
Best Local Similarity 42.9%; Pred. No. 1.6e+02;  
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 6 FECTIGP 12  
: ||: ||  
Db 4 YSCLMGP 10

RESULT 29  
US-08-484-631-218  
; Sequence 218, Application US/08484631  
; Patent No. 5830851  
; GENERAL INFORMATION:  
; APPLICANT: Wrighton, Nicholas C.

APPLICANT: Dower, William J.  
APPLICANT: Chang, Ray S.  
APPLICANT: Kashyap, Arun K.  
APPLICANT: Jolliffe, Linda K.  
APPLICANT: Johnson, Dana  
APPLICANT: Mulcahy, Linda  
TITLE OF INVENTION: Compounds and Peptides That Bind to the  
TITLE OF INVENTION: Erythropoietin Receptor  
NUMBER OF SEQUENCES: 259  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew  
STREET: One Market Plaza, Stewart Street Tower  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105-1492

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/484,631  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/155,940  
FILING DATE: 19-NOV-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Garrett-Wackowek1, Eugenia  
REGISTRATION/DOCKET NUMBER: 37,330  
REFERENCE/DOCKET NUMBER: 16528A-43-1-2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 543-5043  
TELEFAX: (415) 543-9600  
INFORMATION FOR SEQ ID NO: 218:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-484-631-218

Query Match 43.3%; Score 29; DB 1; Length 20;  
Best Local Similarity 42.9%; Pred. No. 1.6e+02;  
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 6 FECTIGP 12  
: ||: ||  
Db 4 YSCLMGP 10

RESULT 30  
US-08-827-570-41  
; Sequence 41, Application US/08827570  
; Patent No. 5986047  
; GENERAL INFORMATION:  
; APPLICANT: Wrighton, Nicholas C.  
; APPLICANT: Dower, William J.  
; APPLICANT: Chang, Ray S.  
; APPLICANT: Kashyap, Arun K.  
; APPLICANT: Jolliffe, Linda K.  
; APPLICANT: Johnson, Dana  
; APPLICANT: Mulcahy, Linda  
; TITLE OF INVENTION: Compounds and Peptides That Bind to the  
; TITLE OF INVENTION: Erythropoietin Receptor  
; NUMBER OF SEQUENCES: 259  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew  
; STREET: One Market Plaza, Stewart Street Tower  
; CITY: San Francisco  
; STATE: California



COUNTRY: USA  
ZIP: 94105-1492  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/827,570  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/484,635  
FILING DATE: 07-JUN-1995  
APPLICATION NUMBER: US 08/155,940  
FILING DATE: 19-NOV-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Garrett-Wackowski, Eugenia  
REGISTRATION NUMBER: 37,330  
REFERENCE/DOCKET NUMBER: 16528A-43-1-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 543-9600  
TELEFAX: (415) 543-5043  
INFORMATION FOR SEQ ID NO: 41:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-827-570-41

Query Match 43.3%; Score 29; DB 1; Length 20;  
Best Local Similarity 57.1%; Pred. No. 1.6e+02;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 6 FRCILGP 12  
DB 4 YECRMGP 10

RESULT 31  
US-08-827-570-42  
Sequence 42, Application US/08827570  
Patent No. 5986047  
GENERAL INFORMATION:  
APPLICANT: Wighton, Nicholas C.  
APPLICANT: Dower, William J.  
APPLICANT: Chang, Ray S.  
APPLICANT: Kashyap, Arun K.  
APPLICANT: Johnson, Dana  
APPLICANT: Jolliffe, Linda K.  
TITLE OF INVENTION: Compounds and Peptides That Bind to the  
TITLE OF INVENTION: Erythropoietin Receptor  
NUMBER OF SEQUENCES: 259  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew  
STREET: One Market Plaza, Stewart Street Tower  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105-1492  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/827,570  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/484,635  
FILING DATE: 07-JUN-1995  
APPLICATION NUMBER: US 08/155,940  
FILING DATE: 19-NOV-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Garrett-Wackowski, Eugenia  
REGISTRATION NUMBER: 37,330  
REFERENCE/DOCKET NUMBER: 16528A-43-1-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 543-9600  
TELEFAX: (415) 543-5043  
INFORMATION FOR SEQ ID NO: 42:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-827-570-42

Query Match 43.3%; Score 29; DB 1; Length 20;  
Best Local Similarity 42.9%; Pred. No. 1.6e+02;  
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 6 FRCILGP 12  
DB 4 YSCILMP 10

RESULT 32  
US-08-827-570-218  
Sequence 218, Application US/08827570  
Patent No. 5986047  
GENERAL INFORMATION:  
APPLICANT: Wighton, Nicholas C.  
APPLICANT: Dower, William J.  
APPLICANT: Chang, Ray S.  
APPLICANT: Kashyap, Arun K.  
APPLICANT: Johnson, Dana  
APPLICANT: Jolliffe, Linda K.  
TITLE OF INVENTION: Compounds and Peptides That Bind to the  
TITLE OF INVENTION: Erythropoietin Receptor  
NUMBER OF SEQUENCES: 259  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew  
STREET: One Market Plaza, Stewart Street Tower  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105-1492  
COMPUTER READABLE FORM:  
MEDIUM TYPE: IBM PC compatible  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/827,570  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/484,635  
FILING DATE: 07-JUN-1995  
APPLICATION NUMBER: US 08/155,940  
FILING DATE: 19-NOV-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Garrett-Wackowski, Eugenia  
REGISTRATION NUMBER: 37,330  
REFERENCE/DOCKET NUMBER: 16528A-43-1-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 543-9600  
TELEFAX: (415) 543-5043  
INFORMATION FOR SEQ ID NO: 218:

/ SEQUENCE CHARACTERISTICS:  
/ LENGTH: 20 amino acids  
/ TYPE: amino acid  
/ STRANDEDNESS:  
/ TOPOLOGY: linear  
/ MOLECULE TYPE: peptide  
US-08-827-570-218

Query Match 43.3%; Score 29; DB 1; Length 20;  
Best Local Similarity 42.9%; Pred. No. 1.6e+02;  
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 6 FPCILGP 12  
: ||: ||  
Db 4 YSCLMGP 10

RESULT 33  
US-09-449-064A-48  
/ Sequence 48, Application US/09449064A  
/ Patent No. 6703480  
/ GENERAL INFORMATION:  
/ APPLICANT: BALU, PALANI  
/ TITLE OF INVENTION: NOVEL PEPTIDE DIMERS AS AGONISTS OF THE ERYTHROPOIETIN  
/ TITLE OF INVENTION: (EPO) RECEPTOR, AND ASSOCIATED METHODS OF SYNTHESIS AND  
/ FILE REFERENCE: 0300-0005  
/ CURRENT APPLICATION NUMBER: US/09/449,064A  
/ CURRENT FILING DATE: 1999-11-24  
/ NUMBER OF SEQ ID NOS: 93  
/ SOFTWARE: PatentIn Ver. 2.1  
/ SEQ ID NO 48  
/ LENGTH: 20  
/ TYPE: PRT  
/ ORGANISM: Artificial Sequence  
/ FEATURE:  
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
/ NAME/KEY: MOD\_RES  
/ LOCATION: (13)  
/ OTHER INFORMATION: 1-Nal  
US-09-449-064A-48

Query Match 43.3%; Score 29; DB 2; Length 20;  
Best Local Similarity 42.9%; Pred. No. 1.6e+02;  
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 6 FPCILGP 12  
: ||: ||  
Db 4 YSCLMGP 10

RESULT 34  
US-09-449-064A-56  
/ Sequence 56, Application US/09449064A  
/ Patent No. 6703480  
/ GENERAL INFORMATION:  
/ APPLICANT: BALU, PALANI  
/ TITLE OF INVENTION: NOVEL PEPTIDE DIMERS AS AGONISTS OF THE ERYTHROPOIETIN  
/ TITLE OF INVENTION: (EPO) RECEPTOR, AND ASSOCIATED METHODS OF SYNTHESIS AND  
/ FILE REFERENCE: 0300-0005  
/ CURRENT APPLICATION NUMBER: US/09/449,064A  
/ CURRENT FILING DATE: 1999-11-24  
/ NUMBER OF SEQ ID NOS: 93  
/ SOFTWARE: PatentIn Ver. 2.1  
/ SEQ ID NO 56  
/ LENGTH: 20  
/ TYPE: PRT  
/ ORGANISM: Artificial Sequence  
/ FEATURE:  
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
/ OTHER INFORMATION: peptide

/ NAME/KEY: MOD\_RES  
/ LOCATION: (13)  
/ OTHER INFORMATION: 1-Nal  
US-09-449-064A-56

Query Match 43.3%; Score 29; DB 2; Length 20;  
Best Local Similarity 57.1%; Pred. No. 1.6e+02;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 6 FPCILGP 12  
: ||: ||  
Db 4 YECRMGP 10

RESULT 35  
US-09-449-064A-81  
/ Sequence 81, Application US/09449064A  
/ Patent No. 6703480  
/ GENERAL INFORMATION:  
/ APPLICANT: BALU, PALANI  
/ TITLE OF INVENTION: NOVEL PEPTIDE DIMERS AS AGONISTS OF THE ERYTHROPOIETIN  
/ TITLE OF INVENTION: (EPO) RECEPTOR, AND ASSOCIATED METHODS OF SYNTHESIS AND  
/ FILE REFERENCE: 0300-0005  
/ CURRENT APPLICATION NUMBER: US/09/449,064A  
/ CURRENT FILING DATE: 1999-11-24  
/ NUMBER OF SEQ ID NOS: 93  
/ SOFTWARE: PatentIn Ver. 2.1  
/ SEQ ID NO 81  
/ LENGTH: 20  
/ TYPE: PRT  
/ ORGANISM: Artificial Sequence  
/ FEATURE:  
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
/ NAME/KEY: MOD\_RES  
/ LOCATION: (13)  
/ OTHER INFORMATION: 1-Nal  
US-09-449-064A-81

Query Match 43.3%; Score 29; DB 2; Length 20;  
Best Local Similarity 42.9%; Pred. No. 1.6e+02;  
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 6 FPCILGP 12  
: ||: ||  
Db 4 YSCLMGP 10

RESULT 36  
US-08-598-873-18  
/ Sequence 18, Application US/08598873  
/ Patent No. 5928864  
/ GENERAL INFORMATION:  
/ APPLICANT: Croce, Carlo M.  
/ TITLE OF INVENTION: PHIT PROTEINS AND NUCLEIC ACIDS AND  
/ NUMBER OF SEQUENCES: 77  
/ CORRESPONDENCE ADDRESS:  
/ ADDRESS: Pennie & Edmonds  
/ STREET: 1155 Avenue of the Americas  
/ CITY: New York  
/ STATE: New York  
/ COUNTRY: U.S.A.  
/ ZIP: 10036-2711  
/ COMPUTER READABLE FORM:  
/ MEDIUM TYPE: Floppy disk  
/ COMPUTER: IBM PC compatible  
/ OPERATING SYSTEM: PC-DOS/MS-DOS  
/ SOFTWARE: PatentIn Release #1.0, Version #1.30  
/ CURRENT APPLICATION DATA:  
/ APPLICATION NUMBER: US/08/598,873

FILING DATE: 09-FEB-1996  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Friebe, Thomas E.  
REGISTRATION NUMBER: 29,258  
REFERENCE/DOCKET NUMBER: 8666-004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-598-873-18

Query Match 41.8%; Score 28; DB 1; Length 8;  
Best Local Similarity 50.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 DEKNSPEC 8  
DB 1 DEBTAFSC 8

RESULT 37  
US-08-605-430-18  
Sequence 18, Application US/08605430  
Patent No. 6242212  
GENERAL INFORMATION:  
APPLICANT: Croce, Carlo M.  
TITLE OF INVENTION: PHIT PROTEINS AND NUCLEIC ACIDS AND  
TITLE OF INVENTION: METHODS BASED THEREON  
NUMBER OF SEQUENCES: 86  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/605,430  
FILING DATE: 22-FEB-1996  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Friebe, Thomas E.  
REGISTRATION NUMBER: 29,258  
REFERENCE/DOCKET NUMBER: 8666-005  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-605-430-18

Query Match 41.8%; Score 28; DB 2; Length 8;  
Best Local Similarity 50.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 DEKNSPEC 8  
DB 1 DEBTAFSC 8

RESULT 38  
US-09-717-054-18  
Sequence 18, Application US/09717054  
Patent No. 6774217  
GENERAL INFORMATION:  
APPLICANT: Croce, Carlo M.  
Huebner, Kay  
TITLE OF INVENTION: PHIT PROTEINS AND NUCLEIC ACIDS AND  
TITLE OF INVENTION: METHODS BASED THEREON  
NUMBER OF SEQUENCES: 86  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/717,054  
FILING DATE: 21-No. 6774217-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/605,430  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Friebe, Thomas E.  
REGISTRATION NUMBER: 29,258  
REFERENCE/DOCKET NUMBER: 8666-005  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 18:  
US-09-717-054-18

Query Match 41.8%; Score 28; DB 2; Length 8;  
Best Local Similarity 50.0%; Pred. No. 4.6e+05;  
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 DEKNSPEC 8  
DB 1 DEBTAFSC 8

RESULT 39  
US-08-893-526A-20  
Sequence 20, Application US/08893526A  
Patent No. 6096707  
GENERAL INFORMATION:  
APPLICANT: Helino, Jyrki  
Ivaska, Johanna  
APPLICANT: K pyl, Jarmo  
TITLE OF INVENTION: Integrin Binding Peptide and Use Thereof  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Sterne, Keesler, Goldstein & Fox P.L.L.C.  
STREET: 1100 New York Ave., N.W.

CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005-3934  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/893,526A  
FILING DATE: 11-JUL-1997  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: KIM, JUDITH U.  
REGISTRATION NUMBER: 40,679  
REFERENCE/DOCKET NUMBER: 1708.0240000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202/371-2600  
TELEFAX: 202/371-2540  
TELEX:  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
TOPOLOGY: circular  
MOLECULE TYPE: peptide  
US-08-893-526A-20

Query Match 41.8%; Score 28; DB 2; Length 10;  
Best Local Similarity 62.5%; Pred. No. 1.2e+02;  
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 DEKNSPEC 8  
DB 3 DESNSTYC 10

RESULT 40  
US-09-177-249-219  
Sequence 219, Application US/09177249  
Patent No. 6229064  
GENERAL INFORMATION:  
APPLICANT: Fischer, Robert L.  
APPLICANT: Ohad, Nir  
APPLICANT: Kiyosue, Tomohiro  
APPLICANT: Yadegari, Ramlin  
APPLICANT: Margosian, Linda  
APPLICANT: Harada, John  
APPLICANT: Goldberg, Robert B.  
TITLE OF INVENTION: The Regents of the University of California  
TITLE OF INVENTION: Nucleic Acids That Control Seed and Fruit  
FILE REFERENCE: 023070-086120US  
CURRENT APPLICATION NUMBER: US/09/177,249  
CURRENT FILING DATE: 1998-10-22  
EARLIER APPLICATION NUMBER: US 09/071,838  
EARLIER FILING DATE: 1998-05-01  
NUMBER OF SEQ ID NOS: 324  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 219  
LENGTH: 12  
TYPE: PRT  
ORGANISM: Arabidopsis sp.  
US-09-177-249-219

Query Match 41.8%; Score 28; DB 2; Length 12;  
Best Local Similarity 44.4%; Pred. No. 1.4e+02;  
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 DEKNSPEC 9  
DB 4 DLRRSPKCV 12

RESULT 41  
US-09-812-283-219  
Sequence 219, Application US/09812283  
Patent No. 6828477  
GENERAL INFORMATION:  
APPLICANT: Fischer, Robert L.  
APPLICANT: Ohad, Nir  
APPLICANT: Kiyosue, Tomohiro  
APPLICANT: Yadegari, Ramlin  
APPLICANT: Margosian, Linda  
APPLICANT: Harada, John  
APPLICANT: Goldberg, Robert B.  
TITLE OF INVENTION: The Regents of the University of California  
TITLE OF INVENTION: Nucleic Acids That Control Seed and Fruit  
FILE REFERENCE: 023070-086120US  
CURRENT APPLICATION NUMBER: US/09/812,283  
CURRENT FILING DATE: 2001-03-19  
PRIOR APPLICATION NUMBER: 09/177,249  
PRIOR FILING DATE: 1998-10-22  
PRIOR APPLICATION NUMBER: US 09/071,838  
PRIOR FILING DATE: 1998-05-01  
NUMBER OF SEQ ID NOS: 324  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 219  
LENGTH: 12  
TYPE: PRT  
ORGANISM: Arabidopsis sp.  
US-09-812-283-219

Query Match 41.8%; Score 28; DB 2; Length 12;  
Best Local Similarity 44.4%; Pred. No. 1.4e+02;  
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 DEKNSPEC 9  
DB 4 DLRRSPKCV 12

RESULT 42  
US-09-774-639-272  
Sequence 272, Application US/09774639  
Patent No. 6806351  
GENERAL INFORMATION:  
APPLICANT: Rosen et al.  
TITLE OF INVENTION: 90 Human Secreted Proteins  
FILE REFERENCE: P2013P1  
CURRENT APPLICATION NUMBER: US/09/774,639  
CURRENT FILING DATE: 2001-07-09  
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/244,112  
PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-04  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 272  
LENGTH: 14  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-774-639-272

Query Match 41.8%; Score 28; DB 2; Length 14;  
Best Local Similarity 55.6%; Pred. No. 1.7e+02;  
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 KNSPECILG 11  
DB 3 KGDLMICIG 11

RESULT 43  
US-08-049-783-11  
Sequence 11, Application US/08049783

Patent No. 5439881  
GENERAL INFORMATION:  
APPLICANT: Narva, Kenneth E  
APPLICANT: Schwab, George E  
APPLICANT: Payne, Jewel M  
TITLE OF INVENTION: Gene Encoding No. 5439881e1 Nematode-Active  
TITLE OF INVENTION: Toxins Cloned from Bacillus thuringiensis Isolates  
NUMBER OF SEQUENCES: 18  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Jeff Lloyd  
STREET: 2421 N.W. 41st Street  
CITY: Gainesville  
STATE: FL  
COUNTRY: USA  
ZIP: 32606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/049,783  
FILING DATE: 19930419  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Lloyd, Jeff  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 904-375-8100  
TELEFAX: 904-372-5800  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: AMINO ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-049-783-11

Query Match 41.8%; Score 28; DB 1; Length 15;  
Best Local Similarity 66.7%; Pred. No. 1.8e+02;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DEKNSPECI 9  
DB 6 DEKLSFOLI 14

RESULT 44  
US-08-158-232-22  
Sequence 22, Application US/08158232  
Patent No. 5596071  
GENERAL INFORMATION:  
APPLICANT: Payne, Jewel  
APPLICANT: Kennedy, M. Keith  
APPLICANT: Randall, John Brooks  
APPLICANT: Meier, Henry  
APPLICANT: Ulick, Heidi Jane  
APPLICANT: Foncetrada, Luis  
APPLICANT: Schnepf, H. Ernest  
APPLICANT: Schwab, George E.  
TITLE OF INVENTION: No. 5596071e1 Bacillus thuringiensis Toxins Active  
TITLE OF INVENTION: Against Hymenopteran Pests  
NUMBER OF SEQUENCES: 51  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: David R. Saliwanchik  
STREET: 2421 N.W. 41st Street, Suite A-1  
CITY: Gainesville  
STATE: FL  
COUNTRY: USA  
ZIP: 32606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/158,232  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/887,980  
FILING DATE: 22-MAY-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/797,645  
FILING DATE: 25-NOV-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/703,977  
FILING DATE: 22-MAY-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Saliwanchik, David R.  
REGISTRATION NUMBER: 31,794  
REFERENCE/DOCKET NUMBER: M/SCU104.C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 904-375-8100  
TELEFAX: 904-372-5800  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-158-232-22

Query Match 41.8%; Score 28; DB 1; Length 15;  
Best Local Similarity 66.7%; Pred. No. 1.8e+02;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DEKNSPECI 9  
DB 6 DEKLSFOLI 14

RESULT 45  
US-08-304-626-22  
Sequence 22, Application US/08304626  
Patent No. 5616495  
GENERAL INFORMATION:  
APPLICANT: Payne, Jewel M.  
APPLICANT: Kennedy, M. Keith  
APPLICANT: Randall, John Brooks  
APPLICANT: Meier, Henry  
APPLICANT: Ulick, Heidi Jane  
APPLICANT: Foncetrada, Luis  
APPLICANT: Schnepf, Harry B.  
TITLE OF INVENTION: No. 5616495e1 Bacillus thuringiensis Isolates  
TITLE OF INVENTION: Active Against Hymenopteran Pests and Genes Encoding  
NUMBER OF SEQUENCES: 39  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: David R. Saliwanchik  
STREET: 2421 N.W. 41st Street, Suite A-1  
CITY: Gainesville  
STATE: FL  
COUNTRY: USA  
ZIP: 32606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/304,626  
FILING DATE:

CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/887,980  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Saliwanchik, David R.  
REGISTRATION NUMBER: 31,794  
REFERENCE/DOCKET NUMBER: M/SCJ 104  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 904-375-8100  
TELEFAX: 904-372-5800  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-304-626-22

Query Match 41.8%; Score 28; DB 1; Length 15;  
Best Local Similarity 66.7%; Pred. No. 1.8e+02;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DEKNSPECI 9  
DB 6 DEKLSFOLI 14

RESULT 46  
US-08-316-301A-23  
Sequence 23, Application US/08316301A

PATENT No. 5753492  
GENERAL INFORMATION:  
APPLICANT: Schmepl, Harry E.  
APPLICANT: Schwab, George E.  
APPLICANT: Payne, Jewel M.  
APPLICANT: Narva, Kenneth E.  
APPLICANT: Foncestrada, Luis  
TITLE OF INVENTION: No. 5753492el Nematode-Active Toxins and Genes  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Saliwanchik & Saliwanchik  
STREET: 2421 N.W. 41st Street, Suite A-1  
CITY: Gainesville  
STATE: FL  
COUNTRY: USA  
ZIP: 32606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/316,301A  
FILING DATE: 30-SEP-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/871,510  
FILING DATE: 23-APR-1992  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/693,018  
FILING DATE: 03-MAY-1991  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/565,544  
FILING DATE: 10-AUG-1990  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/084,653  
FILING DATE: 12-AUG-1987

CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/830,050  
FILING DATE: 31-JAN-1992  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Lloyd, Jeff  
REGISTRATION NUMBER: 35,589  
REFERENCE/DOCKET NUMBER: MA20CCCD1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 904-375-8100  
TELEFAX: 904-372-5800  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-316-301A-23

Query Match 41.8%; Score 28; DB 1; Length 15;  
Best Local Similarity 66.7%; Pred. No. 1.8e+02;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DEKNSPECI 9  
DB 6 DEKLSFOLI 14

RESULT 47  
US-08-611-928-22  
Sequence 22, Application US/08611928

PATENT No. 5824792  
GENERAL INFORMATION:  
APPLICANT: Payne, Jewel  
APPLICANT: Kennedy, M. Keith  
APPLICANT: Randall, John Brooks  
APPLICANT: Meyer, Henry  
APPLICANT: Vick, Heidi Jane  
APPLICANT: Foncestrada, Luis  
APPLICANT: Schmepl, H. Ernest  
APPLICANT: Schwab, George E.  
APPLICANT: Fu, Jenny  
TITLE OF INVENTION: No. 5824792el Bacillus thuringiensis Toxins Active  
NUMBER OF SEQUENCES: 51  
CORRESPONDENCE ADDRESS:  
ADDRESSER: David R. Saliwanchik  
STREET: 2421 N.W. 41st Street, Suite A-1  
CITY: Gainesville  
STATE: FL  
COUNTRY: USA  
ZIP: 32606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/611,928  
FILING DATE: 06-MAR-1996  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/158,232  
FILING DATE: 24-NOV-1993  
APPLICATION NUMBER: US 07/887,980  
FILING DATE: 22-MAY-1992  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/797,645  
FILING DATE: 25-NOV-1991  
CLASSIFICATION: 530

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/703,977  
FILING DATE: 22-MAY-1991  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Saliwanchik, David R.  
REGISTRATION NUMBER: 31,794  
REFERENCE/DOCKET NUMBER: M/SCJ104.C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 904-375-8100  
TELEFAX: 904-372-5800  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-611-928-22

Query Match 41.8%; Score 28; DB 1; Length 15;  
Best local Similarity 66.7%; Pred. No. 1.8e+02;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DEKNSPECI 9  
DB 6 DEKLSFOLI 14

RESULT 48  
US-09-224-024-5  
Sequence 5, Application US/09224024  
Patent No. 6056953

GENERAL INFORMATION:  
APPLICANT: Leslie Hickie  
TITLE OF INVENTION: Materials and Methods for the Control of  
NUMBER OF SEQUENCES: 31  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: David R. Saliwanchik  
STREET: 2421 N.W. 41st Street, Suite A-1  
CITY: Gainesville  
STATE: FL  
COUNTRY: USA  
ZIP: 32606

COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/224,024  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/856,226  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Saliwanchik, David R.  
REGISTRATION NUMBER: 31,794  
REFERENCE/DOCKET NUMBER: M/SCJ104.C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 904-375-8100  
TELEFAX: 904-372-5800  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-224-024-5

Query Match 41.8%; Score 28; DB 2; Length 15;  
Best local Similarity 66.7%; Pred. No. 1.8e+02;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 1 DEKNSPECI 9  
DB 6 DEKLSFOLI 14

RESULT 49  
US-09-173-891-22  
Sequence 22, Application US/09173891  
Patent No. 6077937

GENERAL INFORMATION:  
APPLICANT: Payne, Jewel  
APPLICANT: Kennedy, M. Keith  
APPLICANT: Randall, John Brooks  
APPLICANT: Meier, Henry  
APPLICANT: Wick, Heidi Jane  
APPLICANT: Poncetrada, Luis  
APPLICANT: Schaept, H. Ernest  
APPLICANT: Schwab, George E.  
APPLICANT: Fu, Jenny  
TITLE OF INVENTION: No. 6077937el Bacillus thuringiensis Toxins Active  
NUMBER OF SEQUENCES: 51  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: David R. Saliwanchik  
STREET: 2421 N.W. 41st Street, Suite A-1  
CITY: Gainesville  
STATE: FL  
COUNTRY: USA  
ZIP: 32606

COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/173,891  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/158,232  
FILING DATE:  
APPLICATION NUMBER: US 07/887,980  
FILING DATE: 22-MAY-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/797,645  
FILING DATE: 25-NOV-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/703,977  
FILING DATE: 22-MAY-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Saliwanchik, David R.  
REGISTRATION NUMBER: 31,794  
REFERENCE/DOCKET NUMBER: M/SCJ104.C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 904-375-8100  
TELEFAX: 904-372-5800  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-173-891-22

Query Match 41.8%; Score 28; DB 2; Length 15;  
Best local Similarity 66.7%; Pred. No. 1.8e+02;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DEKNSPECT 9  
||| ||| :  
Db 6 DEKLSFOLI 14

RESULT 50  
US-09-076-137-23  
Sequence 23, Application US/09076137B  
Patent No. 6166195  
GENERAL INFORMATION:  
APPLICANT: Schepf, Harry E.  
APPLICANT: Schepf, George E.  
APPLICANT: Payne, Jewel M.  
APPLICANT: Narva, Kenneth B.  
APPLICANT: Poncetrada, Luis  
TITLE OF INVENTION: No. 6166195el Nematode-Active Toxins and Genes which Code  
FILE REFERENCE: MA-20CCCD2  
CURRENT APPLICATION NUMBER: US/09/076,137B  
EARLIER FILING DATE: 1998-05-12  
EARLIER APPLICATION NUMBER: 08/316,301  
NUMBER OF SEQ ID NOS: 42  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO: 23  
LENGTH: 15  
TYPE: PRT  
ORGANISM: Bacillus thuringiensis  
US-09-076-137-23

Query Match 41.8%; Score 28; DB 2; Length 15;  
Best Local Similarity 66.7%; Pred. No. 1.8e+02;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DEKNSPECT 9  
||| ||| :  
Db 6 DEKLSFOLI 14

RESULT 51  
US-09-738-363-23  
Sequence 23, Application US/09738363  
Patent No. 6632792  
GENERAL INFORMATION:  
APPLICANT: Schepf, Harry E.  
APPLICANT: Schepf, George E.  
APPLICANT: Payne, Jewel M.  
APPLICANT: Narva, Kenneth B.  
APPLICANT: Poncetrada, Luis  
TITLE OF INVENTION: Nematocidal Proteins  
NUMBER OF SEQUENCES: 40  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Jay M. Sanders  
STREET: 2421 N.W. 41st Street, Suite A-1  
CITY: Gainesville  
STATE: FL  
COUNTRY: USA  
ZIP: 32606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/738,363  
FILING DATE: 15-Dec-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/076,137  
FILING DATE: 12-MAY-1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Sanders, Jay

REGISTRATION NUMBER: 39,355  
REFERENCE/DOCKET NUMBER: MA-20CCCD3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 352-375-8100  
TELEFAX: 352-372-5800  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 23:  
US-09-738-363-23

Query Match 41.8%; Score 28; DB 4; Length 15;  
Best Local Similarity 66.7%; Pred. No. 1.8e+02;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DEKNSPECT 9  
||| ||| :  
Db 6 DEKLSFOLI 14

RESULT 52  
PCT-US92-03624-23  
Sequence 23, Application PC/TUS9203624  
GENERAL INFORMATION:  
APPLICANT: Schepf, Harry E.  
APPLICANT: Schepf, George E.  
APPLICANT: Payne, Jewel M.  
APPLICANT: Narva, Kenneth B.  
APPLICANT: Poncetrada, Luis  
TITLE OF INVENTION: Novel Nematode-Active Toxins and Genes  
NUMBER OF SEQUENCES: 40  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: David R. Saliwanchik  
STREET: 2421 N.W. 41st Street, Suite A-1  
CITY: Gainesville  
STATE: FL  
COUNTRY: USA  
ZIP: 32606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/03624  
FILING DATE: 19920501  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Saliwanchik, David R.  
REGISTRATION NUMBER: 31,794  
REFERENCE/DOCKET NUMBER: MA20CC2C1C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 904-375-8100  
TELEFAX: 904-372-5800  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: AMINO ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US92-03624-23

Query Match 41.8%; Score 28; DB 4; Length 15;  
Best Local Similarity 66.7%; Pred. No. 1.8e+02;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DEKNSPECT 9



Db 6 DEKUSFOLI 14

```

RESULT 53
PCT-US94-07902-5
Sequence 5, Application PC/TUS9407902
GENERAL INFORMATION:
APPLICANT:
APPLICANT: Street address: 4980 Carroll Canyon Road
APPLICANT: City: San Diego
APPLICANT: State/Province: California
APPLICANT: Country: US
APPLICANT: Postal code/Zip: 92121
APPLICANT: Phone number: (619) 453-8030
APPLICANT: Fax number: (619) 453-6991
TITLE OF INVENTION: Materials and Methods for the Control of
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSER: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/07902
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: M479
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US94-07902-5

```

Query Match 41.8%; Score 28; DB 4; Length 15;  
 Best Local Similarity 66.7%; Pred. No. 1.8e+02;  
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DEKUSFOLI 9  
 Db 6 DEKUSFOLI 14

```

RESULT 54
US-08-474-696A-7
Sequence 7, Application US/08474696A
Patent No. 5843673
GENERAL INFORMATION:
APPLICANT: Sharpe-Timm, Kathy L.
TITLE OF INVENTION: ENDOMETRIOSIS-SPECIFIC SECRETORY
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSER: Kohn & Associates
STREET: 30500 No. 5843673thwestern Hwy.
CITY: Farmington Hills

```

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STATE: Michigan
COUNTRY: US
ZIP: 48334
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,696A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kohn, Kenneth I.
REGISTRATION NUMBER: 30,955
TELECOMMUNICATION INFORMATION:
TELEPHONE: (810) 539-5050
TELEFAX: (810) 539-5055
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: N-terminal
US-08-474-696A-7

```

Query Match 41.8%; Score 28; DB 1; Length 16;  
 Best Local Similarity 62.5%; Pred. No. 1.9e+02;  
 Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 DEKUSFOLI 8  
 Db 7 DAKUSFOLI 14

```

RESULT 55
US-08-484-635-157
Sequence 157, Application US/08484635
Patent No. 573569
GENERAL INFORMATION:
APPLICANT: Wrighton, Nicholas C.
APPLICANT: Dower, William J.
APPLICANT: Chang, Ray S.
APPLICANT: Kaehyap, Arun K.
APPLICANT: Jolliffe, Linda K.
APPLICANT: Johnson, Dana
APPLICANT: Mulcahy, Linda
TITLE OF INVENTION: Compounds and Peptides That Bind to the
NUMBER OF SEQUENCES: 259
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Crew
STREET: One Market Plaza, Stewart Street Tower
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,635
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/155,940
FILING DATE: 19-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Garrett-Wackowski, Eugenia

```

REGISTRATION NUMBER: 37,330  
REFERENCE/DOCKET NUMBER: 16528A-43-1-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 543-9600  
TELEFAX: (415) 543-5043  
INFORMATION FOR SEQ ID NO: 157:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-484-631-157

Query Match 41.8%; Score 28; DB 1; Length 18;  
Best Local Similarity 36.4%; Pred. No. 2.2e+02;  
Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 EKNSPECTILGP 12  
| : : : | | |  
Db 1 ERRFYKCRFGP 11

RESULT 56  
US-08-484-631-157  
; Sequence 157, Application US/08484631  
; Patent No. 5830851  
; GENERAL INFORMATION:  
; APPLICANT: Wrighton, Nicholas C.  
; APPLICANT: Dower, William J.  
; APPLICANT: Chang, Ray S.  
; APPLICANT: Kashyap, Arun K.  
; APPLICANT: Jolliffe, Linda K.  
; APPLICANT: Johnson, Dana  
; APPLICANT: Mulcahy, Linda  
; TITLE OF INVENTION: Compounds and Peptides That Bind to the  
; TITLE OF INVENTION: Erythropoietin Receptor  
; NUMBER OF SEQUENCES: 259  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSES: Townsend and Townsend and Crew  
; STREET: One Market Plaza, Stewart Street Tower  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94105-1492  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/484,631  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/155,940  
; FILING DATE: 19-NOV-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Garrett-Mackowski, Eugenia  
; REGISTRATION NUMBER: 37,330  
; REFERENCE/DOCKET NUMBER: 16528A-43-1-2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 543-9600  
; TELEFAX: (415) 543-5043  
; INFORMATION FOR SEQ ID NO: 157:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-484-631-157

Query Match 41.8%; Score 28; DB 1; Length 18;  
Best Local Similarity 36.4%; Pred. No. 2.2e+02;  
Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 EKNSPECTILGP 12  
| : : : | | |  
Db 1 ERRFYKCRFGP 11

RESULT 57  
US-08-827-570-157  
; Sequence 157, Application US/08827570  
; Patent No. 5986047  
; GENERAL INFORMATION:  
; APPLICANT: Wrighton, Nicholas C.  
; APPLICANT: Dower, William J.  
; APPLICANT: Chang, Ray S.  
; APPLICANT: Kashyap, Arun K.  
; APPLICANT: Jolliffe, Linda K.  
; APPLICANT: Johnson, Dana  
; APPLICANT: Mulcahy, Linda  
; TITLE OF INVENTION: Compounds and Peptides That Bind to the  
; TITLE OF INVENTION: Erythropoietin Receptor  
; NUMBER OF SEQUENCES: 259  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSES: Townsend and Townsend and Crew  
; STREET: One Market Plaza, Stewart Street Tower  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94105-1492  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/827,570  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/484,635  
; FILING DATE: 07-JUN-1995  
; APPLICATION NUMBER: US 08/155,940  
; FILING DATE: 19-NOV-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Garrett-Mackowski, Eugenia  
; REGISTRATION NUMBER: 37,330  
; REFERENCE/DOCKET NUMBER: 16528A-43-1-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 543-9600  
; TELEFAX: (415) 543-5043  
; INFORMATION FOR SEQ ID NO: 157:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-827-570-157

Query Match 41.8%; Score 28; DB 1; Length 18;  
Best Local Similarity 36.4%; Pred. No. 2.2e+02;  
Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 EKNSPECTILGP 12  
| : : : | | |  
Db 1 ERRFYKCRFGP 11

RESULT 58  
US-08-825-852-66  
; Sequence 66, Application US/08825852

Patent No. 6121416  
GENERAL INFORMATION:  
APPLICANT: Clark, Ross G1  
APPLICANT: Lowman, Henry B.  
APPLICANT: Robinson, Iain C.A.F.  
TITLE OF INVENTION: Insulin-like Growth Factor Agonist Molecules  
NUMBER OF SEQUENCES: 79  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPacIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/825,852  
FILING DATE: 04-Apr-1997  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Hasak, Janet E.  
REGISTRATION NUMBER: 28,616  
REFERENCE/DOCKET NUMBER: P1071  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-1896  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 66:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-08-825-852-66

Query Match 41.8%; Score 28; DB 2; Length 18;  
Best Local Similarity 66.7%; Pred. No. 2.2e+02;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 7 ECIIGP 12  
Db 4 ECIWGP 9

RESULT 59  
US-08-825-852-68  
Sequence 68, Application US/08825852  
Patent No. 6121416  
GENERAL INFORMATION:  
APPLICANT: Clark, Ross G1  
APPLICANT: Lowman, Henry B.  
APPLICANT: Robinson, Iain C.A.F.  
TITLE OF INVENTION: Insulin-like Growth Factor Agonist Molecules  
NUMBER OF SEQUENCES: 79  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPacIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/825,852  
FILING DATE: 04-Apr-1997  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:

NAME: Hasak, Janet E.  
REGISTRATION NUMBER: 28,616  
REFERENCE/DOCKET NUMBER: P1071  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-1896  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 68:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-08-825-852-68

Query Match 41.8%; Score 28; DB 2; Length 18;  
Best Local Similarity 83.3%; Pred. No. 2.2e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 ECIIGP 12  
Db 4 ECIWGP 9

RESULT 60  
US-09-052-888-67  
Sequence 67, Application US/09052888  
Patent No. 6251865  
GENERAL INFORMATION:  
APPLICANT: Clark, Ross G1  
APPLICANT: Lowman, Henry B.  
APPLICANT: Robinson, Iain C.A.F.  
TITLE OF INVENTION: Insulin-like Growth Factor Agonist Molecules  
NUMBER OF SEQUENCES: 109  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPacIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/052,888  
FILING DATE: 31-Mar-1998  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Hasak, Janet E.  
REGISTRATION NUMBER: 28,616  
REFERENCE/DOCKET NUMBER: P1071P1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-1896  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 67:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-09-052-888-67

Query Match 41.8%; Score 28; DB 2; Length 18;  
Best Local Similarity 66.7%; Pred. No. 2.2e+02;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 7 ECIIGP 12  
Db 4 ECIWGP 9

RESULT 61  
US-09-052-888-69

; Sequence 69, Application US/09052888  
; Patent No. 6251865  
; GENERAL INFORMATION:  
; APPLICANT: Clark, Ross G1  
; APPLICANT: Lowman, Henry B.  
; APPLICANT: Robinson, Iain C.A.F.  
; TITLE OF INVENTION: Insulin-like Growth Factor Agonist Molecules  
; NUMBER OF SEQUENCES: 109  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/052,888  
; FILING DATE: 31-Mar-1998  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hasak, Janet E.  
; REGISTRATION NUMBER: 28,616  
; REFERENCE/DOCKET NUMBER: P1071P1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-1896  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 69:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: linear  
; US-09-052-888-69

Query Match 41.8%; Score 28; DB 2; Length 18;  
Best Local Similarity 83.3%; Pred. No. 2.2e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 7 ECICLP 12  
DB 4 ECICGP 9  
RESULT 62  
US-10-158-847-88  
; Sequence 88, Application US/10158847  
; Patent No. 6592865  
; GENERAL INFORMATION:  
; APPLICANT: Tom Parry et al.  
; TITLE OF INVENTION: Method and Compositions for Modulating ACE-2 Activity  
; FILE REFERENCE: PF557  
; CURRENT APPLICATION NUMBER: US/10/158,847  
; PRIOR FILING DATE: 2002-06-03  
; PRIOR APPLICATION NUMBER: 60/295,004  
; NUMBER OF SEQ ID NOS: 158  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO: 88  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: homo sapiens  
; US-10-158-847-88

Query Match 41.8%; Score 28; DB 2; Length 18;  
Best Local Similarity 71.4%; Pred. No. 2.2e+02;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 6 FECICLP 12  
DB 4 ECICGP 9

DB 2 FECICGP 8  
RESULT 63  
US-09-723-890-67  
; Sequence 67, Application US/09723890  
; Patent No. 6608031  
; GENERAL INFORMATION:  
; APPLICANT: Clark, Ross G1  
; APPLICANT: Lowman, Henry B.  
; APPLICANT: Robinson, Iain C.A.F.  
; TITLE OF INVENTION: Insulin-like Growth Factor Agonist Molecules  
; NUMBER OF SEQUENCES: 109  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/723,890  
; FILING DATE: 28-Mar-2000  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/052,888  
; FILING DATE: 31-Mar-1998  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hasak, Janet E.  
; REGISTRATION NUMBER: 28,616  
; REFERENCE/DOCKET NUMBER: P1071P1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-1896  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 67:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: linear  
; SEQUENCE DESCRIPTION: SEQ ID NO: 67:  
; US-09-723-890-67

Query Match 41.8%; Score 28; DB 2; Length 18;  
Best Local Similarity 66.7%; Pred. No. 2.2e+02;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 7 ECICLP 12  
DB 4 ECICGP 9

RESULT 64  
US-09-723-890-69  
; Sequence 69, Application US/09723890  
; Patent No. 6608031  
; GENERAL INFORMATION:  
; APPLICANT: Clark, Ross G1  
; APPLICANT: Lowman, Henry B.  
; APPLICANT: Robinson, Iain C.A.F.  
; TITLE OF INVENTION: Insulin-like Growth Factor Agonist Molecules  
; NUMBER OF SEQUENCES: 109  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Winpatin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/723-890  
FILING DATE: 28-Mar-2000  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/052-888  
FILING DATE: 31-Mar-1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Haasek, Janet E.  
REGISTRATION NUMBER: 28,616  
REFERENCE/DOCKET NUMBER: P1071P1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-1896  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 69:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 69:  
US-09-723-890-69

Query Match 41.8%; Score 28; DB 2; Length 18;  
Best Local Similarity 83.3%; Pred. No. 2.2e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 ECTIGP 12  
DB 4 ECTIGP 9

RESULT 65  
US-09-723-901-67  
Sequence 67, Application US/09723901  
Patent No. 6620789  
GENERAL INFORMATION:  
APPLICANT: Clark, Rose G1  
Lowman, Henry B.  
TITLE OF INVENTION: Insulin-like Growth Factor Agonist Molecules  
NUMBER OF SEQUENCES: 109  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Winpatin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/723-901  
FILING DATE: 28-Mar-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/052-888  
FILING DATE: 31-Mar-1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Haasek, Janet E.  
REGISTRATION NUMBER: 28,616  
REFERENCE/DOCKET NUMBER: P1071P1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-1896  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 67:  
SEQUENCE DESCRIPTION: SEQ ID NO: 67:  
US-09-723-901-67

SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 67:  
US-09-723-901-67

Query Match 41.8%; Score 28; DB 2; Length 18;  
Best Local Similarity 66.7%; Pred. No. 2.2e+02;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 ECTIGP 12  
DB 4 ECTWGP 9

RESULT 66  
US-09-723-901-69  
Sequence 69, Application US/09723901  
Patent No. 6620789  
GENERAL INFORMATION:  
APPLICANT: Clark, Rose G1  
Lowman, Henry B.  
TITLE OF INVENTION: Insulin-like Growth Factor Agonist Molecules  
NUMBER OF SEQUENCES: 109  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Winpatin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/723,901  
FILING DATE: 28-Mar-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/052,888  
FILING DATE: 31-Mar-1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Haasek, Janet E.  
REGISTRATION NUMBER: 28,616  
REFERENCE/DOCKET NUMBER: P1071P1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-1896  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 69:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 69:  
US-09-723-901-69

Query Match 41.8%; Score 28; DB 2; Length 18;  
Best Local Similarity 83.3%; Pred. No. 2.2e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 ECTIGP 12  
DB 4 ECTIGP 9

RESULT 67  
US-09-723-547-67  
Sequence 67, Application US/09723547  
Patent No. 6632794

GENERAL INFORMATION:  
APPLICANT: Clark, Ross G1  
Lowman, Henry B.  
Robinson, Iain C.A.F.  
TITLE OF INVENTION: Insulin-like Growth Factor Agonist Molecules  
NUMBER OF SEQUENCES: 109  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/723,547  
FILING DATE: 28-No. 6632794-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/052,888  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Hasak, Janet E.  
REGISTRATION NUMBER: 28,616  
REFERENCE/DOCKET NUMBER: P1071P1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-1896  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 67:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 67:  
US-09-723-547-67  
Query Match 41.8%; Score 28; DB 2; Length 18;  
Best Local Similarity 66.7%; Pred. No. 2.2e+02;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 7 ECILGP 12  
DB 4 ECVWGP 9  
RESULT 68  
US-09-723-547-69  
Sequence 69, Application US/09723547  
Patent No. 6632794  
GENERAL INFORMATION:  
APPLICANT: Clark, Ross G1  
Lowman, Henry B.  
Robinson, Iain C.A.F.  
TITLE OF INVENTION: Insulin-like Growth Factor Agonist Molecules  
NUMBER OF SEQUENCES: 109  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/723,547

FILING DATE: 28-No. 6632794-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/052,888  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Hasak, Janet E.  
REGISTRATION NUMBER: 28,616  
REFERENCE/DOCKET NUMBER: P1071P1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-1896  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 69:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 69:  
US-09-723-547-69  
Query Match 41.8%; Score 28; DB 2; Length 18;  
Best Local Similarity 83.3%; Pred. No. 2.2e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 7 ECILGP 12  
DB 4 ECVWGP 9  
RESULT 69  
US-09-724-127-67  
Sequence 67, Application US/09724127  
Patent No. 6635619  
GENERAL INFORMATION:  
APPLICANT: Clark, Ross G1  
Lowman, Henry B.  
Robinson, Iain C.A.F.  
TITLE OF INVENTION: Insulin-like Growth Factor Agonist Molecules  
NUMBER OF SEQUENCES: 109  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/724,127  
FILING DATE: 28-No. 6635619-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/052,888  
FILING DATE: 31-Mar-1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Hasak, Janet E.  
REGISTRATION NUMBER: 28,616  
REFERENCE/DOCKET NUMBER: P1071P1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-1896  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 67:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 67:  
US-09-724-127-67

Query Match 41.8%; Score 28; DB 2; Length 18;  
Best Local Similarity 66.7%; Pred. No. 2.2e+02;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 ECLIGP 12  
DB 4 ECVWGP 9

## RESULT 70

US-09-724-127-69  
Sequence 69, Application US/09724127  
Patent No. 6635619  
GENERAL INFORMATION:  
APPLICANT: Clark, Rose G1  
Lowman, Henry B.  
Robinson, Iain C.A.F.  
TITLE OF INVENTION: Insulin-like Growth Factor Agonist Molecules  
NUMBER OF SEQUENCES: 109  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Winpatin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/724,127  
FILING DATE: 28-Mar-1998  
CLASSIFICATION: <Unknown>  
PRIORITY APPLICATION DATA:  
PRIORITY APPLICATION NUMBER: 09/052,888  
FILING DATE: 31-Mar-1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Haasek, Janet E.  
REGISTRATION NUMBER: 28,616  
REFERENCE/DOCKET NUMBER: P1071P1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/952-9881  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 69:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 69:  
US-09-724-127-69  
Query Match 41.8%; Score 28; DB 2; Length 18;  
Best Local Similarity 63.3%; Pred. No. 2.2e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 ECLIGP 12  
DB 4 ECLIGP 9

## RESULT 71

US-09-723-931-67  
Sequence 67, Application US/09723931  
Patent No. 6645775  
GENERAL INFORMATION:  
APPLICANT: Clark, Rose G1  
Lowman, Henry B.  
Robinson, Iain C.A.F.  
TITLE OF INVENTION: Insulin-like Growth Factor Agonist Molecules  
NUMBER OF SEQUENCES: 109  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Winpatin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/723,931

FILING DATE: 28-Mar-1998

CLASSIFICATION: <Unknown>

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: 09/052,888

FILING DATE: 31-Mar-1998

ATTORNEY/AGENT INFORMATION:

NAME: Haasek, Janet E.

REGISTRATION NUMBER: 28,616

REFERENCE/DOCKET NUMBER: P1071P1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/952-9881

TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 67:

SEQUENCE CHARACTERISTICS:

LENGTH: 18 amino acids

TYPE: Amino Acid

TOPOLOGY: Linear

SEQUENCE DESCRIPTION: SEQ ID NO: 67:  
US-09-723-931-67  
Query Match 41.8%; Score 28; DB 2; Length 18;  
Best Local Similarity 66.7%; Pred. No. 2.2e+02;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 ECLIGP 12  
DB 4 ECVWGP 9

## RESULT 72

US-09-723-931-69  
Sequence 69, Application US/09723931  
Patent No. 6645775  
GENERAL INFORMATION:  
APPLICANT: Clark, Rose G1  
Lowman, Henry B.  
Robinson, Iain C.A.F.  
TITLE OF INVENTION: Insulin-like Growth Factor Agonist Molecules  
NUMBER OF SEQUENCES: 109  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Winpatin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/723,931  
FILING DATE: 28-Mar-1998  
CLASSIFICATION: <Unknown>  
PRIORITY APPLICATION DATA:  
PRIORITY APPLICATION NUMBER: 09/052,888  
FILING DATE: 31-Mar-1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Haasek, Janet E.

REGISTRATION NUMBER: 28,616  
REFERENCE/DOCKET NUMBER: P1071P1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/952-1896  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 69:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 69:  
US-09-723-931-69

Query Match 41.8%; Score 28; DB 2; Length 18;  
Best Local Similarity 83.3%; Pred. No. 2.2e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 ECIIGP 12  
Db 4 ECIIGP 9

RESULT 73  
US-09-723-873-67  
Sequence 67, Application US/09723873  
Patent No. 6677305  
GENERAL INFORMATION:  
APPLICANT: Clark, Ross G1  
Lowman, Henry B.  
Robinson, Iain C.A.F.  
TITLE OF INVENTION: Insulin-like Growth Factor Agonist Molecules  
NUMBER OF SEQUENCES: 109  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/723,873  
FILING DATE: 28-No. 6677305-2000  
PRIOR APPLICATION NUMBER: US/09/052,888  
FILING DATE: 31-Mar-1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Hasak, Janet E.  
REGISTRATION NUMBER: 28,616  
REFERENCE/DOCKET NUMBER: P1071P1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/952-1896  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 67:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 67:  
US-09-723-873-67

Query Match 41.8%; Score 28; DB 2; Length 18;  
Best Local Similarity 66.7%; Pred. No. 2.2e+02;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 7 ECIIGP 12  
Db 4 ECIIGP 9

RESULT 74  
US-09-723-873-69  
Sequence 69, Application US/09723873  
Patent No. 6677305  
GENERAL INFORMATION:  
APPLICANT: Clark, Ross G1  
Lowman, Henry B.  
Robinson, Iain C.A.F.  
TITLE OF INVENTION: Insulin-like Growth Factor Agonist Molecules  
NUMBER OF SEQUENCES: 109  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/723,873  
FILING DATE: 28-No. 6677305-2000  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/052,888  
FILING DATE: 31-Mar-1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Hasak, Janet E.  
REGISTRATION NUMBER: 28,616  
REFERENCE/DOCKET NUMBER: P1071P1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/952-1896  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 69:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 69:  
US-09-723-873-69

Query Match 41.8%; Score 28; DB 2; Length 18;  
Best Local Similarity 83.3%; Pred. No. 2.2e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 ECIIGP 12  
Db 4 ECIIGP 9

RESULT 75  
US-09-724-114-67  
Sequence 67, Application US/09724114  
Patent No. 6680298  
GENERAL INFORMATION:  
APPLICANT: Clark, Ross G1  
Lowman, Henry B.  
Robinson, Iain C.A.F.  
TITLE OF INVENTION: Insulin-like Growth Factor Agonist Molecules  
NUMBER OF SEQUENCES: 109  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible



OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPacIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/724,114  
FILING DATE: 28-No. 6680298-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/052,888  
FILING DATE: 31-Mar-1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Hasak, Janet E.  
REGISTRATION NUMBER: 28,616  
REFERENCE/DOCKET NUMBER: P1071P1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-1896  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 67:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-09-724-114-67  
SEQUENCE DESCRIPTION: SEQ ID NO: 67:  
  
Query Match 41.8%; Score 28; DB 2; Length 18;  
Best Local Similarity 66.7%; Pred. No. 2.2e+02;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
  
QY 7 ECIIGP 12  
Db 4 ECVWGP 9  
  
RESULT 76  
US-09-724-114-69  
Sequence 69, Application US/09724114  
Patent No. 6680298  
GENERAL INFORMATION:  
APPLICANT: Clark, Ross G1  
Lowman, Henry B.  
Robinson, Iain C.A.F.  
TITLE OF INVENTION: Insulin-like Growth Factor Agonist Molecules  
NUMBER OF SEQUENCES: 109  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPacIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/724,114  
FILING DATE: 28-No. 6680298-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/052,888  
FILING DATE: 31-Mar-1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Hasak, Janet E.  
REGISTRATION NUMBER: 28,616  
REFERENCE/DOCKET NUMBER: P1071P1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-1896  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 69:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: Amino Acid

TOPOLOGY: Linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 69:  
US-09-724-114-69  
  
Query Match 41.8%; Score 28; DB 2; Length 18;  
Best Local Similarity 83.3%; Pred. No. 2.2e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 7 ECIIGP 12  
Db 4 ECIIGP 9  
  
RESULT 77  
US-09-723-913-67  
Sequence 67, Application US/09723913  
Patent No. 6683053  
GENERAL INFORMATION:  
APPLICANT: Clark, Ross G1  
Lowman, Henry B.  
Robinson, Iain C.A.F.  
TITLE OF INVENTION: Insulin-like Growth Factor Agonist Molecules  
NUMBER OF SEQUENCES: 109  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPacIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/723,913  
FILING DATE: 28-No. 6683053-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/052,888  
FILING DATE: 31-Mar-1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Hasak, Janet E.  
REGISTRATION NUMBER: 28,616  
REFERENCE/DOCKET NUMBER: P1071P1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-1896  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 67:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 67:  
US-09-723-913-67  
  
Query Match 41.8%; Score 28; DB 2; Length 18;  
Best Local Similarity 66.7%; Pred. No. 2.2e+02;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
  
QY 7 ECIIGP 12  
Db 4 ECVWGP 9  
  
RESULT 78  
US-09-723-913-69  
Sequence 69, Application US/09723913  
Patent No. 6683053  
GENERAL INFORMATION:  
APPLICANT: Clark, Ross G1  
Lowman, Henry B.

Robinson, Iain C.A.F.  
TITLE OF INVENTION: Insulin-like Growth Factor Agonist Molecules  
NUMBER OF SEQUENCES: 109  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/723,913  
FILING DATE: 28-No. 6683053-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/052,888  
FILING DATE: 31-Mar-1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Hasak, Janet E.  
REGISTRATION NUMBER: 28,616  
REFERENCE/DOCKET NUMBER: P1071P1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-1896  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 69:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 69:  
US-09-723-913-69  
Query Match 41.8%; Score 28; DB 2; Length 18;  
Best Local Similarity 83.3%; Pred. No. 2.2e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 7 ECIIGP 12  
DB 4 ECIIGP 9  
RESULT 79  
US-09-723-912-67  
Sequence 67, Application US/09723912  
Patent No. 6689751  
GENERAL INFORMATION:  
APPLICANT: Clark, Ross G1  
Lowman, Henry B.  
Robinson, Iain C.A.F.  
TITLE OF INVENTION: Insulin-like Growth Factor Agonist Molecules  
NUMBER OF SEQUENCES: 109  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/723,912  
FILING DATE: 28-No. 6689751-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/052,888  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Hasak, Janet E.  
REGISTRATION NUMBER: 28,616  
REFERENCE/DOCKET NUMBER: P1071P1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-1896  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 67:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 67:  
US-09-723-912-67  
Query Match 41.8%; Score 28; DB 2; Length 18;  
Best Local Similarity 66.7%; Pred. No. 2.2e+02;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 7 ECIIGP 12  
DB 4 ECIIGP 9  
RESULT 80  
US-09-723-912-69  
Sequence 69, Application US/09723912  
Patent No. 6689751  
GENERAL INFORMATION:  
APPLICANT: Clark, Ross G1  
Lowman, Henry B.  
Robinson, Iain C.A.F.  
TITLE OF INVENTION: Insulin-like Growth Factor Agonist Molecules  
NUMBER OF SEQUENCES: 109  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/723,912  
FILING DATE: 28-No. 6689751-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/052,888  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Hasak, Janet E.  
REGISTRATION NUMBER: 28,616  
REFERENCE/DOCKET NUMBER: P1071P1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-1896  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 69:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 69:  
US-09-723-912-69  
Query Match 41.8%; Score 28; DB 2; Length 18;  
Best Local Similarity 83.3%; Pred. No. 2.2e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 ECIIGP 12  
|||  
Db 4 ECIIGP 9

RESULT 81  
US-09-724-095-67  
Sequence 67, Application US/09724095  
Patent No. 6693078  
GENERAL INFORMATION:  
APPLICANT: Clark, Ross G1  
Lowman, Henry B.  
Robinson, Iain C.A.F.  
TITLE OF INVENTION: Insulin-like Growth Factor Agonist Molecules  
NUMBER OF SEQUENCES: 109  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/724,095  
FILING DATE: 28-Mar-1998  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/052,888  
FILING DATE: 31-Mar-1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Haseak, Janet B.  
REGISTRATION NUMBER: 28,616  
REFERENCE/DOCKET NUMBER: P1071P1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-1896  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 67:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 67:  
US-09-724-095-67

Query Match 41.8%; Score 28; DB 2; Length 18;  
Best Local Similarity 66.7%; Pred. No. 2.2e+02;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 ECIIGP 12  
|||  
Db 4 ECIIGP 9

RESULT 82  
US-09-724-095-69  
Sequence 69, Application US/09724095  
Patent No. 6693078  
GENERAL INFORMATION:  
APPLICANT: Clark, Ross G1  
Lowman, Henry B.  
Robinson, Iain C.A.F.  
TITLE OF INVENTION: Insulin-like Growth Factor Agonist Molecules  
NUMBER OF SEQUENCES: 109  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco

STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/724,095  
FILING DATE: 28-Mar-1998  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/052,888  
FILING DATE: 31-Mar-1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Haseak, Janet B.  
REGISTRATION NUMBER: 28,616  
REFERENCE/DOCKET NUMBER: P1071P1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-1896  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 69:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 69:  
US-09-724-095-69

Query Match 41.8%; Score 28; DB 2; Length 18;  
Best Local Similarity 83.3%; Pred. No. 2.2e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 ECIIGP 12  
|||  
Db 4 ECIIGP 9

RESULT 83  
US-09-724-157-67  
Sequence 67, Application US/09724157  
Patent No. 6693079  
GENERAL INFORMATION:  
APPLICANT: Clark, Ross G1  
Lowman, Henry B.  
Robinson, Iain C.A.F.  
TITLE OF INVENTION: Insulin-like Growth Factor Agonist Molecules  
NUMBER OF SEQUENCES: 109  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/724,157  
FILING DATE: 28-Mar-1998  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/052888  
FILING DATE: 31-Mar-1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Haseak, Janet B.  
REGISTRATION NUMBER: 28,616  
REFERENCE/DOCKET NUMBER: P1071P1  
TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-1896  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 67:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 67:  
US-09-724-157-67

Query Match 41.8%; Score 28; DB 2; Length 18;  
Best Local Similarity 66.7%; Pred. No. 2.2e+02;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 ECLIGP 12  
||: ||  
DB 4 ECVWGP 9

RESULT 84  
US-09-724-157-69

Sequence 69, Application US/09724157  
Patent No. 6693079  
GENERAL INFORMATION:  
APPLICANT: Clark, Rose G1  
Lowman, Henry B.  
Robinson, Iain C.A.F.  
TITLE OF INVENTION: Insulin-like Growth Factor Agonist Molecules  
NUMBER OF SEQUENCES: 109  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Winpactin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/724,157  
FILING DATE: 28-Mar-1998  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/052888  
FILING DATE: 31-Mar-1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Hasak, Janet E.  
REGISTRATION/DOCKET NUMBER: 28,616  
REFERENCE/DOCKET NUMBER: P1071P1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-1896  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 69:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 69:  
US-09-724-157-69

Query Match 41.8%; Score 28; DB 2; Length 18;  
Best Local Similarity 83.3%; Pred. No. 2.2e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 ECLIGP 12  
||: ||  
DB 4 ECLIGP 9

RESULT 85

US-09-724-062-67  
Sequence 67, Application US/09724062  
Patent No. 6713451  
GENERAL INFORMATION:  
APPLICANT: Clark, Rose G1  
Lowman, Henry B.  
Robinson, Iain C.A.F.  
TITLE OF INVENTION: Insulin-like Growth Factor Agonist Molecules  
NUMBER OF SEQUENCES: 109  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Winpactin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/724,062  
FILING DATE: 28-Mar-1998  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/052,888  
FILING DATE: 31-Mar-1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Hasak, Janet E.  
REGISTRATION/DOCKET NUMBER: 28,616  
REFERENCE/DOCKET NUMBER: P1071P1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-1896  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 67:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 67:  
US-09-724-062-67

Query Match 41.8%; Score 28; DB 2; Length 18;  
Best Local Similarity 66.7%; Pred. No. 2.2e+02;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 ECLIGP 12  
||: ||  
DB 4 ECVWGP 9

RESULT 86  
US-09-724-062-69

Sequence 69, Application US/09724062  
Patent No. 6713451  
GENERAL INFORMATION:  
APPLICANT: Clark, Rose G1  
Lowman, Henry B.  
Robinson, Iain C.A.F.  
TITLE OF INVENTION: Insulin-like Growth Factor Agonist Molecules  
NUMBER OF SEQUENCES: 109  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/724,062  
FILING DATE: 28-No. 6713451-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/052,888  
FILING DATE: 31-Mar-1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Haasek, Janet E.  
REGISTRATION NUMBER: 28,616  
REFERENCE/DOCKET NUMBER: P1071P1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/952-9881  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 69:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 69:  
US-09-724-062-69

Query Match 41.8%; Score 28; DB 2; Length 18;  
Best Local Similarity 83.3%; Pred. No. 2.2e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 ECLIGP 12  
DB 4 ECTIGP 9

RESULT 87  
US-09-724-065-67  
Sequence 67, Application US/09724065  
Patent No. 6716586  
GENERAL INFORMATION:  
APPLICANT: Clark, Rose G1  
Lowman, Henry B.  
Robinson, Iain C.A.F.  
TITLE OF INVENTION: Insulin-like Growth Factor Agonist Molecules  
NUMBER OF SEQUENCES: 109  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/724,065  
FILING DATE: 28-No. 6716586-2000  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/052,888  
FILING DATE: 31-Mar-1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Haasek, Janet E.  
REGISTRATION NUMBER: 28,616  
REFERENCE/DOCKET NUMBER: P1071P1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/952-9881  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 67:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 67:

US-09-724-065-67

Query Match 41.8%; Score 28; DB 2; Length 18;  
Best Local Similarity 66.7%; Pred. No. 2.2e+02;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 ECLIGP 12  
DB 4 ECTWGP 9

RESULT 88  
US-09-724-065-69  
Sequence 69, Application US/09724065  
Patent No. 6716586  
GENERAL INFORMATION:  
APPLICANT: Clark, Rose G1  
Lowman, Henry B.  
Robinson, Iain C.A.F.  
TITLE OF INVENTION: Insulin-like Growth Factor Agonist Molecules  
NUMBER OF SEQUENCES: 109  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/724,065  
FILING DATE: 28-No. 6716586-2000  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/052,888  
FILING DATE: 31-Mar-1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Haasek, Janet E.  
REGISTRATION NUMBER: 28,616  
REFERENCE/DOCKET NUMBER: P1071P1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/952-9881  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 69:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 69:  
US-09-724-065-69

Query Match 41.8%; Score 28; DB 2; Length 18;  
Best Local Similarity 83.3%; Pred. No. 2.2e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 ECLIGP 12  
DB 4 ECTIGP 9

RESULT 89  
US-10-158-825-88  
Sequence 88, Application US/10158825  
Patent No. 6900033  
GENERAL INFORMATION:  
APPLICANT: Tom Parry et al.  
TITLE OF INVENTION: Method and Compositions for Modulating ACE-2 Activity  
FILE REFERENCE: PF555  
CURRENT APPLICATION NUMBER: US/10/158,825  
CURRENT FILING DATE: 2002-06-03

PRIOR APPLICATION NUMBER: 60/294,976  
PRIOR FILING DATE: 2001-06-04  
NUMBER OF SEQ ID NOS: 158  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO: 88  
LENGTH: 18  
TYPE: PRT  
ORGANISM: homo sapiens  
US-10-158-825-88

Query Match 41.8%; Score 28; DB 2; Length 18;  
Best Local Similarity 71.4%; Pred. No. 2.2e+02;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 ECICGP 12  
DB 2 ECICWGP 8

RESULT 90  
US-09-724-481-67  
Sequence 67, Application US/09724481  
Patent No. 6949349  
GENERAL INFORMATION:  
APPLICANT: Clark, Ross G1  
Lowman, Henry B.  
Robinson, Iain C.A.F.  
TITLE OF INVENTION: Insulin-like Growth Factor Agonist Molecules  
NUMBER OF SEQUENCES: 109  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Winpatin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/724,481  
FILING DATE: 28-Mar-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/052,888  
FILING DATE: 31-Mar-1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Haasak, Janet E.  
REGISTRATION NUMBER: 28,616  
REFERENCE/DOCKET NUMBER: P1071P1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-1896  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 67:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 67:  
US-09-724-481-67

Query Match 41.8%; Score 28; DB 2; Length 18;  
Best Local Similarity 66.7%; Pred. No. 2.2e+02;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 ECICGP 12  
DB 4 ECICWGP 9

RESULT 91

US-09-724-481-69  
Sequence 69, Application US/09724481  
Patent No. 6949349  
GENERAL INFORMATION:  
APPLICANT: Clark, Ross G1  
Lowman, Henry B.  
Robinson, Iain C.A.F.

TITLE OF INVENTION: Insulin-like Growth Factor Agonist Molecules  
NUMBER OF SEQUENCES: 109  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Winpatin (Genentech)

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/724,481  
FILING DATE: 28-Mar-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/052,888  
FILING DATE: 31-Mar-1998

ATTORNEY/AGENT INFORMATION:  
NAME: Haasak, Janet E.  
REGISTRATION NUMBER: 28,616  
REFERENCE/DOCKET NUMBER: P1071P1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-1896  
TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 69:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 69:  
US-09-724-481-69

Query Match 41.8%; Score 28; DB 2; Length 18;  
Best Local Similarity 83.3%; Pred. No. 2.2e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 ECICGP 12  
DB 4 ECICWGP 9

RESULT 92  
US-08-474-696A-1  
Sequence 1, Application US/08474696A  
Patent No. 5843673  
GENERAL INFORMATION:  
APPLICANT: Sharpe-Timm, Kathy L.  
TITLE OF INVENTION: ENDOMETRIOSIS-SPECIFIC SECRETORY  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Kohn & Associates  
STREET: 30500 No. 5843673thwestern Hwy.  
CITY: Farmington Hills  
STATE: Michigan  
COUNTRY: US  
ZIP: 48334  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/474,696A  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Kohn, Kenneth I.  
REGISTRATION NUMBER: 30,955  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (810) 539-5050  
TELEFAX: (810) 539-5055  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: N-terminal  
US-08-474-696A-1

Query Match 41.8%; Score 28; DB 1; Length 19;  
Best Local Similarity 62.5%; Pred. No. 2.3e+02;  
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 DEKNSPEC 8  
DB 7 DAKGSFPC 14

RESULT 93  
US-08-474-696A-3  
Sequence 3, Application US/08474696A  
Patent No. 5843673

GENERAL INFORMATION:  
APPLICANT: Sharpe-Tilms, Kathy L.  
TITLE OF INVENTION: ENDOMETRIOSIS-SPECIFIC SECRETORY  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Kohn & Associates  
STREET: 30500 No. 5843673thwestern Hwy.  
CITY: Farmington Hills  
STATE: Michigan  
COUNTRY: US  
ZIP: 48334  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/474,696A  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Kohn, Kenneth I.  
REGISTRATION NUMBER: 30,955  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (810) 539-5050  
TELEFAX: (810) 539-5055  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: N-terminal  
US-08-474-696A-3

Query Match 41.8%; Score 28; DB 1; Length 19;  
Best Local Similarity 62.5%; Pred. No. 2.3e+02;  
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 DEKNSPEC 8  
DB 7 DAKGSFPC 14

RESULT 94  
US-09-044-604-3

Sequence 3, Application US/09044604  
Patent No. 6531277  
GENERAL INFORMATION:  
APPLICANT: Tilms, Kathy L.  
TITLE OF INVENTION: ENDOMETRIOSIS-SPECIFIC SECRETORY  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: KOHN & ASSOCIATES  
STREET: 30500 No. 6531277thwestern Hwy. Suite 410  
CITY: Farmington Hills  
STATE: Michigan  
COUNTRY: US  
ZIP: 48334  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/044,604  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Montgomery, Ilene N.  
REGISTRATION NUMBER: 38,972  
REFERENCE/DOCKET NUMBER: 0994.00084  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (248) 539-5050  
TELEFAX: (248) 539-5055  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: N-terminal  
US-09-044-604-3

Query Match 41.8%; Score 28; DB 2; Length 19;  
Best Local Similarity 62.5%; Pred. No. 2.3e+02;  
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 DEKNSPEC 8  
DB 7 DAKGSFPC 14

RESULT 95  
US-08-484-135-51  
Sequence 51, Application US/08484135  
Patent No. 5767078

GENERAL INFORMATION:  
APPLICANT: Johnson, Dana L.  
TITLE OF INVENTION: AGONIST PEPTIDE DIMERS  
NUMBER OF SEQUENCES: 93  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Frank S. Digiglio  
STREET: 400 Garden City Plaza  
CITY: Garden City  
STATE: New York

COUNTRY: U.S.A..  
ZIP: 11530  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/484,135  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: DIGIGLIO, Frank S  
REGISTRATION NUMBER: 31,346  
REFERENCE/DOCKET NUMBER: 9594  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (516) 742-4343  
TELEFAX: (516) 742-4366  
INFORMATION FOR SEQ ID NO: 51:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-484-135-51

Query Match 41.8%; Score 28; DB 1; Length 20;  
Best Local Similarity 50.0%; Pred. No. 2.4e+02;  
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 SPECIILGP 12  
|:|:|:  
DB 3 SMDCRIGP 10

RESULT 96  
US-08-484-135-75  
Sequence 75, Application US/08484135  
Patent No. 5767078  
GENERAL INFORMATION:  
APPLICANT: Johnson, Dana L  
APPLICANT: Zivlin, Robert A  
TITLE OF INVENTION: AGONIST PEPTIDE DIMERS  
NUMBER OF SEQUENCES: 93  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Frank S. Digiglio  
STREET: 400 Garden City Plaza  
CITY: Garden City  
STATE: New York  
COUNTRY: U.S.A..  
ZIP: 11530  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/484,135  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: DIGIGLIO, Frank S  
REGISTRATION NUMBER: 31,346  
REFERENCE/DOCKET NUMBER: 9594  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (516) 742-4343  
TELEFAX: (516) 742-4366  
INFORMATION FOR SEQ ID NO: 75:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
STRANDEDNESS: single

TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-484-135-75

Query Match 41.8%; Score 28; DB 1; Length 20;  
Best Local Similarity 50.0%; Pred. No. 2.4e+02;  
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 5 SPECIILGP 12  
|:|:|:  
DB 3 SMDCRIGP 10

RESULT 97  
US-08-484-635-35  
Sequence 35, Application US/08484635  
Patent No. 5773569  
GENERAL INFORMATION:  
APPLICANT: Wrighton, Nicholas C.  
APPLICANT: Dower, William J.  
APPLICANT: Chang, Ray S.  
APPLICANT: Kashyap, Arun K.  
APPLICANT: Jolliffe, Linda K.  
APPLICANT: Johnson, Dana  
APPLICANT: Mulcahy, Linda  
TITLE OF INVENTION: Compounds and Peptides That Bind to the  
NUMBER OF SEQUENCES: 259  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew  
STREET: One Market Plaza, Stuart Street Tower  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105-1492  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/484,635  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/155,940  
FILING DATE: 19-NOV-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Garrett-Mackowski, Eugenia  
REGISTRATION NUMBER: 37,330  
REFERENCE/DOCKET NUMBER: 16528A-43-1-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 543-9600  
TELEFAX: (415) 543-5043  
INFORMATION FOR SEQ ID NO: 35:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-484-635-35

Query Match 41.8%; Score 28; DB 1; Length 20;  
Best Local Similarity 50.0%; Pred. No. 2.4e+02;  
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 5 SPECIILGP 12  
|:|:|:  
DB 3 SMDCRIGP 10

RESULT 98



US-08-484-635-167  
Sequence 167, Application US/08484635  
Patent No. 5773569  
GENERAL INFORMATION:  
APPLICANT: Wrighton, Nicholas C.  
APPLICANT: Dower, William J.  
APPLICANT: Chang, Ray S.  
APPLICANT: Kaahyap, Arun K.  
APPLICANT: Jolliffe, Linda K.  
APPLICANT: Johnson, Dana  
APPLICANT: Mulcahy, Linda  
TITLE OF INVENTION: Compounds and Peptides That Bind to the  
TITLE OF INVENTION: Erythropoietin Receptor  
NUMBER OF SEQUENCES: 259  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Townsend and Townsend and Crew  
STREET: One Market Plaza, Stewart Street Tower  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105-1492  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/484,635  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/155,940  
FILING DATE: 19-NOV-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Garrett-Wackowski, Eugenia  
REGISTRATION NUMBER: 37,330  
REFERENCE/DOCKET NUMBER: 16528A-43-1-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 543-9600  
TELEFAX: (415) 543-5043  
INFORMATION FOR SEQ ID NO: 167:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULAR TYPE: peptide  
US-08-484-635-167  
Query Match 41.8%; Score 28; DB 1; Length 20;  
Best Local Similarity 50.0%; Pred. No. 2.4e+02;  
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
QY 5 SPECIAGP 12  
DB 4 SYSCARGP 11  
RESULT 99  
US-08-484-635-224  
Sequence 224, Application US/08484635  
Patent No. 5773569  
GENERAL INFORMATION:  
APPLICANT: Wrighton, Nicholas C.  
APPLICANT: Dower, William J.  
APPLICANT: Chang, Ray S.  
APPLICANT: Kaahyap, Arun K.  
APPLICANT: Jolliffe, Linda K.  
APPLICANT: Johnson, Dana  
APPLICANT: Mulcahy, Linda  
TITLE OF INVENTION: Compounds and Peptides That Bind to the  
TITLE OF INVENTION: Erythropoietin Receptor  
NUMBER OF SEQUENCES: 259

CORRESPONDENCE ADDRESS:  
ADDRESSER: Townsend and Townsend and Crew  
STREET: One Market Plaza, Stewart Street Tower  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105-1492  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/484,635  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/155,940  
FILING DATE: 19-NOV-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Garrett-Wackowski, Eugenia  
REGISTRATION NUMBER: 37,330  
REFERENCE/DOCKET NUMBER: 16528A-43-1-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 543-9600  
TELEFAX: (415) 543-5043  
INFORMATION FOR SEQ ID NO: 224:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULAR TYPE: peptide  
US-08-484-635-224  
Query Match 41.8%; Score 28; DB 1; Length 20;  
Best Local Similarity 50.0%; Pred. No. 2.4e+02;  
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
QY 5 SPECIAGP 12  
DB 3 SYSCARGP 10  
RESULT 100  
US-08-484-631-35  
Sequence 35, Application US/08484631  
Patent No. 5830851  
GENERAL INFORMATION:  
APPLICANT: Wrighton, Nicholas C.  
APPLICANT: Dower, William J.  
APPLICANT: Chang, Ray S.  
APPLICANT: Kaahyap, Arun K.  
APPLICANT: Jolliffe, Linda K.  
APPLICANT: Johnson, Dana  
APPLICANT: Mulcahy, Linda  
TITLE OF INVENTION: Compounds and Peptides That Bind to the  
TITLE OF INVENTION: Erythropoietin Receptor  
NUMBER OF SEQUENCES: 259  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Townsend and Townsend and Crew  
STREET: One Market Plaza, Stewart Street Tower  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105-1492  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/484,631

; FILING DATE: 07-JUN-1995  
 ; CLASSIFICATION: 514  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/155,940  
 ; FILING DATE: 19-NOV-1993  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Garrett-Wackowski, Eugenia  
 ; REGISTRATION NUMBER: 37,330  
 ; REFERENCE/DOCKET NUMBER: 16528A-43-1-2  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (415) 543-9600  
 ; TELEFAX: (415) 543-5043  
 ; INFORMATION FOR SEQ ID NO: 35:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 20 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS:  
 ; TOPOLOGY: linear  
 ; MOLBCULE TYPE: peptide  
 ; US-08-484-631-35

Query Match 41.8%; Score 28; DB 1; Length 20;  
 Best Local Similarity 50.0%; Pred. No. 2.4e+02;  
 Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 5 SPECIIGP 12  
 DB 3 SWDCRIGP 10

Search completed: January 20, 2006, 19:14:14  
 Job time : 13.5769 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 20, 2006, 19:11:21 : Search time 43.2692 Seconds  
(without alignments)  
115.878 Million cell updates/sec

Title: US-09-662-293-5  
Perfect score: 67  
Sequence: 1 DEKNSPEICILGP 12

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 380452

Minimum DB seq length: 0  
Maximum DB seq length: 20

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : Published Applications AA Main:\*  
1: /cgn2\_6/prodata/1/pubppaa/US07\_PUBCOMB.pep:\*  
2: /cgn2\_6/prodata/1/pubppaa/US08\_PUBCOMB.pep:\*  
3: /cgn2\_6/prodata/1/pubppaa/US09\_PUBCOMB.pep:\*  
4: /cgn2\_6/prodata/1/pubppaa/US10A\_PUBCOMB.pep:\*  
5: /cgn2\_6/prodata/1/pubppaa/US10B\_PUBCOMB.pep:\*  
6: /cgn2\_6/prodata/1/pubppaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	67	100.0	12	4	US-10-218-743-5
2	33	49.3	18	4	US-10-381-112-6
3	32	47.8	13	5	US-10-488-671-20
4	32	47.8	13	5	US-10-488-707-795
5	31	46.3	20	4	US-10-225-567A-1942
6	30	44.8	16	3	US-09-824-637-6
7	30	44.8	18	4	US-10-098-093-41
8	30	44.8	19	4	US-10-378-557-55
9	30	44.8	19	5	US-10-661-156-220
10	29	43.3	10	5	US-10-808-187-1834
11	29	43.3	10	5	US-10-807-807-1834
12	29	43.3	19	5	US-10-792-582-57
13	28	41.8	8	5	US-10-889-934-18
14	28	41.8	9	4	US-10-913-228-18
15	28	41.8	9	4	US-10-448-521-1
16	28	41.8	9	4	US-10-448-521-43
17	28	41.8	12	3	US-09-071-838-219
18	28	41.8	12	4	US-10-213-512-219
19	28	41.8	13	4	US-10-481-180-109
20	28	41.8	14	3	US-09-774-639-272
21	28	41.8	14	3	US-09-969-730-340
22	28	41.8	14	3	US-09-932-613-59
23	28	41.8	14	3	US-09-932-322-59
24	28	41.8	14	4	US-10-621-363-340
25	28	41.8	15	3	US-09-738-363-23
26	28	41.8	15	4	US-10-633-023-23
27	28	41.8	15	4	US-10-481-180-116

28	28	41.8	15	4	US-10-481-180-117	Sequence 117, App
29	28	41.8	16	4	US-10-481-180-120	Sequence 120, App
30	28	41.8	17	4	US-10-481-180-122	Sequence 122, App
31	28	41.8	18	3	US-09-864-761-43665	Sequence 43665, A
32	28	41.8	18	3	US-09-858-935B-107	Sequence 107, App
33	28	41.8	18	3	US-09-858-935B-110	Sequence 110, App
34	28	41.8	18	4	US-10-158-847-88	Sequence 88, App1
35	28	41.8	18	4	US-10-158-847-88	Sequence 88, App1
36	28	41.8	18	4	US-10-271-869-107	Sequence 107, App
37	28	41.8	18	4	US-10-271-869-110	Sequence 110, App
38	28	41.8	18	4	US-10-158-825-88	Sequence 88, App1
39	28	41.8	19	3	US-09-044-604-3	Sequence 3, App11
40	28	41.8	19	4	US-10-306-903-3	Sequence 3, App11
41	28	41.8	20	5	US-10-690-276-662	Sequence 662, App
42	27	40.3	20	4	US-10-196-394-65	Sequence 65, App1
43	27	40.3	9	4	US-10-357-175-89	Sequence 89, App1
44	27	40.3	9	4	US-10-357-175-115	Sequence 115, App
45	27	40.3	9	4	US-10-455-720-89	Sequence 89, App1
46	27	40.3	9	4	US-10-455-720-115	Sequence 115, App
47	27	40.3	9	4	US-10-350-508-55	Sequence 55, App
48	27	40.3	12	5	US-10-838-289-227	Sequence 227, App
49	27	40.3	12	5	US-10-607-595-435	Sequence 435, App
50	27	40.3	13	5	US-10-488-671-21	Sequence 21, App1
51	27	40.3	20	4	US-10-269-695-147	Sequence 147, App
52	27	40.3	20	4	US-10-410-998-147	Sequence 147, App
53	27	40.3	20	4	US-10-432-465-65	Sequence 65, App1
54	27	40.3	20	4	US-10-433-091-34	Sequence 34, App1
55	26	38.8	9	4	US-10-286-457-230	Sequence 230, App
56	26	38.8	10	4	US-10-352-786-455	Sequence 455, App
57	26	38.8	10	4	US-10-352-786-454	Sequence 454, App
58	26	38.8	11	4	US-10-114-500-19	Sequence 19, App1
59	26	38.8	11	4	US-10-352-786-541	Sequence 541, App
60	26	38.8	11	4	US-10-352-786-542	Sequence 542, App
61	26	38.8	11	5	US-10-471-346-19	Sequence 19, App1
62	26	38.8	12	4	US-10-352-786-627	Sequence 627, App
63	26	38.8	12	4	US-10-352-786-628	Sequence 628, App
64	26	38.8	13	3	US-09-880-713A-30	Sequence 30, App1
65	26	38.8	13	3	US-09-888-493-302	Sequence 302, App1
66	26	38.8	13	4	US-10-352-786-717	Sequence 717, App
67	26	38.8	13	4	US-10-352-786-718	Sequence 718, App
68	26	38.8	13	4	US-10-412-964-40	Sequence 40, App1
69	26	38.8	13	5	US-10-948-707-1280	Sequence 1280, App
70	26	38.8	14	4	US-10-352-786-813	Sequence 813, App
71	26	38.8	14	4	US-10-352-786-814	Sequence 814, App
72	26	38.8	14	4	US-10-615-659-45	Sequence 45, App1
73	26	38.8	14	4	US-10-635-977-45	Sequence 45, App1
74	26	38.8	14	5	US-10-473-287-39	Sequence 39, App1
75	26	38.8	15	3	US-09-767-460-29	Sequence 29, App1
76	26	38.8	15	3	US-10-352-786-913	Sequence 913, App
77	26	38.8	15	4	US-10-352-786-914	Sequence 914, App
78	26	38.8	15	5	US-10-777-829-29	Sequence 29, App1
79	26	38.8	15	5	US-10-818-067-29	Sequence 29, App1
80	26	38.8	15	3	US-09-774-639-245	Sequence 245, App
81	26	38.8	16	3	US-10-969-730-344	Sequence 344, App
82	26	38.8	16	4	US-10-114-500-15	Sequence 1017, App
83	26	38.8	16	4	US-10-352-786-1017	Sequence 1017, App
84	26	38.8	16	4	US-10-352-786-1018	Sequence 1018, App
85	26	38.8	16	4	US-10-621-363-344	Sequence 344, App
86	26	38.8	17	5	US-10-471-346-15	Sequence 15, App1
87	26	38.8	17	4	US-10-352-786-1127	Sequence 1127, App
88	26	38.8	17	4	US-10-352-786-1128	Sequence 1128, App
89	26	38.8	18	3	US-09-858-935B-121	Sequence 121, App
90	26	38.8	18	4	US-10-271-869-121	Sequence 121, App
91	26	38.8	18	4	US-10-352-786-1243	Sequence 1243, App
92	26	38.8	18	4	US-10-352-786-1244	Sequence 1244, App
93	26	38.8	18	4	US-10-754-437-25	Sequence 25, App1
94	26	38.8	18	4	US-10-754-437-29	Sequence 29, App1
95	26	38.8	18	4	US-10-754-437-31	Sequence 31, App1
96	26	38.8	19	3	US-09-864-761-43430	Sequence 43430, A
97	26	38.8	19	4	US-10-225-567A-1330	Sequence 1330, App
98	26	38.8	19	4	US-10-352-786-1365	Sequence 1365, App
99	26	38.8	19	4	US-10-352-786-1366	Sequence 1366, App
100	26	38.8	19	4	US-10-352-786-1366	Sequence 1366, App

## ALIGNMENTS

## RESULT 1

US-10-218-743-5  
 ; Sequence 5, Application US/10218743  
 ; Publication No. US20030096779A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: McCall, Catherine A.  
 ; APPLICANT: Hunter, Shirley Wu  
 ; APPLICANT: Weber, Eric R.  
 ; TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS  
 ; TITLE OF INVENTION: AND USES THEREOF  
 ; FILE REFERENCE: AL-2-C3  
 ; CURRENT APPLICATION NUMBER: US/10/218,743  
 ; CURRENT FILING DATE: 2002-08-13  
 ; PRIOR APPLICATION NUMBER: US/09/292,225  
 ; PRIOR FILING DATE: 1999-04-15  
 ; PRIOR APPLICATION NUMBER: 60/098,909  
 ; PRIOR FILING DATE: 1998-09-02  
 ; PRIOR APPLICATION NUMBER: 60/085,295  
 ; PRIOR FILING DATE: 1998-05-13  
 ; PRIOR APPLICATION NUMBER: 60/098,565  
 ; PRIOR FILING DATE: 1998-04-17  
 ; PRIOR APPLICATION NUMBER: 09/062,013  
 ; PRIOR FILING DATE: 1998-04-17  
 ; NUMBER OF SEQ ID NOS: 49  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 5  
 ; LENGTH: 12  
 ; TYPE: PRT  
 ; ORGANISM: Dermatophagoides farinae  
 US-10-218-743-5

## Query Match

Best Local Similarity 100.0%; Score 67; DB 4; Length 12;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEKNSFECTLGP 12  
 |||||

Db 1 DEKNSFECTLGP 12

## RESULT 2

US-10-381-112-6  
 ; Sequence 6, Application US/10381112  
 ; Publication No. US20040086942A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Lowman, Henry B.  
 ; APPLICANT: Nakamura, Gerald R.  
 ; APPLICANT: Reynolds, Mark E.  
 ; APPLICANT: Starovaanik, Melissa A.  
 ; TITLE OF INVENTION: IGR RECEPTOR ANTAGONISTS  
 ; FILE REFERENCE: P1816R1  
 ; CURRENT APPLICATION NUMBER: US/10/381,112  
 ; CURRENT FILING DATE: 2003-10-27  
 ; PRIOR APPLICATION NUMBER: US 60/278,540  
 ; PRIOR FILING DATE: 2001-03-23  
 ; PRIOR APPLICATION NUMBER: US 60/235,353  
 ; PRIOR FILING DATE: 2000-09-26  
 ; NUMBER OF SEQ ID NOS: 595  
 ; SEQ ID NO 6  
 ; LENGTH: 18  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: clone g8b.22 shown in Table 2  
 US-10-381-112-6

Query Match 49.3%; Score 33; DB 4; Length 18;  
 Best Local Similarity 55.6%; Pred. No. 76;

Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 4 NSPFCITLGP 12  
 |||||

Db 1 NYEBCWMP 9

## RESULT 3

US-10-488-671-20  
 ; Sequence 20, Application US/10488671  
 ; Publication No. US20040254106A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Carr, Francis J.  
 ; APPLICANT: Carter, Graham  
 ; TITLE OF INVENTION: Modified Factor IX  
 ; FILE REFERENCE: MER-128  
 ; CURRENT APPLICATION NUMBER: US/10/488,671  
 ; CURRENT FILING DATE: 2004-03-04  
 ; PRIOR APPLICATION NUMBER: PCT/EP02/09717  
 ; PRIOR FILING DATE: 2002-08-30  
 ; PRIOR APPLICATION NUMBER: EP 01121154.7  
 ; PRIOR FILING DATE: 2001-09-04  
 ; NUMBER OF SEQ ID NOS: 126  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 20  
 ; LENGTH: 13  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-488-671-20

## Query Match

Best Local Similarity 47.8%; Score 32; DB 5; Length 13;  
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DEKNSFEC 8  
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Db 1 DDINSYEC 8

## RESULT 4

US-10-948-707-795  
 ; Sequence 795, Application US/10948707  
 ; Publication No. US20050187147A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ballatore, Carlo  
 ; APPLICANT: Castellino, Angelo  
 ; APPLICANT: Deshmatais, Joel  
 ; APPLICANT: Guo, Zijian  
 ; APPLICANT: Li, Qing  
 ; APPLICANT: Newman, Michael James  
 ; APPLICANT: Sun, Chengzao  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INCREASING  
 ; FILE REFERENCE: 17967-003001  
 ; CURRENT APPLICATION NUMBER: US/10/948,707  
 ; CURRENT FILING DATE: 2004-09-22  
 ; PRIOR APPLICATION NUMBER: 60/505,325  
 ; PRIOR FILING DATE: 2003-09-22  
 ; PRIOR APPLICATION NUMBER: 60/568,340  
 ; PRIOR FILING DATE: 2004-05-04  
 ; PRIOR APPLICATION NUMBER: 60/581,835  
 ; PRIOR FILING DATE: 2004-06-22  
 ; NUMBER OF SEQ ID NOS: 1422  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 795  
 ; LENGTH: 13  
 ; TYPE: PRT  
 ; ORGANISM: Homo Sapiens  
 US-10-948-707-795

Query Match 47.8%; Score 32; DB 5; Length 13;  
 Best Local Similarity 62.5%; Pred. No. 82;  
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 DEKNSPEC 8  
|:|:|:  
Db 4 DDINSYEC 11

RESULT 5  
US-10-225-567A-1942  
; Sequence 1942, Application US/10225567A  
; Publication No. US2003011798A1  
; GENERAL INFORMATION:  
; APPLICANT: Lifespan Biosciences  
; APPLICANT: Brown, Joseph P.  
; APPLICANT: Burner, Glenn C.  
; APPLICANT: Roush, Christine L.  
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS  
; FILE REFERENCE: 1920-4-4  
; CURRENT APPLICATION NUMBER: US/10/225,567A  
; CURRENT FILING DATE: 2001-12-19  
; PRIOR APPLICATION NUMBER: 60/257,144  
; PRIOR FILING DATE: 2000-12-19  
; NUMBER OF SEQ ID NOS: 2292  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1942  
; LENGTH: 20  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-225-567A-1942

Query Match 46.3%; Score 31; DB 4; Length 20;  
Best Local Similarity 62.5%; Pred. No. 2e+02;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 DEKNSPEC 8  
|:|:|:  
Db 13 DEKNTKC 20

RESULT 6  
US-09-824-637-6  
; Sequence 6, Application US/09824637  
; Patent No. US2002004226A1  
; GENERAL INFORMATION:  
; APPLICANT: RUBINSTEIN, Menachem  
; APPLICANT: NOVICK, Daniela  
; APPLICANT: TAL, Nathan  
; APPLICANT: Fischer, Dina  
; TITLE OF INVENTION: SOLUBLE LDL RECEPTOR, ITS PRODUCTION AND USE  
; FILE REFERENCE: RUBINSTEIN-5D  
; CURRENT APPLICATION NUMBER: US/09/824,637  
; CURRENT FILING DATE: 2001-04-04  
; PRIOR APPLICATION NUMBER: US 08/485,128  
; PRIOR FILING DATE: 1995-06-07  
; PRIOR APPLICATION NUMBER: US 08/092,817  
; PRIOR FILING DATE: 1993-07-19  
; PRIOR APPLICATION NUMBER: IL 100696  
; PRIOR FILING DATE: 1992-01-19  
; PRIOR APPLICATION NUMBER: IL 102915  
; PRIOR FILING DATE: 1992-08-23  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 6  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-824-637-6

Query Match 44.8%; Score 30; DB 3; Length 16;  
Best Local Similarity 57.1%; Pred. No. 2.4e+02;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 4 ERNEFOC 10

RESULT 7  
US-10-098-093-41  
; Sequence 41, Application US/10098093  
; Publication No. US20030092631A1  
; GENERAL INFORMATION:  
; APPLICANT: Debnayes, Kurt D.  
; APPLICANT: Lowman, Henry B.  
; APPLICANT: Schaffer, Michelle L.  
; APPLICANT: Sidhu, Sachdev S.  
; TITLE OF INVENTION: IGF ANTAGONIST PEPTIDES  
; FILE REFERENCE: P1863R1  
; CURRENT APPLICATION NUMBER: US/10/098,093  
; CURRENT FILING DATE: 2002-03-13  
; PRIOR APPLICATION NUMBER: US 60/275,904  
; PRIOR FILING DATE: 2001-03-14  
; NUMBER OF SEQ ID NOS: 122  
; SEQ ID NO 41  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Sequence is synthesized  
US-10-098-093-41

Query Match 44.8%; Score 30; DB 4; Length 18;  
Best Local Similarity 33.3%; Pred. No. 2.7e+02;  
Matches 3; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 4 NSPECTIP 12  
:::|:|:  
Db 1 DAMDCVGP 9

RESULT 8  
US-10-378-557-55  
; Sequence 55, Application US/10378557  
; Publication No. US20030186223A1  
; GENERAL INFORMATION:  
; APPLICANT: Ladner, Robert C.  
; TITLE OF INVENTION: MODULAR RECOMBINANTORIAL DISPLAY  
; FILE REFERENCE: 3421.1013-001  
; CURRENT APPLICATION NUMBER: US/10/378,557  
; CURRENT FILING DATE: 2003-03-03  
; PRIOR APPLICATION NUMBER: 60/361,121  
; PRIOR FILING DATE: 2002-03-01  
; NUMBER OF SEQ ID NOS: 65  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 55  
; LENGTH: 19  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Selected library sequence  
US-10-378-557-55

Query Match 44.8%; Score 30; DB 4; Length 19;  
Best Local Similarity 100.0%; Pred. No. 2.8e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 NSPEC 8  
|:|:|:  
Db 12 NSPEC 16

RESULT 9  
US-10-661-156-220  
; Sequence 220, Application US/10661156  
; Publication No. US20050100963A1  
; GENERAL INFORMATION:

```
/ APPLICANT: Sato, Aaron K.
/ APPLICANT: Sexton, Daniel J.
/ APPLICANT: Dransfield, Daniel T.
/ APPLICANT: Ladner, Robert C.
/ APPLICANT: Arbogast, Christophe
/ APPLICANT: Bussac, Philippe
/ APPLICANT: Fan, Hong
/ APPLICANT: Khurana, Sudha
/ APPLICANT: Linder, Karen E.
/ APPLICANT: Marinelli, Edmund R.
/ APPLICANT: Nanjappan, Palanippa
/ APPLICANT: Nunn, Adrian
/ APPLICANT: Pillai, Radhakrishna
/ APPLICANT: Pochon, Sibylle
/ APPLICANT: Ramalingam, Kondareddiar
/ APPLICANT: Shrivastava, Ajay
/ APPLICANT: Song, Bo
/ APPLICANT: Swenson, Rolf E.
/ APPLICANT: Von Wronski, Mathew A.
/ TITLE OF INVENTION: KDR and VEGF/KDR Binding Peptides and
/ TITLE OF INVENTION: Their Use in Diagnosis and Therapy
/ FILE REFERENCE: D0617.70012US00
/ CURRENT APPLICATION NUMBER: US/10/661,156
/ PRIOR FILING DATE: 2003-09-11
/ PRIOR APPLICATION NUMBER: PCT/US03/06731
/ PRIOR FILING DATE: 2003-03-03
/ PRIOR APPLICATION NUMBER: PCT/US03/06731
/ PRIOR FILING DATE: 2003-03-03
/ PRIOR APPLICATION NUMBER: US 60/440,411
/ PRIOR FILING DATE: 2003-01-15
/ PRIOR APPLICATION NUMBER: US 60/360,851
/ PRIOR FILING DATE: 2002-03-01
/ NUMBER OF SEQ ID NOS: 617
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 220
/ LENGTH: 19
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Library Isolate
/
US-10-661-156-220

Query Match          44.8%; Score 30; DB 5; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 NSPEC 8
DB 12 NSPEC 16

RESULT 10
/ Sequence 1834, Application US/10808187
/ Publication No. US2005009009A1
/ GENERAL INFORMATION:
/ APPLICANT: PEIRIS, JOSEPH S. M.
/ APPLICANT: YUEN, KWOK YUNG
/ APPLICANT: POON, LIT MAN
/ APPLICANT: GUAN, YI
/ APPLICANT: CHAN, KWOK HUNG
/ APPLICANT: NICHOLLS, JOHN
/ TITLE OF INVENTION: A DIAGNOSTIC ASSAY FOR THE HUMAN VIRUS CAUSING SEVERE ACUTE
/ TITLE OF INVENTION: RESPIRATORY SYNDROME (SARS)
/ FILE REFERENCE: V9661.0078
/ CURRENT APPLICATION NUMBER: US/10/808,187
/ PRIOR FILING DATE: 2004-03-24
/ PRIOR APPLICATION NUMBER: 60/457,031
/ PRIOR FILING DATE: 2003-03-24
/ PRIOR APPLICATION NUMBER: 60/457,730
/ PRIOR FILING DATE: 2003-03-26
/ PRIOR APPLICATION NUMBER: 60/459,931
/ PRIOR FILING DATE: 2003-04-02
```

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/ PRIOR APPLICATION NUMBER: 60/460,357
/ PRIOR FILING DATE: 2003-04-03
/ PRIOR APPLICATION NUMBER: 60/461,265
/ PRIOR FILING DATE: 2003-04-08
/ PRIOR APPLICATION NUMBER: 60/462,805
/ PRIOR FILING DATE: 2003-04-14
/ PRIOR APPLICATION NUMBER: 60/468,139
/ PRIOR FILING DATE: 2003-05-05
/ PRIOR APPLICATION NUMBER: 60/464,886
/ PRIOR FILING DATE: 2003-04-23
/ PRIOR APPLICATION NUMBER: 60/471,200
/ PRIOR FILING DATE: 2003-05-16
/ NUMBER OF SEQ ID NOS: 2476
/ SOFTWARE: PatentIn ver. 3.2
/ SEQ ID NO 1834
/ LENGTH: 10
/ TYPE: PRT
/ ORGANISM: Human severe acute respiratory system virus
/
US-10-808-187-1834

Query Match          43.3%; Score 29; DB 5; Length 10;
Best Local Similarity 55.6%; Pred. No. 2.2e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 EKNSPECIL 10
DB 2 KNSDHCVL 10

RESULT 11
/ Sequence 1834, Application US/10807807
/ Publication No. US20050181357A1
/ GENERAL INFORMATION:
/ APPLICANT: LEUNG, FREDERICK C.
/ APPLICANT: PEIRIS, JOSEPH S. M.
/ APPLICANT: YUEN, KWOK YUNG
/ APPLICANT: POON, LIT MAN
/ APPLICANT: GUAN, YI
/ APPLICANT: CHAN, KWOK HUNG
/ APPLICANT: NICHOLLS, JOHN M.
/ TITLE OF INVENTION: A HIGH-THROUGHPUT DIAGNOSTIC ASSAY FOR THE HUMAN VIRUS
/ TITLE OF INVENTION: CAUSING SEVERE ACUTE RESPIRATORY SYNDROME (SARS)
/ FILE REFERENCE: V9661.0077
/ CURRENT APPLICATION NUMBER: US/10/807,807
/ PRIOR FILING DATE: 2004-03-24
/ PRIOR APPLICATION NUMBER: 60/457,031
/ PRIOR FILING DATE: 2003-03-24
/ PRIOR APPLICATION NUMBER: 60/457,730
/ PRIOR FILING DATE: 2003-03-26
/ PRIOR APPLICATION NUMBER: 60/459,931
/ PRIOR FILING DATE: 2003-04-02
/ PRIOR APPLICATION NUMBER: 60/460,357
/ PRIOR FILING DATE: 2003-04-03
/ PRIOR APPLICATION NUMBER: 60/461,265
/ PRIOR FILING DATE: 2003-04-08
/ PRIOR APPLICATION NUMBER: 60/462,805
/ PRIOR FILING DATE: 2003-04-14
/ PRIOR APPLICATION NUMBER: 60/464,886
/ PRIOR FILING DATE: 2003-04-23
/ PRIOR APPLICATION NUMBER: 60/465,738
/ PRIOR FILING DATE: 2003-04-25
/ PRIOR APPLICATION NUMBER: 60/470,935
/ PRIOR FILING DATE: 2003-05-14
/ NUMBER OF SEQ ID NOS: 2487
/ SOFTWARE: PatentIn ver. 3.2
/ SEQ ID NO 1834
/ LENGTH: 10
/ TYPE: PRT
/ ORGANISM: Human severe acute respiratory system virus
/
US-10-807-807-1834

Query Match          43.3%; Score 29; DB 5; Length 10;
```

Best Local Similarity 55.6%; Pred. No. 2.2e+02;  
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 EKNSPECIL 10  
DB 2 KNSDHCVL 10

## RESULT 12

US-10-792-582-57  
Sequence 57, Application US/10792582  
Publication No. US20050214859A1  
GENERAL INFORMATION:  
APPLICANT: Dransfield, Daniel T.  
APPLICANT: Sato, Aaron K.  
APPLICANT: Ladner, Robert C.  
APPLICANT: Smlvascava, Ajay  
APPLICANT: Thomas, Regl  
TITLE OF INVENTION: PEPTIDES THAT SPECIFICALLY BIND HGF  
TITLE OF INVENTION: RECEPTOR (CMET) AND USES THEREOF  
FILE REFERENCE: D0617,70013US01  
CURRENT APPLICATION NUMBER: US/10/792,582  
CURRENT FILING DATE: 2004-03-03  
PRIOR APPLICATION NUMBER: US 60/451,588  
PRIOR FILING DATE: 2003-03-03  
NUMBER OF SEQ ID NOS: 619  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 57  
LENGTH: 19  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetically generated cMet-binding peptide  
US-10-792-582-57

Query Match 43.3%; Score 29; DB 5; Length 19;  
Best Local Similarity 83.3%; Pred. No. 4.3e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 SPECIL 10  
DB 11 TPECIL 16

## RESULT 13

US-10-889-934-18  
Sequence 18, Application US/10889934  
Publication No. US20040265316A1  
GENERAL INFORMATION:  
APPLICANT: Croce, Carlo M.  
Huebner, Kay  
TITLE OF INVENTION: PHIT PROTEINS AND NUCLEIC ACIDS AND  
METHODS BASED THEREON  
NUMBER OF SEQUENCES: 86  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/889,934  
FILING DATE: 13-Jul-2004  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/605,430

FILING DATE: 22-FEB-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Friedel, Thomas B.  
REGISTRATION NUMBER: 29,258  
REFERENCE/DOCKET NUMBER: 8666-005  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 866-9741/8864  
TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 18:  
US-10-889-934-18

Query Match 41.8%; Score 28; DB 5; Length 8;  
Best Local Similarity 50.0%; Pred. No. 1.7e+06;  
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 DEKNSPEC 8  
DB 1 DEETAFSC 8

## RESULT 14

US-10-913-228-18  
Sequence 18, Application US/10913228  
Publication No. US20050074797A1  
GENERAL INFORMATION:  
APPLICANT: Croce, Carlo M.  
Huebner, Kay

TITLE OF INVENTION: PHIT PROTEINS AND NUCLEIC ACIDS AND  
METHODS BASED THEREON

NUMBER OF SEQUENCES: 86  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/913,228  
FILING DATE: 06-Aug-2004  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/605,430  
FILING DATE: 22-FEB-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Friedel, Thomas B.  
REGISTRATION NUMBER: 29,258  
REFERENCE/DOCKET NUMBER: 8666-005  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 866-9741/8864  
TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 18:  
US-10-913-228-18

Query Match 41.8%; Score 28; DB 5; Length 8;  
Best Local Similarity 50.0%; Pred. No. 1.7e+06;  
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DEKNSPEC 8  
| : | : |  
Db 1 DETAFCSC 8

## RESULT 15

US-10-448-521-1  
; Sequence 1, Application US/10448521  
; Publication No. US20040018205A1  
; GENERAL INFORMATION:  
; APPLICANT: FIRAT, HUSEYIN  
; APPLICANT: LANGLADE-DEMOYAN, PIERRE  
; APPLICANT: VILMER, ETIENNE  
; APPLICANT: LEMONNIER, FRANCOIS  
; APPLICANT: ROHRLICH, PIERRE  
; APPLICANT: YOTUNDA, PATRICIA  
; TITLE OF INVENTION: MUTATED IMMUNOGENIC PEPTIDES DERIVED FROM R9M,  
; TITLE OF INVENTION: POLYNUCLEOTIDES CODING FOR SAME AND THERAPEUTIC USES  
; TITLE OF INVENTION: THEREOF  
; FILE REFERENCE: 02356.0082  
; CURRENT APPLICATION NUMBER: US/10/448,521  
; PRIOR FILING DATE: 2003-05-30  
; PRIOR APPLICATION NUMBER: PCT/FR01/03779  
; PRIOR FILING DATE: 2001-11-29  
; PRIOR APPLICATION NUMBER: CA 2,325,666  
; PRIOR FILING DATE: 2000-12-01  
; NUMBER OF SEQ ID NOS: 45  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-448-521-1

Query Match 41.8%; Score 28; DB 4; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 ECIIG 11  
| : | : | : |  
Db 4 ECIIG 8

## RESULT 16

US-10-448-521-43  
; Sequence 43, Application US/10448521  
; Publication No. US20040018205A1  
; GENERAL INFORMATION:  
; APPLICANT: FIRAT, HUSEYIN  
; APPLICANT: LANGLADE-DEMOYAN, PIERRE  
; APPLICANT: VILMER, ETIENNE  
; APPLICANT: LEMONNIER, FRANCOIS  
; APPLICANT: ROHRLICH, PIERRE  
; APPLICANT: YOTUNDA, PATRICIA  
; TITLE OF INVENTION: MUTATED IMMUNOGENIC PEPTIDES DERIVED FROM R9M,  
; TITLE OF INVENTION: POLYNUCLEOTIDES CODING FOR SAME AND THERAPEUTIC USES  
; TITLE OF INVENTION: THEREOF  
; FILE REFERENCE: 02356.0082  
; CURRENT APPLICATION NUMBER: US/10/448,521  
; PRIOR FILING DATE: 2003-05-30  
; PRIOR APPLICATION NUMBER: PCT/FR01/03779  
; PRIOR FILING DATE: 2001-11-29  
; PRIOR APPLICATION NUMBER: CA 2,325,666  
; PRIOR FILING DATE: 2000-12-01  
; NUMBER OF SEQ ID NOS: 45  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 43  
; LENGTH: 9  
; TYPE: PRT

; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: peptide  
US-10-448-521-43

Query Match 41.8%; Score 28; DB 4; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 ECIIG 11  
| : | : | : |  
Db 4 ECIIG 8

RESULT 17  
US-09-071-838-219  
; Sequence 219, Application US/09071838  
; Patent No. US20020152501A1  
; GENERAL INFORMATION:  
; APPLICANT: Fischer, Robert L.  
; APPLICANT: Ohad, Nir  
; APPLICANT: Kiyosue, Tomohiro  
; APPLICANT: Yadegari, Ramin  
; APPLICANT: Margosian, Linda  
; APPLICANT: Harada, John  
; APPLICANT: Goldberg, Robert B.  
; TITLE OF INVENTION: Nucleic Acids That Control Seed and  
; TITLE OF INVENTION: Fruit Development in Plants  
; NUMBER OF SEQUENCES: 324  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC Compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/071,838  
; FILING DATE: 01-MAY-1998  
; CLASSIFICATION: 800  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Bastian, Kevin L.  
; REGISTRATION NUMBER: 34,774  
; REFERENCE/DOCKET NUMBER: 023070-086100US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 219:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 12 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-09-071-838-219

Query Match 41.8%; Score 28; DB 3; Length 12;  
Best Local Similarity 44.4%; Pred. No. 4.1e+02;  
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DEKNSPEC 9  
| : | : | : |  
Db 4 DLRRSFVCV 12

RESULT 18  
US-10-213-512-219  
; Sequence 219, Application US/10213512



Publication No. US20030110536A1  
GENERAL INFORMATION:  
APPLICANT: Fischer, Robert L.  
APPLICANT: Ohad, Nir  
APPLICANT: Kiyosue, Tomohiro  
APPLICANT: Yadegari, Ramlin  
APPLICANT: Margossian, Linda  
APPLICANT: Harada, John  
APPLICANT: Goldberg, Robert B.  
TITLE OF INVENTION: The Regents of the University of California  
TITLE OF INVENTION: Combinations of Nucleic Acids That Control Seed and  
FILE REFERENCE: 023070-086110US  
CURRENT APPLICATION NUMBER: US/10/213,512  
CURRENT FILING DATE: 2002-08-06  
PRIOR APPLICATION NUMBER: US/09/177,206  
PRIOR FILING DATE: 1998-10-22  
PRIOR APPLICATION NUMBER: US 09/071,838  
PRIOR FILING DATE: 1998-05-01  
NUMBER OF SEQ ID NOS: 324  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 219  
LENGTH: 12  
TYPE: PRT  
ORGANISM: Arabidopsis sp.  
US-10-213-512-219

Query Match 41.8%; Score 28; DB 4; Length 12;  
Best Local Similarity 44.4%; Pred. No. 4.1e+02;  
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 DEKNSPECI 9  
| : || : |  
DB 4 DLRRSFKCV 12

RESULT 19  
US-10-481-180-109  
Sequence 109, Application US/10481180  
Publication No. US20040171821A1  
GENERAL INFORMATION:  
APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS  
APPLICANT: REPRESENTED BY THE SECRETARY OF THE DEPARTMENT OF HEALTH AND  
APPLICANT: HUMAN SERVICES  
APPLICANT: Valenzuela, Jesus G.  
APPLICANT: Belkaid, Yasmine  
APPLICANT: Kambawi, Shaden  
APPLICANT: Sacks, David  
APPLICANT: Ribeiro, Jose M. C.  
TITLE OF INVENTION: ANTI-ARTHRITIS VECTOR VACCINES, METHODS  
TITLE OF INVENTION: OF SELECTING AND USES THEREOF  
FILE REFERENCE: 4239-67347  
CURRENT APPLICATION NUMBER: US/10/481,180  
CURRENT FILING DATE: 2003-12-17  
PRIOR APPLICATION NUMBER: PCT/US02/19663  
PRIOR FILING DATE: 2002-06-18  
PRIOR APPLICATION NUMBER: US 60/299,391  
PRIOR FILING DATE: 2001-06-19  
NUMBER OF SEQ ID NOS: 884  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 109  
LENGTH: 13  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURES:  
OTHER INFORMATION: Description of Artificial Sequence; NOTE =  
US-10-481-180-109

Query Match 41.8%; Score 28; DB 4; Length 13;  
Best Local Similarity 100.0%; Pred. No. 4.4e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PECTL 10  
|||||  
DB 5 PECTL 9

RESULT 20  
US-09-774-639-272  
Sequence 272, Application US/09774639  
Publication No. US2003003555A1  
GENERAL INFORMATION:  
APPLICANT: Rosen et al.  
TITLE OF INVENTION: 90 Human Secreted Proteins  
FILE REFERENCE: P2013P1  
CURRENT APPLICATION NUMBER: US/09/774,639  
CURRENT FILING DATE: 2001-07-09  
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/244,112  
PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-04  
NUMBER OF SEQ ID NOS: 371  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 272  
LENGTH: 14  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-774-639-272

Query Match 41.8%; Score 28; DB 3; Length 14;  
Best Local Similarity 55.6%; Pred. No. 4.8e+02;  
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 KNSPECILG 11  
|||||  
DB 3 KGDHCLIG 11

RESULT 21  
US-09-969-730-340  
Sequence 340, Application US/09969730  
Publication No. US2003005443A1  
GENERAL INFORMATION:  
APPLICANT: Ruben et al.  
TITLE OF INVENTION: 90 Human Secreted Proteins  
FILE REFERENCE: P2013P2  
CURRENT APPLICATION NUMBER: US/09/969,730  
CURRENT FILING DATE: 2001-10-04  
PRIOR APPLICATION NUMBER: 09/774,639  
PRIOR FILING DATE: 2001-02-01  
PRIOR APPLICATION NUMBER: 60/238,291  
PRIOR FILING DATE: 2000-10-06  
PRIOR APPLICATION NUMBER: 09/244,112  
PRIOR FILING DATE: 1999-02-04  
PRIOR APPLICATION NUMBER: PCT/US98/16235  
PRIOR FILING DATE: 1998-08-04  
PRIOR APPLICATION NUMBER: 60/056,371  
PRIOR FILING DATE: 1997-08-19  
PRIOR APPLICATION NUMBER: 60/056,732  
PRIOR FILING DATE: 1997-08-19  
PRIOR APPLICATION NUMBER: 60/056,366  
PRIOR FILING DATE: 1997-08-19  
PRIOR APPLICATION NUMBER: 60/056,364  
PRIOR FILING DATE: 1997-08-19  
PRIOR APPLICATION NUMBER: 60/056,370  
PRIOR FILING DATE: 1997-08-19  
PRIOR APPLICATION NUMBER: 60/056,367  
PRIOR FILING DATE: 1997-08-19  
PRIOR APPLICATION NUMBER: 60/056,365  
PRIOR FILING DATE: 1997-08-19  
PRIOR APPLICATION NUMBER: 60/056,731  
PRIOR FILING DATE: 1997-08-19  
PRIOR APPLICATION NUMBER: 60/056,557  
PRIOR FILING DATE: 1997-08-19  
PRIOR APPLICATION NUMBER: 60/056,563  
PRIOR FILING DATE: 1997-08-19  
PRIOR APPLICATION NUMBER: 60/055,970

PRIOR FILING DATE: 1997-08-18  
PRIOR APPLICATION NUMBER: 60/055,986  
PRIOR FILING DATE: 1997-08-18  
PRIOR APPLICATION NUMBER: 60/055,311  
PRIOR FILING DATE: 1997-08-05  
PRIOR APPLICATION NUMBER: 60/054,808  
PRIOR FILING DATE: 1997-08-05  
PRIOR APPLICATION NUMBER: 60/054,803  
PRIOR FILING DATE: 1997-08-05  
PRIOR APPLICATION NUMBER: 60/054,804  
PRIOR FILING DATE: 1997-08-05  
PRIOR APPLICATION NUMBER: 60/054,809  
PRIOR FILING DATE: 1997-08-05  
PRIOR APPLICATION NUMBER: 60/054,806  
PRIOR FILING DATE: 1997-08-05  
PRIOR APPLICATION NUMBER: 60/055,310  
PRIOR FILING DATE: 1997-08-05  
PRIOR APPLICATION NUMBER: 60/054,798  
PRIOR FILING DATE: 1997-08-05  
PRIOR APPLICATION NUMBER: 60/055,309  
PRIOR FILING DATE: 1997-08-05  
PRIOR APPLICATION NUMBER: 60/055,312  
PRIOR FILING DATE: 1997-08-05  
PRIOR APPLICATION NUMBER: 60/054,807  
PRIOR FILING DATE: 1997-08-05  
PRIOR APPLICATION NUMBER: 60/055,386  
PRIOR FILING DATE: 1997-08-05  
NUMBER OF SEQ ID NOS: 373  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 340  
LENGTH: 14  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-969-730-340

Query Match 41.8%; Score 28; DB 3; Length 14;  
Best Local Similarity 55.6%; Pred. No. 4.8e+02;  
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 KNSFCLIG 11  
Db 3 KGDILCIG 11

RESULT 22  
US-09-932-613-59  
Sequence 59, Application US/09932613  
Publication No. US20030091565A1  
GENERAL INFORMATION:  
APPLICANT: Human Genome Sciences, Inc.  
APPLICANT: Belzer, James P.  
APPLICANT: Potter, M. Daniel  
APPLICANT: Fleming, Tony J.  
APPLICANT: Rosen, Craig A.  
TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON  
FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US  
CURRENT APPLICATION NUMBER: US/09/932,613  
CURRENT FILING DATE: 2001-08-17  
NUMBER OF SEQ ID NOS: 458  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 59  
LENGTH: 14  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Blys binding polypeptide  
US-09-932-613-59

Query Match 41.8%; Score 28; DB 3; Length 14;  
Best Local Similarity 57.1%; Pred. No. 4.8e+02;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 6 FDCILGP 12

Db 2 FDCILGP 8

RESULT 23  
US-09-932-322-59  
Sequence 59, Application US/09932322  
Publication No. US20030194743A1  
GENERAL INFORMATION:  
APPLICANT: Dyax Corp.  
APPLICANT: Belzer, James P.  
APPLICANT: Potter, M. Daniel  
APPLICANT: Fleming, Tony J.  
APPLICANT: Ladner, Robert Charles  
TITLE OF INVENTION: BINDING POLYPEPTIDES FOR B LYMPHOCYTE STIMULATOR PROTEIN (BLYS)  
FILE REFERENCE: DYX-018.1 PCT; DYX-018.1 US  
CURRENT APPLICATION NUMBER: US/09/932,322  
CURRENT FILING DATE: 2001-08-17  
NUMBER OF SEQ ID NOS: 458  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 59  
LENGTH: 14  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Blys binding polypeptide  
US-09-932-322-59

Query Match 41.8%; Score 28; DB 3; Length 14;  
Best Local Similarity 57.1%; Pred. No. 4.8e+02;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 6 FDCILGP 12  
Db 2 FDCILGP 8

RESULT 24  
US-10-621-363-340  
Sequence 340, Application US/10621363  
Publication No. US20040023283A1  
GENERAL INFORMATION:  
APPLICANT: Ruben et al.  
TITLE OF INVENTION: 90 Human Secreted Proteins  
FILE REFERENCE: PZ013P2C1  
CURRENT APPLICATION NUMBER: US/10/621,363  
CURRENT FILING DATE: 2003-07-18  
PRIOR APPLICATION NUMBER: 09/969,730  
PRIOR FILING DATE: 2001-10-06  
PRIOR APPLICATION NUMBER: 09/774,639  
PRIOR FILING DATE: 2001-02-01  
PRIOR APPLICATION NUMBER: 60/238,291  
PRIOR FILING DATE: 2000-10-06  
PRIOR APPLICATION NUMBER: 09/244,112  
PRIOR FILING DATE: 1999-02-04  
PRIOR APPLICATION NUMBER: PCT/US98/16235  
PRIOR FILING DATE: 1998-08-04  
PRIOR APPLICATION NUMBER: 60/056,371  
PRIOR FILING DATE: 1997-08-19  
PRIOR APPLICATION NUMBER: 60/056,732  
PRIOR FILING DATE: 1997-08-19  
PRIOR APPLICATION NUMBER: 60/056,366  
PRIOR FILING DATE: 1997-08-19  
PRIOR APPLICATION NUMBER: 60/056,364  
PRIOR FILING DATE: 1997-08-19  
PRIOR APPLICATION NUMBER: 60/056,370  
PRIOR FILING DATE: 1997-08-19  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 373  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 340  
LENGTH: 14  
TYPE: PRT

ORGANISM: Homo sapiens  
US-10-621-363-340

Query Match 41.8%; Score 28; DB 4; Length 14;  
Best Local Similarity 55.6%; Pred. No. 4.8e+02;  
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 KNSPCTIG 11  
| | | | |  
DB 3 KQDLHCLIG 11

RESULT 25  
US-09-738-363-23  
Sequence 23, Application US/09738363  
Patent No. US20010010932A1

GENERAL INFORMATION:

APPLICANT: Schepf, Harry E.

Schwab, George E.

Payne, Jewel M.

Narva, Kenneth E.

Poncetrada, Luis

TITLE OF INVENTION: Nematocidal Proteins

NUMBER OF SEQUENCES: 40

CORRESPONDENCE ADDRESS:

ADDRESSEE: Jay M. Sanders

STREET: 2421 N.W. 41st Street, Suite A-1

CITY: Gainesville

STATE: FL

COUNTRY: USA

ZIP: 32606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/738,363

FILING DATE: 15-Dec-2000

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/076,137

FILING DATE: 12-MAY-1998

ATTORNEY/AGENT INFORMATION:

NAME: Sanders, Jay

REGISTRATION NUMBER: 39,355

REFERENCE/DOCKET NUMBER: MA-20CCCD3

TELECOMMUNICATION INFORMATION:

TELEPHONE: 352-375-8100

TELEFAX: 352-372-5800

INFORMATION FOR SEQ ID NO: 23:

SEQUENCE CHARACTERISTICS:

LENGTH: 15 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 23:

US-09-738-363-23

Query Match 41.8%; Score 28; DB 3; Length 15;

Best Local Similarity 66.7%; Pred. No. 5.1e+02;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DEKNSPCTI 9  
| | | | |  
DB 6 DEKLSFQLI 14

RESULT 26  
US-10-633-023-23  
Sequence 23, Application US/10633023  
Publication No. US20040018982A1

GENERAL INFORMATION:

APPLICANT: Schepf, H. Ernest

Schwab, George

Payne, Jewel

Narva, Kenneth

APPLICANT: Poncetrada, Luis

TITLE OF INVENTION: Nematocidal Proteins

FILE REFERENCE: MA-20CCCD4

CURRENT APPLICATION NUMBER: US/10/633,023

CURRENT FILING DATE: 2003-07-31

PRIOR APPLICATION NUMBER: US 09/738,363

PRIOR FILING DATE: 2000-12-15

PRIOR APPLICATION NUMBER: US 09/076,137

PRIOR FILING DATE: 1998-05-12

PRIOR APPLICATION NUMBER: US 08/316,301

PRIOR FILING DATE: 1994-09-30

PRIOR APPLICATION NUMBER: US 07/871,510

PRIOR FILING DATE: 1992-04-23

PRIOR APPLICATION NUMBER: US 07/830,050

PRIOR FILING DATE: 1992-01-31

PRIOR APPLICATION NUMBER: US 07/693,018

PRIOR FILING DATE: 1991-05-03

PRIOR APPLICATION NUMBER: US 07/675,772

PRIOR FILING DATE: 1991-03-27

PRIOR APPLICATION NUMBER: US 07/565,544

PRIOR FILING DATE: 1990-08-10

PRIOR APPLICATION NUMBER: US 07/557,246

PRIOR FILING DATE: 1990-07-24

PRIOR APPLICATION NUMBER: US 07/535,810

PRIOR FILING DATE: 1990-06-11

Remaining Prior Application data removed - See file wrapper or PALM.

NUMBER OF SEQ ID NOS: 40

SOFTWARE: Patentin version 3.2

SEQ ID NO 23

LENGTH: 15

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURES:

OTHER INFORMATION: Internal amino acid sequence for 63B.

US-10-633-023-23

Query Match 41.8%; Score 28; DB 4; Length 15;

Best Local Similarity 66.7%; Pred. No. 5.1e+02;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DEKNSPCTI 9  
| | | | |  
DB 6 DEKLSFQLI 14

RESULT 27  
US-10-481-180-116

Sequence 116, Application US/10481180

Publication No. US20040171821A1

GENERAL INFORMATION:

APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS

APPLICANT: REPRESENTED BY THE SECRETARY OF THE DEPARTMENT OF HEALTH AND

APPLICANT: HUMAN SERVICES

APPLICANT: Valenzuela, Jesus G.

APPLICANT: Belkaid, Yasmine

APPLICANT: Kanhaw, Shaden

APPLICANT: Sacks, David

APPLICANT: Ribeiro, Jose M. C.

TITLE OF INVENTION: ANTI-ARTHOPOD VECTOR VACCINES, METHODS

OF SELECTING AND USING THEREOF

FILE REFERENCE: 4239-67347

CURRENT APPLICATION NUMBER: US/10/481,180

CURRENT FILING DATE: 2003-12-17

PRIOR APPLICATION NUMBER: PCT/US02/19663

PRIOR FILING DATE: 2002-06-18

PRIOR APPLICATION NUMBER: US 60/299,391

PRIOR FILING DATE: 2001-06-19

NUMBER OF SEQ ID NOS: 884

```
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 116
/ LENGTH: 15
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence; NOTE =
US-10-481-180-116

Query Match      41.8%; Score 28; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      6  FECTIL 10
        |||||
Db      7  FECTIL 11

RESULT 28
US-10-481-180-117
/ Sequence 117, Application US/10481180
/ Publication No. US20040171821A1
/ GENERAL INFORMATION:
/ APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS
/ APPLICANT: REPRESENTED BY THE SECRETARY OF THE DEPARTMENT OF HEALTH AND
/ APPLICANT: HUMAN SERVICES
/ APPLICANT: Valenzuela, Jesus G.
/ APPLICANT: Belkaid, Yasmine
/ APPLICANT: Kamhawi, Shaden
/ APPLICANT: Sacks, David
/ APPLICANT: Ribeiro, Jose M. C.
/ TITLE OF INVENTION: ANTI-ARTHROPOD VECTOR VACCINES, METHODS
/ TITLE OF INVENTION: OF SELECTING AND USES THEREOF
/ FILE REFERENCE: 4239-67347
/ CURRENT APPLICATION NUMBER: US/10/481,180
/ PRIOR FILING DATE: 2003-12-17
/ PRIOR APPLICATION NUMBER: PCT/US02/19663
/ PRIOR FILING DATE: 2002-06-18
/ PRIOR APPLICATION NUMBER: US 60/299,391
/ NUMBER OF SEQ ID NOS: 884
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 117
/ LENGTH: 15
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence; NOTE =
US-10-481-180-117

Query Match      41.8%; Score 28; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      6  FECTIL 10
        |||||
Db      5  FECTIL 9

RESULT 29
US-10-481-180-120
/ Sequence 120, Application US/10481180
/ Publication No. US20040171821A1
/ GENERAL INFORMATION:
/ APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS
/ APPLICANT: REPRESENTED BY THE SECRETARY OF THE DEPARTMENT OF HEALTH AND
/ APPLICANT: HUMAN SERVICES
/ APPLICANT: Valenzuela, Jesus G.
/ APPLICANT: Belkaid, Yasmine
/ APPLICANT: Kamhawi, Shaden
/ APPLICANT: Sacks, David
```

```
/ APPLICANT: Ribeiro, Jose M. C.
/ TITLE OF INVENTION: ANTI-ARTHROPOD VECTOR VACCINES, METHODS
/ TITLE OF INVENTION: OF SELECTING AND USES THEREOF
/ FILE REFERENCE: 4239-67347
/ CURRENT APPLICATION NUMBER: US/10/481,180
/ PRIOR FILING DATE: 2003-12-17
/ PRIOR APPLICATION NUMBER: PCT/US02/19663
/ PRIOR FILING DATE: 2002-06-18
/ PRIOR APPLICATION NUMBER: US 60/299,391
/ NUMBER OF SEQ ID NOS: 884
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 120
/ LENGTH: 16
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence; NOTE =
US-10-481-180-120

Query Match      41.8%; Score 28; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      6  FECTIL 10
        |||||
Db      8  FECTIL 12

RESULT 30
US-10-481-180-122
/ Sequence 122, Application US/10481180
/ Publication No. US20040171821A1
/ GENERAL INFORMATION:
/ APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS
/ APPLICANT: REPRESENTED BY THE SECRETARY OF THE DEPARTMENT OF HEALTH AND
/ APPLICANT: HUMAN SERVICES
/ APPLICANT: Valenzuela, Jesus G.
/ APPLICANT: Belkaid, Yasmine
/ APPLICANT: Kamhawi, Shaden
/ APPLICANT: Sacks, David
/ APPLICANT: Ribeiro, Jose M. C.
/ TITLE OF INVENTION: ANTI-ARTHROPOD VECTOR VACCINES, METHODS
/ TITLE OF INVENTION: OF SELECTING AND USES THEREOF
/ FILE REFERENCE: 4239-67347
/ CURRENT APPLICATION NUMBER: US/10/481,180
/ PRIOR FILING DATE: 2003-12-17
/ PRIOR APPLICATION NUMBER: PCT/US02/19663
/ PRIOR FILING DATE: 2002-06-18
/ PRIOR APPLICATION NUMBER: US 60/299,391
/ NUMBER OF SEQ ID NOS: 884
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 122
/ LENGTH: 17
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence; NOTE =
US-10-481-180-122

Query Match      41.8%; Score 28; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      6  FECTIL 10
        |||||
Db      7  FECTIL 11

RESULT 31
```

```

US-09-864-761-43665
/ Sequence 43665, Application US/09864761
/ Patent No. US20020048763A1
/ GENERAL INFORMATION:
/ APPLICANT: Penn, Sharon G.
/ APPLICANT: Rank, David R.
/ APPLICANT: Hanzel, David K.
/ APPLICANT: Chen, Wensheng
/ TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
/ FILE REFERENCE: Aeomica-X-1
/ CURRENT FILING DATE: US/09/864, 761
/ PRIOR APPLICATION NUMBER: 2001-05-23
/ PRIOR FILING DATE: US 60/180,312
/ PRIOR APPLICATION NUMBER: US 60/207,456
/ PRIOR FILING DATE: 2000-05-26
/ PRIOR APPLICATION NUMBER: US 09/632,366
/ PRIOR FILING DATE: 2000-08-03
/ PRIOR APPLICATION NUMBER: GB 24263.6
/ PRIOR FILING DATE: 2000-10-04
/ PRIOR APPLICATION NUMBER: US 60/236,359
/ PRIOR FILING DATE: 2000-09-27
/ PRIOR APPLICATION NUMBER: PCT/US01/00666
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00667
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00664
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00669
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00665
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00668
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00663
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00662
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00661
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00670
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: US 60/234,687
/ PRIOR FILING DATE: 2000-09-21
/ PRIOR APPLICATION NUMBER: US 09/608,408
/ PRIOR FILING DATE: 2000-06-30
/ PRIOR APPLICATION NUMBER: US 09/774,203
/ PRIOR FILING DATE: 2001-01-29
/ NUMBER OF SEQ ID NOS: 49117
/ SOFTWARE: Annotmax Sequence Listing Engine vers. 1.1
/ SEQ ID NO 43665
/ LENGTH: 18
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ OTHER INFORMATION: MAP TO AC005104.1
/ OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.2
/ OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.88
/ OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.1
/ OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.1
/ OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.1
/ OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.2
/ OTHER INFORMATION: EST_HUMAN HIT: BR901608.1, EVALUATE 1.00e-03
US-09-864-761-43665

Query Match      41.8%; Score 28; DB 3; Length 18;
Best Local Similarity 62.5%; Pred. No. 6.2e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```

```

RESULT 32
US-09-858-935B-107
/ Sequence 107, Application US/09858935B
/ Publication No. US20030069177A1
/ GENERAL INFORMATION:
/ APPLICANT: Dubnagie, Yves
/ APPLICANT: Filvaroff, Ellen
/ APPLICANT: Lowman, Henry B.
/ TITLE OF INVENTION: METHOD FOR TREATING CARTILAGE DISORDERS
/ FILE REFERENCE: P1794R1
/ CURRENT APPLICATION NUMBER: US/09/858, 935B
/ CURRENT FILING DATE: 2002-07-02
/ PRIOR APPLICATION NUMBER: US 60/248,985
/ PRIOR FILING DATE: 2000-11-15
/ PRIOR APPLICATION NUMBER: US 60/204,490
/ PRIOR FILING DATE: 2000-05-16
/ NUMBER OF SEQ ID NOS: 153
/ SEQ ID NO 107
/ LENGTH: 18
/ TYPE: PRT
/ ORGANISM: Artificial sequence
/ FEATURE:
/ OTHER INFORMATION: Sequence is synthesized
US-09-858-935B-107

Query Match      41.8%; Score 28; DB 3; Length 18;
Best Local Similarity 66.7%; Pred. No. 6.2e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

```

RESULT 33
US-09-858-935B-110
/ Sequence 110, Application US/09858935B
/ Publication No. US20030069177A1
/ GENERAL INFORMATION:
/ APPLICANT: Dubnagie, Yves
/ APPLICANT: Filvaroff, Ellen
/ APPLICANT: Lowman, Henry B.
/ TITLE OF INVENTION: METHOD FOR TREATING CARTILAGE DISORDERS
/ FILE REFERENCE: P1794R1
/ CURRENT APPLICATION NUMBER: US/09/858, 935B
/ CURRENT FILING DATE: 2002-07-02
/ PRIOR APPLICATION NUMBER: US 60/248,985
/ PRIOR FILING DATE: 2000-11-15
/ PRIOR APPLICATION NUMBER: US 60/204,490
/ PRIOR FILING DATE: 2000-05-16
/ NUMBER OF SEQ ID NOS: 153
/ SEQ ID NO 110
/ LENGTH: 18
/ TYPE: PRT
/ ORGANISM: Artificial sequence
/ FEATURE:
/ OTHER INFORMATION: Sequence is synthesized
US-09-858-935B-110

Query Match      41.8%; Score 28; DB 3; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.2e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Query Match      41.8%; Score 28; DB 3; Length 18;
Best Local Similarity 62.5%; Pred. No. 6.2e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```

```

RESULT 34
US-10-158-847-88
/ Sequence 88, Application US/10158847

```

```
/ Publication No. US20030091557A1
/ GENERAL INFORMATION:
/ APPLICANT: Tom Parry et al.
/ TITLE OF INVENTION: Method and Compositions for Modulating ACE-2 Activity
/ FILE REFERENCE: PF557
/ CURRENT APPLICATION NUMBER: US/10/158,847
/ PRIOR FILING DATE: 2002-06-03
/ PRIOR APPLICATION NUMBER: 60/295,004
/ PRIOR FILING DATE: 2001-06-04
/ NUMBER OF SEQ ID NOS: 158
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 88
/ TYPE: PRT
/ ORGANISM: homo sapiens
US-10-158-847-88

Query Match          41.8%; Score 28; DB 4; Length 18;
Best Local Similarity 71.4%; Pred. No. 6.2e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      6 ECICGP 12
      ||| |||
Db      2 ECDCWGP 8

RESULT 35
US-10-158-825-88
/ Sequence 88, Application US/10158825
/ Publication No. US20030138894A1
/ GENERAL INFORMATION:
/ APPLICANT: Tom Parry et al.
/ TITLE OF INVENTION: Method and Compositions for Modulating ACE-2 Activity
/ FILE REFERENCE: PF555
/ CURRENT APPLICATION NUMBER: US/10/158,825
/ PRIOR FILING DATE: 2002-06-03
/ PRIOR APPLICATION NUMBER: 60/294,976
/ PRIOR FILING DATE: 2001-06-04
/ NUMBER OF SEQ ID NOS: 158
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 88
/ LENGTH: 18
/ TYPE: PRT
/ ORGANISM: homo sapiens
US-10-158-825-88

Query Match          41.8%; Score 28; DB 4; Length 18;
Best Local Similarity 71.4%; Pred. No. 6.2e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      6 ECICGP 12
      ||| |||
Db      2 ECDCWGP 8

RESULT 36
US-10-271-869-107
/ Sequence 107, Application US/10271869
/ Publication No. US20030211992A1
/ GENERAL INFORMATION:
/ APPLICANT: Dubaigle, Yves
/ APPLICANT: Filvaroff, Ellen
/ APPLICANT: Lowman, Henry B.
/ TITLE OF INVENTION: METHOD FOR TREATING CARTILAGE DISORDERS
/ FILE REFERENCE: P1794R1
/ CURRENT APPLICATION NUMBER: US/10/271,869
/ PRIOR FILING DATE: 2002-10-16
/ PRIOR APPLICATION NUMBER: US/09/858,935
/ PRIOR FILING DATE: 2002-07-02
/ PRIOR APPLICATION NUMBER: US 60/248,985
/ PRIOR FILING DATE: 2000-11-15
/ PRIOR APPLICATION NUMBER: US 60/204,490
/ PRIOR FILING DATE: 2000-05-16
```

```
/ NUMBER OF SEQ ID NOS: 153
/ SEQ ID NO 107
/ LENGTH: 18
/ TYPE: PRT
/ ORGANISM: Artificial sequence
/ FEATURE:
/ OTHER INFORMATION: Sequence is synthesized
US-10-271-869-107

Query Match          41.8%; Score 28; DB 4; Length 18;
Best Local Similarity 66.7%; Pred. No. 6.2e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      7 ECICGP 12
      ||| |||
Db      4 ECWGP 9

RESULT 37
US-10-271-869-110
/ Sequence 110, Application US/10271869
/ Publication No. US20030211992A1
/ GENERAL INFORMATION:
/ APPLICANT: Dubaigle, Yves
/ APPLICANT: Filvaroff, Ellen
/ APPLICANT: Lowman, Henry B.
/ TITLE OF INVENTION: METHOD FOR TREATING CARTILAGE DISORDERS
/ FILE REFERENCE: P1794R1
/ CURRENT APPLICATION NUMBER: US/10/271,869
/ PRIOR FILING DATE: 2002-10-16
/ PRIOR APPLICATION NUMBER: US/09/858,935
/ PRIOR FILING DATE: 2002-07-02
/ PRIOR APPLICATION NUMBER: US 60/248,985
/ PRIOR FILING DATE: 2000-11-15
/ PRIOR APPLICATION NUMBER: US 60/204,490
/ PRIOR FILING DATE: 2000-05-16
/ NUMBER OF SEQ ID NOS: 153
/ SEQ ID NO 110
/ LENGTH: 18
/ TYPE: PRT
/ ORGANISM: Artificial sequence
/ FEATURE:
/ OTHER INFORMATION: Sequence is synthesized
US-10-271-869-110

Query Match          41.8%; Score 28; DB 4; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.2e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      7 ECICGP 12
      ||| |||
Db      4 ECICGP 9

RESULT 38
US-10-158-825-88
/ Sequence 88, Application US/10158825
/ Publication No. US20040121429A9
/ GENERAL INFORMATION:
/ APPLICANT: Tom Parry et al.
/ TITLE OF INVENTION: Method and Compositions for Modulating ACE-2 Activity
/ FILE REFERENCE: PF555
/ CURRENT APPLICATION NUMBER: US/10/158,825
/ PRIOR FILING DATE: 2002-06-03
/ PRIOR APPLICATION NUMBER: 60/294,976
/ PRIOR FILING DATE: 2001-06-04
/ NUMBER OF SEQ ID NOS: 158
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 88
/ LENGTH: 18
/ TYPE: PRT
/ ORGANISM: homo sapiens
US-10-158-825-88
```

Query Match 41.8%; Score 28; DB 4; Length 18;  
Best Local Similarity 71.4%; Pred. No. 6.2e+02;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 PECILGP 12  
DB 2 FECDWGP 8

RESULT 39  
US-09-044-604-3

/ Sequence 3, Application US/09044604  
/ Patent No. US20020009718A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Tims, Kathy L.  
/ TITLE OF INVENTION: ENDOMETRIOSIS-SPECIFIC SECRETORY  
/ NUMBER OF SEQUENCES: 11  
/ CORRESPONDENCE ADDRESS:  
/ ADDRESSES: KOHN & ASSOCIATES  
/ STREET: 30500 NO. US20020009718A1Western Hwy. Suite 410  
/ CITY: Farmington Hills  
/ STATE: Michigan  
/ COUNTRY: US  
/ ZIP: 48334  
/ COMPUTER READABLE FORM:  
/ MEDIUM TYPE: Floppy disk  
/ COMPUTER: IBM PC compatible  
/ OPERATING SYSTEM: PC-DOS/MS-DOS  
/ SOFTWARE: Patent Release #1.0, Version #1.30  
/ CURRENT APPLICATION DATA:  
/ APPLICATION NUMBER: US/09/044,604  
/ FILING DATE:  
/ CLASSIFICATION:  
/ ATTORNEY/AGENT INFORMATION:  
/ NAME: Montgomery, Ilene N.  
/ REGISTRATION NUMBER: 38,972  
/ REFERENCE/DOCKET NUMBER: 0994.00084  
/ TELECOMMUNICATION INFORMATION:  
/ TELEPHONE: (248) 539-5050  
/ TELEFAX: (248) 539-5055  
/ INFORMATION FOR SEQ ID NO: 3:  
/ SEQUENCE CHARACTERISTICS:  
/ LENGTH: 19 amino acids  
/ TYPE: amino acid  
/ STRANDEDNESS: single  
/ TOPOLOGY: linear  
/ MOLECULE TYPE: peptide  
/ HYPOTHETICAL: NO  
/ ANTI-SENSE: NO  
/ FRAGMENT TYPE: N-terminal  
/ US-09-044-604-3

Query Match 41.8%; Score 28; DB 3; Length 19;  
Best Local Similarity 62.5%; Pred. No. 6.6e+02;  
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 DEKNSPEC 8  
DB 7 DAKGSFPC 14

RESULT 40  
US-10-306-903-3

/ Sequence 3, Application US/10306903  
/ Publication No. US20030166014A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Tims, Kathy  
/ TITLE OF INVENTION: ENDOMETRIOSIS-SPECIFIC SECRETORY PROTEIN  
/ FILE REFERENCE: 0994.00137  
/ CURRENT APPLICATION NUMBER: US/10/306,903  
/ CURRENT FILING DATE: 2002-11-27

/ PRIOR APPLICATION NUMBER: 09/044,604  
/ PRIOR FILING DATE: 1998-03-19  
/ PRIOR APPLICATION NUMBER: 08/328,451  
/ PRIOR FILING DATE: 1994-10-25  
/ NUMBER OF SEQ ID NOS: 16  
/ SOFTWARE: Patent version 3.2  
/ SEQ ID NO 3  
/ LENGTH: 19  
/ TYPE: PRT  
/ ORGANISM: Homo sapien  
/ US-10-306-903-3

Query Match 41.8%; Score 28; DB 4; Length 19;  
Best Local Similarity 62.5%; Pred. No. 6.6e+02;  
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 DEKNSPEC 8  
DB 7 DAKGSFPC 14

RESULT 41

US-10-690-276-662  
/ Sequence 662, Application US/10690276  
/ Publication No. US20050112118A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Myriad Genetics, Incorporated  
/ APPLICANT: Climbora, Daniel  
/ APPLICANT: Heichman, Karen  
/ APPLICANT: Bartel, Paul  
/ APPLICANT: Mauck, Kimberly  
/ APPLICANT: Bush, Angie  
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING INFLAMMATORY DISORDERS  
/ FILE REFERENCE: 1834.01  
/ CURRENT APPLICATION NUMBER: US/10/690,276  
/ CURRENT FILING DATE: 2003-10-20  
/ PRIOR APPLICATION NUMBER: 09/727,384  
/ PRIOR FILING DATE: 2000-12-01  
/ PRIOR APPLICATION NUMBER: 60/168,377  
/ PRIOR FILING DATE: 1999-12-02  
/ PRIOR APPLICATION NUMBER: 60/168,379  
/ PRIOR FILING DATE: 1999-12-02  
/ PRIOR APPLICATION NUMBER: 60/185,056  
/ PRIOR FILING DATE: 2000-02-25  
/ PRIOR APPLICATION NUMBER: 10/035,344  
/ PRIOR FILING DATE: 2002-01-04  
/ PRIOR APPLICATION NUMBER: 60/259,571  
/ PRIOR FILING DATE: 2001-01-04  
/ PRIOR APPLICATION NUMBER: 10/035,343  
/ PRIOR FILING DATE: 2002-01-04  
/ PRIOR APPLICATION NUMBER: 60/259,572  
/ PRIOR FILING DATE: 2001-01-04  
/ PRIOR APPLICATION NUMBER: 10/099,924  
/ PRIOR FILING DATE: 2002-03-14  
/ PRIOR APPLICATION NUMBER: 60/276,179  
/ PRIOR FILING DATE: 2001-03-15  
/ Remaining Prior Application data removed - See File Wrapper or PAM.  
/ NUMBER OF SEQ ID NOS: 728  
/ SOFTWARE: Patent version 3.2  
/ SEQ ID NO 662  
/ LENGTH: 20  
/ TYPE: PRT  
/ ORGANISM: Homo sapiens  
/ US-10-690-276-662

Query Match 41.8%; Score 28; DB 5; Length 20;  
Best Local Similarity 80.0%; Pred. No. 6.9e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 CILGP 12  
DB 6 CILGP 10

```
RESULT 42
US-10-196-394-65
; Sequence 65, Application US/10196394
; Publication No. US20030171278A1
; GENERAL INFORMATION:
; APPLICANT: Mark S. Dennis
; TITLE OF INVENTION: Compounds that Bind HER2
; FILE REFERENCE: P1713R1
; CURRENT APPLICATION NUMBER: US/10/196,394
; PRIOR FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: US/09/609,721
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/142,232
; PRIOR FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 162
; SEQ ID NO 65
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide sequence
US-10-196-394-65

Query Match          41.0%; Score 27.5; DB 4; Length 20;
Best Local Similarity 58.3%; Pred. No. 8.6e+02;
Matches 7; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

QY      1 DKNRSPECTLGP 12
        |||:|:|
Db       1 DEVESWGCIGP 11

RESULT 43
US-10-357-175-89
; Sequence 89, Application US/10357175
; Publication No. US20030170707A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; TITLE OF INVENTION: Transmembrane Serine Protease Overexpressed
; FILE REFERENCE: D6192CIP/D/CIP
; CURRENT APPLICATION NUMBER: US/10/357,175
; PRIOR FILING DATE: 2003-02-03
; PRIOR APPLICATION NUMBER: 09/650,371
; PRIOR FILING DATE: 2000-08-28
; NUMBER OF SEQ ID NOS: 158
; SEQ ID NO 89
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; LOCATION: 81..89
; OTHER INFORMATION: TADG-12 peptide
US-10-357-175-89

Query Match          40.3%; Score 27; DB 4; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      3 KNSPECTI 9
        ::||:|
Db       1 RSSFKCI 7

RESULT 44
US-10-357-175-115
; Sequence 115, Application US/10357175
; Publication No. US20030170707A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; TITLE OF INVENTION: Transmembrane Serine Protease Overexpressed
; FILE REFERENCE: D6192CIP/D/CIP
; CURRENT APPLICATION NUMBER: US/10/357,175
; PRIOR FILING DATE: 2003-02-03
; PRIOR APPLICATION NUMBER: 09/650,371
; PRIOR FILING DATE: 2000-08-28
; NUMBER OF SEQ ID NOS: 153
; SEQ ID NO 89
```

```
FILE REFERENCE: D6192CIP/D/CIP
; CURRENT APPLICATION NUMBER: US/10/357,175
; CURRENT FILING DATE: 2003-02-03
; PRIOR APPLICATION NUMBER: 09/650,371
; PRIOR FILING DATE: 2000-08-28
; NUMBER OF SEQ ID NOS: 158
; SEQ ID NO 115
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; LOCATION: 79...87
; OTHER INFORMATION: TADG-12 peptide
US-10-357-175-115

Query Match          40.3%; Score 27; DB 4; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      3 KNSPECTI 9
        ::||:|
Db       3 RSSFKCI 9

RESULT 45
US-10-455-720-89
; Sequence 89, Application US/10455720
; Publication No. US20030207316A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; TITLE OF INVENTION: Transmembrane Serine Protease Overexpressed
; FILE REFERENCE: D6192CIP/D/2
; CURRENT APPLICATION NUMBER: US/10/455,720
; PRIOR FILING DATE: 2003-06-05
; PRIOR APPLICATION NUMBER: 09/650,371
; PRIOR FILING DATE: 2000-08-28
; NUMBER OF SEQ ID NOS: 153
; SEQ ID NO 89
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; LOCATION: 81..89
; OTHER INFORMATION: TADG-12 peptide
US-10-455-720-89

Query Match          40.3%; Score 27; DB 4; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      3 KNSPECTI 9
        ::||:|
Db       1 RSSFKCI 7

RESULT 46
US-10-455-720-115
; Sequence 115, Application US/10455720
; Publication No. US20030207316A1
; GENERAL INFORMATION:
; APPLICANT: Underwood, Lowell J.
; TITLE OF INVENTION: Transmembrane Serine Protease Overexpressed
; FILE REFERENCE: D6192CIP/D/2
; CURRENT APPLICATION NUMBER: US/10/455,720
; PRIOR FILING DATE: 2003-06-05
; PRIOR APPLICATION NUMBER: 09/650,371
; PRIOR FILING DATE: 2000-08-28
; NUMBER OF SEQ ID NOS: 153
; SEQ ID NO 115
```



```
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ LOCATION: 79...87
/ OTHER INFORMATION: TADG-12 peptide
US-10-455-720-115
```

```
Query Match          40.3%; Score 27; DB 4; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 3 KNSPECI 9
Db 3 RSSFKCI 9
```

```
RESULT 47
US-10-250-508-55
/ Sequence 55, Application US/10250508
/ Publication No. US20040121327A1
/ GENERAL INFORMATION:
/ APPLICANT: Manns, Michael
/ APPLICANT: Strauszburg, Christian
/ TITLE OF INVENTION: Method for Predicting the Potential Risk of Carcinomas and
/ TITLE OF INVENTION: Inflammatory Bowel Diseases and Relevant Tests
/ FILE REFERENCE: 0310017848
/ CURRENT APPLICATION NUMBER: US/10/250,508
/ CURRENT FILING DATE: 2003-12-08
/ PRIOR APPLICATION NUMBER: PCT/DE02/00003
/ PRIOR FILING DATE: 2002-01-03
/ PRIOR APPLICATION NUMBER: DE 101 00 238.6
/ PRIOR FILING DATE: 2001-01-05
/ NUMBER OF SEQ ID NOS: 57
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 55
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: MISC_FEATURE
/ LOCATION: (1)..(9)
/ OTHER INFORMATION: amino acid residues 7-15 of UGT1A10 as shown in Figure 4
US-10-250-508-55
```

```
Query Match          40.3%; Score 27; DB 4; Length 9;
Best Local Similarity 44.4%; Pred. No. 1.7e+06;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 1 DEKNSPECI 9
Db 1 DQPRSFMCV 9
```

```
RESULT 48
US-10-838-289-227
/ Sequence 227, Application US/10838289
/ Publication No. US20050058603A1
/ GENERAL INFORMATION:
/ APPLICANT: Gao, Jinning
/ APPLICANT: Ai, Hua
/ TITLE OF INVENTION: DRUG DELIVERY SYSTEM BASED ON POLYMER
/ TITLE OF INVENTION: NANOSHIELDS
/ FILE REFERENCE: CMRU-P01-040
/ CURRENT APPLICATION NUMBER: US/10/838,289
/ PRIOR FILING DATE: 2004-05-03
/ PRIOR APPLICATION NUMBER: US 60/502,429
/ PRIOR FILING DATE: 2003-09-12
/ PRIOR APPLICATION NUMBER: US 60/467,389
/ PRIOR FILING DATE: 2003-05-02
/ NUMBER OF SEQ ID NOS: 756
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 227
```

```
/ LENGTH: 12
/ TYPE: PRT
/ ORGANISM: Unknown
/ FEATURE:
/ OTHER INFORMATION: Lung homing peptide
US-10-838-289-227
```

```
Query Match          40.3%; Score 27; DB 5; Length 12;
Best Local Similarity 57.1%; Pred. No. 6.2e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 5 SPECIIG 11
Db 5 NPDCTIG 11
```

```
RESULT 49
US-10-607-595-435
/ Sequence 435, Application US/10607595
/ Publication No. US20050074812A1
/ GENERAL INFORMATION:
/ APPLICANT: Ruoslahti, Erkki
/ APPLICANT: Pasqualini, Renata
/ TITLE OF INVENTION: Molecules that Home to Various Selected Organs or
/ TITLE OF INVENTION: Tissues
/ FILE REFERENCE: P-LJ 4514
/ CURRENT APPLICATION NUMBER: US/10/607,595
/ CURRENT FILING DATE: 2003-06-27
/ PRIOR APPLICATION NUMBER: US/09/722,250
/ PRIOR FILING DATE: 2000-11-22
/ PRIOR APPLICATION NUMBER: US 09/042,107
/ PRIOR FILING DATE: 1998-03-13
/ NUMBER OF SEQ ID NOS: 437
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 435
/ LENGTH: 12
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-607-595-435
```

```
Query Match          40.3%; Score 27; DB 5; Length 12;
Best Local Similarity 57.1%; Pred. No. 6.2e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 5 SPECIIG 11
Db 5 NPDCTIG 11
```

```
RESULT 50
US-10-488-671-21
/ Sequence 21, Application US/10488671
/ Publication No. US20040254106A1
/ GENERAL INFORMATION:
/ APPLICANT: Carr, Francis J.
/ APPLICANT: Carter, Graham
/ TITLE OF INVENTION: Modified Factor IX
/ FILE REFERENCE: MER-128
/ CURRENT APPLICATION NUMBER: US/10/488,671
/ CURRENT FILING DATE: 2004-03-04
/ PRIOR APPLICATION NUMBER: PCT/EP02/09717
/ PRIOR FILING DATE: 2002-08-30
/ PRIOR APPLICATION NUMBER: EP 01121154.7
/ PRIOR FILING DATE: 2001-09-04
/ NUMBER OF SEQ ID NOS: 126
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 21
/ LENGTH: 13
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-488-671-21
```

Query Match 40.3%; Score 27; DB 5; Length 13;  
Best Local Similarity 80.0%; Pred. No. 6.7e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 NSPEC 8  
DB 1 NSPEC 5

RESULT 51  
US-10-269-695-147  
Sequence 147, Application US/10269695  
Publication No. US20030229023A1  
GENERAL INFORMATION:  
APPLICANT: OLINER, JONATHAN DANIEL  
APPLICANT: MIN, HOSUNG  
TITLE OF INVENTION: SPECIFIC BINDING AGENTS OF HUMAN ANGIOPOIETIN-2  
FILE REFERENCE: A-801A  
CURRENT APPLICATION NUMBER: US/10/269,695  
CURRENT FILING DATE: 2002-10-10  
PRIOR APPLICATION NUMBER: US 60/414,155  
PRIOR FILING DATE: 2002-09-27  
PRIOR APPLICATION NUMBER: US 60/328,624  
PRIOR FILING DATE: 2001-10-11  
NUMBER OF SEQ ID NOS: 359  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 147  
LENGTH: 20  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Polypeptide capable of binding to Ang-2  
US-10-269-695-147

Query Match 40.3%; Score 27; DB 4; Length 20;  
Best Local Similarity 40.0%; Pred. No. 1.1e+03;  
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 EKNSPECITG 11  
DB 3 DKRPLECMFG 12

RESULT 52  
US-10-410-998-147  
Sequence 147, Application US/10410998  
Publication No. US20030236193A1  
GENERAL INFORMATION:  
APPLICANT: OLINER, JONATHAN DANIEL  
APPLICANT: MIN, HOSUNG  
TITLE OF INVENTION: SPECIFIC BINDING AGENTS OF HUMAN ANGIOPOIETIN-2  
FILE REFERENCE: A-801A  
CURRENT APPLICATION NUMBER: US/10/410,998  
CURRENT FILING DATE: 2003-04-09  
PRIOR APPLICATION NUMBER: US/10/269,695  
PRIOR FILING DATE: 2002-10-10  
PRIOR APPLICATION NUMBER: US 60/414,155  
PRIOR FILING DATE: 2002-09-27  
PRIOR APPLICATION NUMBER: US 60/328,624  
PRIOR FILING DATE: 2001-10-11  
NUMBER OF SEQ ID NOS: 359  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 147  
LENGTH: 20  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Polypeptide capable of binding to Ang-2  
US-10-410-998-147

Query Match 40.3%; Score 27; DB 4; Length 20;  
Best Local Similarity 40.0%; Pred. No. 1.1e+03;

Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 EKNSPECITG 11  
DB 3 DKRPLECMFG 12

RESULT 53  
US-10-432-465-65  
Sequence 65, Application US/10432465  
Publication No. US20040091479A1  
GENERAL INFORMATION:  
APPLICANT: Nieland, John  
APPLICANT: Kaufmann, Andreas  
APPLICANT: Kather, Angela  
APPLICANT: Schinz, Manuela  
TITLE OF INVENTION: T-Cell Epitopes of the Papillomavirus L1  
TITLE OF INVENTION: Protein and E7 Protein and Their Use in Diagnosis and  
FILE REFERENCE: 50125/077001  
CURRENT APPLICATION NUMBER: US/10/432,465  
CURRENT FILING DATE: 2003-12-10  
PRIOR APPLICATION NUMBER: PCT/EP01/14037  
PRIOR FILING DATE: 2001-11-30  
PRIOR APPLICATION NUMBER: DE 10059631.2  
PRIOR FILING DATE: 2000-12-01  
NUMBER OF SEQ ID NOS: 116  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 65  
LENGTH: 20  
TYPE: PRT  
ORGANISM: Human papillomavirus  
US-10-432-465-65

Query Match 40.3%; Score 27; DB 4; Length 20;  
Best Local Similarity 54.5%; Pred. No. 1.1e+03;  
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 DEKNSPECITG 11  
DB 7 DYKOTOLCITG 17

RESULT 54  
US-10-433-091-34  
Sequence 34, Application US/10433091  
Publication No. US20040101533A1  
GENERAL INFORMATION:  
APPLICANT: MÜLLER, RAINER  
APPLICANT: NIELAND, JOHN  
APPLICANT: GABELSBERGER, JOSEF  
APPLICANT: HERBST, RUTH  
TITLE OF INVENTION: MEDICAMENT FOR PREVENTING OR TREATING TUMORS CAUSED BY  
FILE REFERENCE: 037067/0115  
CURRENT APPLICATION NUMBER: US/10/433,091  
CURRENT FILING DATE: 2003-11-25  
PRIOR APPLICATION NUMBER: PCT/EP01/14038  
PRIOR FILING DATE: 2001-11-30  
PRIOR APPLICATION NUMBER: DE 100 59 630.4  
PRIOR FILING DATE: 2000-12-01  
NUMBER OF SEQ ID NOS: 72  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 34  
LENGTH: 20  
TYPE: PRT  
ORGANISM: Human papillomavirus type 18  
US-10-433-091-34

Query Match 40.3%; Score 27; DB 4; Length 20;  
Best Local Similarity 54.5%; Pred. No. 1.1e+03;  
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 DEKNSPECTIG 11  
| | | | |  
DB 7 DYKOTOLCTIG 17

RESULT 55  
US-10-286-457-230  
; Sequence 230, Application US/10286457  
; Publication No. US20030166004A1  
; GENERAL INFORMATION:  
; APPLICANT: JENO GYURIS et al.  
; TITLE OF INVENTION: ENDOTHELIAL-CELL BINDING PEPTIDES FOR DIAGNOSIS AND THERAPY  
; FILE REFERENCE: GPCI-PO1-178  
; CURRENT APPLICATION NUMBER: US/10/286,457  
; PRIOR FILING DATE: 2002-11-01  
; PRIOR APPLICATION NUMBER: 60/334822  
; NUMBER OF SEQ ID NOS: 684  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 230  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: artificial sequence isolated from random peptide libraries, based  
US-10-286-457-230

Query Match 38.8%; Score 26; DB 4; Length 9;  
Best Local Similarity 66.7%; Pred. No. 1.7e+06;  
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 KNSPEC 8  
| | | | |  
DB 4 KNOFHC 9

RESULT 56  
US-10-352-786-454  
; Sequence 454, Application US/10352786  
; Publication No. US20030228353A1  
; GENERAL INFORMATION:  
; APPLICANT: Cowart, Donald R.  
; TITLE OF INVENTION: Bioactive Keratin Peptides  
; FILE REFERENCE: KER020/4-024US  
; CURRENT APPLICATION NUMBER: US/10/352,786  
; PRIOR FILING DATE: 2003-06-06  
; PRIOR APPLICATION NUMBER: 60/352,396  
; PRIOR FILING DATE: 2002-01-28  
; NUMBER OF SEQ ID NOS: 468  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 454  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Consensus Peptide  
US-10-352-786-454

Query Match 38.8%; Score 26; DB 4; Length 10;  
Best Local Similarity 50.0%; Pred. No. 7.8e+02;  
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 EKNSPECTIG 11  
| | | | |  
DB 1 EVNTLRCLG 10

RESULT 57  
US-10-352-786-455  
; Sequence 455, Application US/10352786  
; Publication No. US20030228353A1  
; GENERAL INFORMATION:

; APPLICANT: Cowart, Donald R.  
; TITLE OF INVENTION: Bioactive Keratin Peptides  
; FILE REFERENCE: KER020/4-024US  
; CURRENT APPLICATION NUMBER: US/10/352,786  
; PRIOR FILING DATE: 2003-06-06  
; PRIOR APPLICATION NUMBER: 60/352,396  
; PRIOR FILING DATE: 2002-01-28  
; NUMBER OF SEQ ID NOS: 468  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 455  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Consensus Peptide  
US-10-352-786-455

Query Match 38.8%; Score 26; DB 4; Length 10;  
Best Local Similarity 50.0%; Pred. No. 7.8e+02;  
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 EKNSPECTIG 11  
| | | | |  
DB 1 EVNTLRCLG 10

RESULT 58  
US-10-114-500-19  
; Sequence 19, Application US/10114500  
; Publication No. US20030100746A1  
; GENERAL INFORMATION:  
; APPLICANT: Godbole, Shubhada  
; APPLICANT: Boyle, Bryan J  
; APPLICANT: Arterburn, Matthew C  
; APPLICANT: Liu, Chenghua  
; APPLICANT: Tang, Y Tom  
; APPLICANT: Dmanac, Radoje T  
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO FIBULIN-LIKE POLYPEPTIDES AND  
; FILE REFERENCE: HYS-40CON  
; CURRENT APPLICATION NUMBER: US/10/114,500  
; PRIOR FILING DATE: 2002-04-01  
; PRIOR APPLICATION NUMBER: US 09/802,704  
; PRIOR FILING DATE: 2001-03-08  
; PRIOR APPLICATION NUMBER: US 09/560,875  
; PRIOR FILING DATE: 2000-04-27  
; PRIOR APPLICATION NUMBER: US 09/496,914  
; PRIOR FILING DATE: 2000-02-03  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 19  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-114-500-19

Query Match 38.8%; Score 26; DB 4; Length 11;  
Best Local Similarity 44.4%; Pred. No. 8.6e+02;  
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 4 NSPECTIG 12  
| | | | |  
DB 1 NOYRCICPP 9

RESULT 59  
US-10-352-786-541  
; Sequence 541, Application US/10352786  
; Publication No. US20030228353A1  
; GENERAL INFORMATION:  
; APPLICANT: Cowart, Donald R.  
; TITLE OF INVENTION: Bioactive Keratin Peptides  
; FILE REFERENCE: KER020/4-024US

```
/ CURRENT APPLICATION NUMBER: US/10/352,786
/ CURRENT FILING DATE: 2003-06-06
/ PRIOR APPLICATION NUMBER: 630/352,396
/ PRIOR FILING DATE: 2002-01-28
/ NUMBER OF SEQ ID NOS: 4468
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 541
/ LENGTH: 11
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: Consensus Peptide
US-10-352-786-541
```

```
Query Match          38.8%; Score 26; DB 4; Length 11;
Best Local Similarity 50.0%; Pred. No. 8.6e+02;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
```

```
Qy      2 EKNSPECILG 11
      ||: |||
Db      1 EVNTRLRCQLG 10
```

```
RESULT 60
US-10-352-786-542
/ Sequence 542, Application US/10352786
/ Publication No. US20030228353A1
/ GENERAL INFORMATION:
/ APPLICANT: Cowser, Donald R.
/ TITLE OF INVENTION: Bioactive Keratin Peptides
/ FILE REFERENCE: KER020/4-024US
/ CURRENT APPLICATION NUMBER: US/10/352,786
/ CURRENT FILING DATE: 2003-06-06
/ PRIOR APPLICATION NUMBER: 630/352,396
/ PRIOR FILING DATE: 2002-01-28
/ NUMBER OF SEQ ID NOS: 4468
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 542
/ LENGTH: 11
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: Consensus Peptide
US-10-352-786-542
```

```
Query Match          38.8%; Score 26; DB 4; Length 11;
Best Local Similarity 50.0%; Pred. No. 8.6e+02;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
```

```
Qy      2 EKNSPECILG 11
      ||: |||
Db      1 EVNTRLRCPLG 10
```

```
RESULT 61
US-10-471-346-19
/ Sequence 19, Application US/10471346
/ Publication No. US20040236050A1
/ GENERAL INFORMATION:
/ APPLICANT: Hyseq, Inc
/ APPLICANT: Godbole, Shubhada D
/ APPLICANT: Boyle, Bryan J
/ APPLICANT: Arterburn, Matthew C
/ APPLICANT: Liu, Chenghua
/ APPLICANT: Tang, Y Tom
/ APPLICANT: Dimaqac, Radoje T
/ TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO FIBULIN-LIKE POLYPEPTIDES AND
/ FILE REFERENCE: POLYNCLB0TIDES
/ FILE REFERENCE: 24059-040-061
/ CURRENT APPLICATION NUMBER: US/10/471,346
/ CURRENT FILING DATE: 2003-09-08
/ PRIOR APPLICATION NUMBER: US 09/802,704
/ PRIOR FILING DATE: 2001-03-08
```

```
/ PRIOR APPLICATION NUMBER: US 09/560,875
/ PRIOR FILING DATE: 2000-04-27
/ PRIOR APPLICATION NUMBER: US 09/496,914
/ PRIOR FILING DATE: 2000-02-03
/ NUMBER OF SEQ ID NOS: 22
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 19
/ LENGTH: 11
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-471-346-19
```

```
Query Match          38.8%; Score 26; DB 5; Length 11;
Best Local Similarity 44.4%; Pred. No. 8.6e+02;
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
```

```
Qy      4 NSFECILGP 12
      ||: |||
Db      1 NQYRCICPP 9
```

```
RESULT 62
US-10-352-786-627
/ Sequence 627, Application US/10352786
/ Publication No. US20030228353A1
/ GENERAL INFORMATION:
/ APPLICANT: Cowser, Donald R.
/ TITLE OF INVENTION: Bioactive Keratin Peptides
/ FILE REFERENCE: KER020/4-024US
/ CURRENT APPLICATION NUMBER: US/10/352,786
/ CURRENT FILING DATE: 2003-06-06
/ PRIOR APPLICATION NUMBER: 630/352,396
/ PRIOR FILING DATE: 2002-01-28
/ NUMBER OF SEQ ID NOS: 4468
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 627
/ LENGTH: 12
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: Consensus Peptide
US-10-352-786-627
```

```
Query Match          38.8%; Score 26; DB 4; Length 12;
Best Local Similarity 50.0%; Pred. No. 9.4e+02;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
```

```
Qy      2 EKNSPECILG 11
      ||: |||
Db      1 EVNTRLRCQLG 10
```

```
RESULT 63
US-10-352-786-628
/ Sequence 628, Application US/10352786
/ Publication No. US20030228353A1
/ GENERAL INFORMATION:
/ APPLICANT: Cowser, Donald R.
/ TITLE OF INVENTION: Bioactive Keratin Peptides
/ FILE REFERENCE: KER020/4-024US
/ CURRENT APPLICATION NUMBER: US/10/352,786
/ CURRENT FILING DATE: 2003-06-06
/ PRIOR APPLICATION NUMBER: 630/352,396
/ PRIOR FILING DATE: 2002-01-28
/ NUMBER OF SEQ ID NOS: 4468
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 628
/ LENGTH: 12
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: Consensus Peptide
US-10-352-786-628
```

Query Match 38.8%; Score 26; DB 4; Length 12;  
 Best Local Similarity 50.0%; Pred. No. 9,4e+02;  
 Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 EKNSPECTIG 11  
 DB 1 EVNTLRCPG 10

RESULT 64  
 US-09-880-713A-30  
 ; Sequence 30, Application US/09880713A  
 ; Patent No. US20020049307A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Aebersold, Ruedi  
 ; APPLICANT: Zhou, Huijin  
 ; TITLE OF INVENTION: Selective labeling and isolation of phosphopeptides and  
 ; FILE REFERENCE: 39-00  
 ; CURRENT APPLICATION NUMBER: US/09/880,713A  
 ; PRIOR FILING DATE: 2001-06-12  
 ; PRIOR APPLICATION NUMBER: US 60/210,972  
 ; PRIOR FILING DATE: 2000-06-12  
 ; NUMBER OF SEQ ID NOS: 34  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 30  
 ; LENGTH: 13  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-880-713A-30

Query Match 38.8%; Score 26; DB 3; Length 13;  
 Best Local Similarity 62.5%; Pred. No. 1e+03;  
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 SPECIIGP 12  
 DB 5 APELIISP 12

RESULT 65  
 US-09-988-493-302  
 ; Sequence 302, Application US/09988493  
 ; Publication No. US20030064419A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Herath, Herath Mudiyanselage Achula Chandrasiri  
 ; APPLICANT: O'Hare, Michael John  
 ; APPLICANT: Page, Martin John  
 ; APPLICANT: Parekh, Rajesh Bhikhu  
 ; APPLICANT: Waterfield, Michael Derek  
 ; TITLE OF INVENTION: Proteins, Genes, and Their Use for  
 ; FILE REFERENCE: 2543-1-024  
 ; CURRENT APPLICATION NUMBER: US/09/988,493  
 ; PRIOR FILING DATE: 2002-05-21  
 ; PRIOR APPLICATION NUMBER: PCT/GB01/01219  
 ; PRIOR FILING DATE: 2001-03-20  
 ; PRIOR APPLICATION NUMBER: GB 0006695.1  
 ; PRIOR FILING DATE: 2000-03-20  
 ; PRIOR APPLICATION NUMBER: GB 0007265.2  
 ; PRIOR FILING DATE: 2000-02-24  
 ; NUMBER OF SEQ ID NOS: 308  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 302  
 ; LENGTH: 13  
 ; TYPE: PRT  
 ; ORGANISM: homo sapien  
 US-09-988-493-302

Query Match 38.8%; Score 26; DB 3; Length 13;  
 Best Local Similarity 62.5%; Pred. No. 1e+03;  
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 SPECIIGP 12  
 DB 5 APELIISP 12

RESULT 66  
 US-10-352-786-717  
 ; Sequence 717, Application US/10352786  
 ; Publication No. US20030228353A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Cowart, Donald R.  
 ; TITLE OF INVENTION: Bioactive keratin peptides  
 ; FILE REFERENCE: KER020/4-024US  
 ; CURRENT APPLICATION NUMBER: US/10/352,786  
 ; PRIOR FILING DATE: 2003-06-06  
 ; PRIOR APPLICATION NUMBER: 630/352,396  
 ; PRIOR FILING DATE: 2002-01-28  
 ; NUMBER OF SEQ ID NOS: 4468  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 717  
 ; LENGTH: 13  
 ; TYPE: PRT  
 ; ORGANISM: Artificial  
 ; FEATURE:  
 ; OTHER INFORMATION: Consensus Peptide  
 US-10-352-786-717

Query Match 38.8%; Score 26; DB 4; Length 13;  
 Best Local Similarity 50.0%; Pred. No. 1e+03;  
 Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 EKNSPECTIG 11  
 DB 1 EVNTLRCPG 10

RESULT 67  
 US-10-352-786-718  
 ; Sequence 718, Application US/10352786  
 ; Publication No. US20030228353A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Cowart, Donald R.  
 ; TITLE OF INVENTION: Bioactive Keratin Peptides  
 ; FILE REFERENCE: KER020/4-024US  
 ; CURRENT APPLICATION NUMBER: US/10/352,786  
 ; PRIOR FILING DATE: 2003-06-06  
 ; PRIOR APPLICATION NUMBER: 630/352,396  
 ; PRIOR FILING DATE: 2002-01-28  
 ; NUMBER OF SEQ ID NOS: 4468  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 718  
 ; LENGTH: 13  
 ; TYPE: PRT  
 ; ORGANISM: Artificial  
 ; FEATURE:  
 ; OTHER INFORMATION: Consensus Peptide  
 US-10-352-786-718

Query Match 38.8%; Score 26; DB 4; Length 13;  
 Best Local Similarity 50.0%; Pred. No. 1e+03;  
 Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 EKNSPECTIG 11  
 DB 1 EVNTLRCPG 10

RESULT 68  
 US-10-412-964-40  
 ; Sequence 40, Application US/10412964  
 ; Publication No. US20040106150A1  
 ; GENERAL INFORMATION:

```
/ APPLICANT: Wang, Yinqi Karen
/ TITLE OF INVENTION: Inverse Labeling Method for the Rapid
/ FILE REFERENCE: 4-31692B
/ CURRENT APPLICATION NUMBER: US/10/412,964
/ PRIOR FILING DATE: 2003-04-14
/ PRIOR APPLICATION NUMBER: 60/257,559
/ PRIOR FILING DATE: 2000-12-22
/ PRIOR APPLICATION NUMBER: 60/332,965
/ PRIOR FILING DATE: 2001-11-19
/ PRIOR APPLICATION NUMBER: 10/016,627
/ PRIOR FILING DATE: 2001-12-10
/ NUMBER OF SEQ ID NOS: 83
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 40
/ LENGTH: 13
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Peptide obtained from Oncoprotein 18
/ NAME/KEY: PHOSPHORYLATION
/ LOCATION: 11
/ OTHER INFORMATION: The serine is phosphorylated
US-10-412-964-40
```

```
Query Match          38.8%; Score 26; DB 4; Length 13;
Best Local Similarity 62.5%; Pred. No. 1e+03;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

QY 5 SPECIFIC 12  
DB 5 APELILSP 12

```
RESULT 69
US-10-948-707-1280
/ Sequence 1280, Application US/10948707
/ Publication No. US20050187147A1
/ GENERAL INFORMATION:
/ APPLICANT: Ballatore, Carlo
/ APPLICANT: Castellino, Angelo
/ APPLICANT: Desharnais, Joel
/ APPLICANT: Guo, Zijian
/ APPLICANT: Li, Qing
/ APPLICANT: Newman, Michael James
/ APPLICANT: Sun, Chengzao
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INCREASING
/ FILE REFERENCE: 17967-003001
/ CURRENT APPLICATION NUMBER: US/10/948,707
/ CURRENT FILING DATE: 2004-09-22
/ PRIOR APPLICATION NUMBER: 60/505,325
/ PRIOR FILING DATE: 2003-09-22
/ PRIOR APPLICATION NUMBER: 60/568,340
/ PRIOR FILING DATE: 2004-05-04
/ PRIOR APPLICATION NUMBER: 60/581,835
/ PRIOR FILING DATE: 2004-06-22
/ NUMBER OF SEQ ID NOS: 1422
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 1280
/ LENGTH: 13
/ TYPE: PRT
/ ORGANISM: Homo Sapiens
US-10-948-707-1280
```

```
Query Match          38.8%; Score 26; DB 5; Length 13;
Best Local Similarity 62.5%; Pred. No. 1e+03;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

QY 5 SPECIFIC 12  
DB 2 APELILSP 9

```
RESULT 70
US-10-352-786-813
/ Sequence 813, Application US/10352786
/ Publication No. US20030228353A1
/ GENERAL INFORMATION:
/ APPLICANT: Cowbar, Donald R.
/ TITLE OF INVENTION: Bioactive Keratin Peptides
/ FILE REFERENCE: KER020/4-024US
/ CURRENT APPLICATION NUMBER: US/10/352,786
/ CURRENT FILING DATE: 2003-06-06
/ PRIOR APPLICATION NUMBER: 60/352,396
/ PRIOR FILING DATE: 2002-01-28
/ NUMBER OF SEQ ID NOS: 4468
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 813
/ LENGTH: 14
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: Consensus Peptide
US-10-352-786-813
```

```
Query Match          38.8%; Score 26; DB 4; Length 14;
Best Local Similarity 50.0%; Pred. No. 1.1e+03;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
```

QY 2 EKNSPECTIG 11  
DB 1 EYNTLRCPDG 10

```
RESULT 71
US-10-352-786-814
/ Sequence 814, Application US/10352786
/ Publication No. US20030228353A1
/ GENERAL INFORMATION:
/ APPLICANT: Cowbar, Donald R.
/ TITLE OF INVENTION: Bioactive Keratin Peptides
/ FILE REFERENCE: KER020/4-024US
/ CURRENT APPLICATION NUMBER: US/10/352,786
/ CURRENT FILING DATE: 2003-06-06
/ PRIOR APPLICATION NUMBER: 60/352,396
/ PRIOR FILING DATE: 2002-01-28
/ NUMBER OF SEQ ID NOS: 4468
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 814
/ LENGTH: 14
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: Consensus Peptide
US-10-352-786-814
```

```
Query Match          38.8%; Score 26; DB 4; Length 14;
Best Local Similarity 50.0%; Pred. No. 1.1e+03;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
```

QY 2 EKNSPECTIG 11  
DB 1 EYNTLRCPDG 10

```
RESULT 72
US-10-615-659-45
/ Sequence 45, Application US/10615659
/ Publication No. US2004015734A1
/ GENERAL INFORMATION:
/ APPLICANT: Bristol-Myers Squibb Company
/ TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING A NOVEL TESTIS-SPECIFIC TUBULIN
/ FILE REFERENCE: D0283 NP
```

/ CURRENT APPLICATION NUMBER: US/10/615,659  
/ CURRENT FILING DATE: 2003-07-09  
/ PRIOR APPLICATION NUMBER: U.S. 60/394,725  
/ PRIOR FILING DATE: 2002-07-09  
/ NUMBER OF SEQ ID NOS: 102  
/ SOFTWARE: PatentIn version 3.2  
/ SEQ ID NO 45  
/ LENGTH: 14  
/ TYPE: PRT  
/ ORGANISM: Homo sapiens  
US-10-615-659-45

Query Match 38.8%; Score 26; DB 4; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KNSFE 7  
| | | | |  
| | | | |  
DB 7 KNSFE 11

RESULT 73  
US-10-635-977-45  
/ Sequence 45, Application US/10635977  
/ Publication No. US20040171131A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Bristol-Myers Squibb Company  
/ TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING A NOVEL TESTIS-SPECIFIC TUBULIN  
/ FILE REFERENCE: D0283A CIP  
/ CURRENT APPLICATION NUMBER: US/10/635,977  
/ CURRENT FILING DATE: 2003-08-07  
/ PRIOR APPLICATION NUMBER: U.S. 60/394,725  
/ PRIOR FILING DATE: 2002-07-09  
/ PRIOR APPLICATION NUMBER: U.S. 10/615,659  
/ PRIOR FILING DATE: 2003-07-09  
/ NUMBER OF SEQ ID NOS: 103  
/ SOFTWARE: PatentIn version 3.2  
/ SEQ ID NO 45  
/ LENGTH: 14  
/ TYPE: PRT  
/ ORGANISM: Homo sapiens  
US-10-635-977-45

Query Match 38.8%; Score 26; DB 4; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KNSFE 7  
| | | | |  
| | | | |  
DB 7 KNSFE 11

RESULT 74  
US-10-473-287-39  
/ Sequence 39, Application US/10473287  
/ Publication No. US20040221327A1  
/ GENERAL INFORMATION:  
/ APPLICANT: GERSHWIN, M. ERIC  
/ TITLE OF INVENTION: ANTIBODIES AGAINST AUTOANTIGENS OF PRIMARY BILIARY  
/ TITLE OF INVENTION: CIRRHOSIS AND METHODS OF MAKING AND USING THEM  
/ FILE REFERENCE: ABX-UCD PCT  
/ CURRENT APPLICATION NUMBER: US/10/473,287  
/ CURRENT FILING DATE: 2003-09-26  
/ NUMBER OF SEQ ID NOS: 64  
/ SOFTWARE: PatentIn Ver. 2.1  
/ SEQ ID NO 39  
/ LENGTH: 14  
/ TYPE: PRT  
/ ORGANISM: Artificial Sequence  
/ FEATURE:  
/ OTHER INFORMATION: Description of Artificial Sequence: Human mab  
US-10-473-287-39

Query Match 38.8%; Score 26; DB 5; Length 14;  
Best Local Similarity 45.5%; Pred. No. 1.1e+03;  
Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 2 EKNSPECILGP 12  
: | | | |  
: | | | |  
DB 3 QANSFPPTFGP 13

RESULT 75  
US-10-473-287-43  
/ Sequence 43, Application US/10473287  
/ Publication No. US20040221327A1  
/ GENERAL INFORMATION:  
/ APPLICANT: GERSHWIN, M. ERIC  
/ TITLE OF INVENTION: ANTIBODIES AGAINST AUTOANTIGENS OF PRIMARY BILIARY  
/ TITLE OF INVENTION: CIRRHOSIS AND METHODS OF MAKING AND USING THEM  
/ FILE REFERENCE: ABX-UCD PCT  
/ CURRENT APPLICATION NUMBER: US/10/473,287  
/ CURRENT FILING DATE: 2003-09-26  
/ NUMBER OF SEQ ID NOS: 64  
/ SOFTWARE: PatentIn Ver. 2.1  
/ SEQ ID NO 43  
/ LENGTH: 14  
/ TYPE: PRT  
/ ORGANISM: Artificial Sequence  
/ FEATURE:  
/ OTHER INFORMATION: Description of Artificial Sequence: Human mab  
US-10-473-287-43

Query Match 38.8%; Score 26; DB 5; Length 14;  
Best Local Similarity 40.0%; Pred. No. 1.1e+03;  
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 EKNSPECILG 11  
: | | | |  
: | | | |  
DB 3 QHNSYPCSRG 12

RESULT 76  
US-09-767-460-29  
/ Sequence 29, Application US/09767460  
/ Patent No. US20020009756A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Mandell, Arnold  
/ APPLICANT: Selz, Karen  
/ APPLICANT: Shlesinger, Michael  
/ TITLE OF INVENTION: Algorithmic Design of Peptides for Binding and/or Modulation of  
/ TITLE OF INVENTION: Functions of Receptors and/or Other Proteins  
/ FILE REFERENCE: 01561-0002-CPUS01  
/ CURRENT APPLICATION NUMBER: US/09/767,460  
/ CURRENT FILING DATE: 2001-01-23  
/ NUMBER OF SEQ ID NOS: 96  
/ SOFTWARE: PatentIn version 3.0  
/ SEQ ID NO 29  
/ LENGTH: 15  
/ TYPE: PRT  
/ ORGANISM: Artificial Sequence  
/ FEATURE:  
/ OTHER INFORMATION: Synthetic  
US-09-767-460-29

Query Match 38.8%; Score 26; DB 3; Length 15;  
Best Local Similarity 42.9%; Pred. No. 1.2e+03;  
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 EKNSFEC 8  
: | | | |  
: | | | |  
DB 6 DRNHDFC 12

RESULT 77

US-10-352-786-913  
; Sequence 913, Application US/10352786  
; Publication No. US20030228353A1  
; GENERAL INFORMATION:  
; APPLICANT: Cowart, Donald R.  
; TITLE OF INVENTION: Bioactive Keratin Peptides  
; FILE REFERENCE: KER020/4-024US  
; CURRENT APPLICATION NUMBER: US/10/352,786  
; CURRENT FILING DATE: 2003-06-06  
; PRIOR APPLICATION NUMBER: 670/352,396  
; PRIOR FILING DATE: 2002-01-28  
; NUMBER OF SEQ ID NOS: 4468  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 913  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Consensus Peptide  
US-10-352-786-913

Query Match 38.8%; Score 26; DB 4; Length 15;  
Best Local Similarity 50.0%; Pred. No. 1.2e+03;  
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 EKNSFECIG 11  
| | | | |  
| | | | |  
DB 1 EVNITLRCPLG 10

RESULT 78  
US-10-352-786-914  
; Sequence 914, Application US/10352786  
; Publication No. US20030228353A1  
; GENERAL INFORMATION:  
; APPLICANT: Cowart, Donald R.  
; TITLE OF INVENTION: Bioactive Keratin Peptides  
; FILE REFERENCE: KER020/4-024US  
; CURRENT APPLICATION NUMBER: US/10/352,786  
; CURRENT FILING DATE: 2003-06-06  
; PRIOR APPLICATION NUMBER: 670/352,396  
; PRIOR FILING DATE: 2002-01-28  
; NUMBER OF SEQ ID NOS: 4468  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 914  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Consensus Peptide  
US-10-352-786-914

Query Match 38.8%; Score 26; DB 4; Length 15;  
Best Local Similarity 50.0%; Pred. No. 1.2e+03;  
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 EKNSFECIG 11  
| | | | |  
| | | | |  
DB 1 EVNITLRCPLG 10

RESULT 79  
US-10-777-829-29  
; Sequence 29, Application US/10777829  
; Publication No. US20050027457A1  
; GENERAL INFORMATION:  
; APPLICANT: MANDELL, ARNOLD J.  
; APPLICANT: SELZ, KAREN A.  
; APPLICANT: SHLESINGER, MICHAEL F.  
; TITLE OF INVENTION: ALGORITHMIC DESIGN OF PEPTIDES FOR BINDING AND/OR MODULATION OF  
; FILE REFERENCE: 31010-701.301  
; CURRENT APPLICATION NUMBER: US/10/777,829

; CURRENT FILING DATE: 2004-02-11  
; PRIOR APPLICATION NUMBER: 09/767,460  
; PRIOR FILING DATE: 2001-01-23  
; PRIOR APPLICATION NUMBER: 09/490,701  
; PRIOR FILING DATE: 2000-01-24  
; NUMBER OF SEQ ID NOS: 99  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 29  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic peptide  
US-10-777-829-29

Query Match 38.8%; Score 26; DB 5; Length 15;  
Best Local Similarity 42.9%; Pred. No. 1.2e+03;  
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 EKNSPEC 8  
| | | | |  
| | | | |  
DB 6 DRNHFDG 12

RESULT 80  
US-10-818-067-29  
; Sequence 29, Application US/10818067  
; Publication No. US20050119454A1  
; GENERAL INFORMATION:  
; APPLICANT: MANDELL, ARNOLD J.  
; APPLICANT: SELZ, KAREN A.  
; APPLICANT: SHLESINGER, MICHAEL F.  
; TITLE OF INVENTION: ALGORITHMIC DESIGN OF PEPTIDES FOR BINDING AND/OR MODULATION OF  
; FILE REFERENCE: 31010-701.502  
; CURRENT APPLICATION NUMBER: US/10/818,067  
; CURRENT FILING DATE: 2004-04-02  
; PRIOR APPLICATION NUMBER: 10/777,829  
; PRIOR FILING DATE: 2004-02-11  
; PRIOR APPLICATION NUMBER: 09/767,460  
; PRIOR FILING DATE: 2000-01-23  
; PRIOR APPLICATION NUMBER: 09/490,701  
; PRIOR FILING DATE: 2000-01-24  
; NUMBER OF SEQ ID NOS: 107  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 29  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic peptide  
US-10-818-067-29

Query Match 38.8%; Score 26; DB 5; Length 15;  
Best Local Similarity 42.9%; Pred. No. 1.2e+03;  
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 EKNSPEC 8  
| | | | |  
| | | | |  
DB 6 DRNHFDG 12

RESULT 81  
US-09-774-639-245  
; Sequence 245, Application US/09774639  
; Publication No. US2003003555A1  
; GENERAL INFORMATION:  
; APPLICANT: ROSEN et al.  
; TITLE OF INVENTION: 90 Human Secreted Proteins  
; FILE REFERENCE: P2013p1  
; CURRENT APPLICATION NUMBER: US/09/774,639  
; CURRENT FILING DATE: 2001-07-09  
; PRIOR APPLICATION NUMBER: 09/244,112



```
/ PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-04
/ NUMBER OF SEQ ID NOS: 371
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 245
/ LENGTH: 16
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-774-639-245

Query Match          38.8%; Score 26; DB 3; Length 16;
Best Local Similarity 50.0%; Pred. No. 1.3e+03;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY      3 KNSFECTILGP 12
         | | | | |
Db       4 KTRPACTILVP 13

RESULT 82
US-09-969-730-344
/ Sequence 344, Application US/09969730
/ Publication No. US2003005443A1
/ GENERAL INFORMATION:
/ APPLICANT: Ruben et al.
/ TITLE OF INVENTION: 90 Human Secreted Proteins
/ FILE REFERENCE: P2013P2
/ CURRENT APPLICATION NUMBER: US/09/969,730
/ PRIOR FILING DATE: 2001-10-04
/ PRIOR APPLICATION NUMBER: 09/774,639
/ PRIOR FILING DATE: 2001-02-01
/ PRIOR APPLICATION NUMBER: 60/238,291
/ PRIOR FILING DATE: 2000-10-06
/ PRIOR APPLICATION NUMBER: 09/244,112
/ PRIOR FILING DATE: 1999-02-04
/ PRIOR APPLICATION NUMBER: PCT/US98/16235
/ PRIOR FILING DATE: 1998-08-04
/ PRIOR APPLICATION NUMBER: 60/056,371
/ PRIOR FILING DATE: 1997-08-19
/ PRIOR APPLICATION NUMBER: 60/056,732
/ PRIOR FILING DATE: 1997-08-19
/ PRIOR APPLICATION NUMBER: 60/056,366
/ PRIOR FILING DATE: 1997-08-19
/ PRIOR APPLICATION NUMBER: 60/056,364
/ PRIOR FILING DATE: 1997-08-19
/ PRIOR APPLICATION NUMBER: 60/056,370
/ PRIOR FILING DATE: 1997-08-19
/ PRIOR APPLICATION NUMBER: 60/056,367
/ PRIOR FILING DATE: 1997-08-19
/ PRIOR APPLICATION NUMBER: 60/056,365
/ PRIOR FILING DATE: 1997-08-19
/ PRIOR APPLICATION NUMBER: 60/056,731
/ PRIOR FILING DATE: 1997-08-19
/ PRIOR APPLICATION NUMBER: 60/056,557
/ PRIOR FILING DATE: 1997-08-19
/ PRIOR APPLICATION NUMBER: 60/056,563
/ PRIOR FILING DATE: 1997-08-19
/ PRIOR APPLICATION NUMBER: 60/055,970
/ PRIOR FILING DATE: 1997-08-18
/ PRIOR APPLICATION NUMBER: 60/055,986
/ PRIOR FILING DATE: 1997-08-18
/ PRIOR APPLICATION NUMBER: 60/055,311
/ PRIOR FILING DATE: 1997-08-05
/ PRIOR APPLICATION NUMBER: 60/054,808
/ PRIOR FILING DATE: 1997-08-05
/ PRIOR APPLICATION NUMBER: 60/054,803
/ PRIOR FILING DATE: 1997-08-05
/ PRIOR APPLICATION NUMBER: 60/054,804
/ PRIOR FILING DATE: 1997-08-05
/ PRIOR APPLICATION NUMBER: 60/054,809
/ PRIOR FILING DATE: 1997-08-05
/ PRIOR APPLICATION NUMBER: 60/054,806
/ PRIOR FILING DATE: 1997-08-05
/ PRIOR APPLICATION NUMBER: 60/055,310
```

```
/ PRIOR FILING DATE: 1997-08-05
/ PRIOR APPLICATION NUMBER: 60/054,798
/ PRIOR FILING DATE: 1997-08-05
/ PRIOR APPLICATION NUMBER: 60/055,309
/ PRIOR FILING DATE: 1997-08-05
/ PRIOR APPLICATION NUMBER: 60/055,312
/ PRIOR FILING DATE: 1997-08-05
/ PRIOR APPLICATION NUMBER: 60/054,807
/ PRIOR FILING DATE: 1997-08-05
/ PRIOR APPLICATION NUMBER: 60/055,386
/ PRIOR FILING DATE: 1997-08-05
/ NUMBER OF SEQ ID NOS: 373
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 344
/ LENGTH: 16
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-969-730-344

Query Match          38.8%; Score 26; DB 3; Length 16;
Best Local Similarity 50.0%; Pred. No. 1.3e+03;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY      3 KNSFECTILGP 12
         | | | | |
Db       4 KTRPACTILVP 13

RESULT 83
US-10-114-500-15
/ Sequence 15, Application US/10114500
/ Publication No. US20030100746A1
/ GENERAL INFORMATION:
/ APPLICANT: Godbole, Shubhada
/ APPLICANT: Boyle, Bryan J
/ APPLICANT: Atterburn, Matthew C
/ APPLICANT: Liu, Chenghua
/ APPLICANT: Tang, Y Tom
/ APPLICANT: Dimauc, Radoje T
/ TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO FIBULIN-LIKE POLYPEPTIDES AND
/ FILE REFERENCE: HYS-40CON
/ CURRENT APPLICATION NUMBER: US/10/114,500
/ PRIOR FILING DATE: 2002-04-01
/ PRIOR APPLICATION NUMBER: US 09/802,704
/ PRIOR FILING DATE: 2001-03-08
/ PRIOR APPLICATION NUMBER: US 09/560,875
/ PRIOR FILING DATE: 2000-04-27
/ PRIOR APPLICATION NUMBER: US 09/496,914
/ PRIOR FILING DATE: 2000-02-03
/ NUMBER OF SEQ ID NOS: 22
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 15
/ LENGTH: 16
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-114-500-15

Query Match          38.8%; Score 26; DB 4; Length 16;
Best Local Similarity 44.4%; Pred. No. 1.3e+03;
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY      4 NSFECTILGP 12
         | | | | |
Db       6 NGYRCICPP 14

RESULT 84
US-10-352-786-1017
/ Sequence 1017, Application US/10352786
/ Publication No. US20030228353A1
/ GENERAL INFORMATION:
/ APPLICANT: Cowart, Donald R.
```

```
/ TITLE OF INVENTION: Bioactive Keratin Peptides
/ FILE REFERENCE: KER020/4-024US
/ CURRENT APPLICATION NUMBER: US/10/352,786
/ CURRENT FILING DATE: 2003-06-06
/ PRIOR APPLICATION NUMBER: 6J0/352,396
/ PRIOR FILING DATE: 2002-01-28
/ NUMBER OF SEQ ID NOS: 4468
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO: 1017
/ LENGTH: 16
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: Consensus Peptide
US-10-352-786-1017

Query Match      38.8%; Score 26; DB 4; Length 16;
Best Local Similarity 50.0%; Pred. No. 1.3e+03;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
```

```
QY      2 EKNSPECTIG 11
| | | | |
Db      1 EVNTRCOLG 10

RESULT 85
US-10-352-786-1018
/ Sequence 1018, Application US/10352786
/ Publication No. US20030228353A1
/ GENERAL INFORMATION:
/ APPLICANT: Cowbat, Donald R.
/ TITLE OF INVENTION: Bioactive Keratin Peptides
/ FILE REFERENCE: KER020/4-024US
/ CURRENT APPLICATION NUMBER: US/10/352,786
/ CURRENT FILING DATE: 2003-06-06
/ PRIOR APPLICATION NUMBER: 6J0/352,396
/ PRIOR FILING DATE: 2002-01-28
/ NUMBER OF SEQ ID NOS: 4468
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO: 1018
/ LENGTH: 16
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: Consensus Peptide
US-10-352-786-1018

Query Match      38.8%; Score 26; DB 4; Length 16;
Best Local Similarity 50.0%; Pred. No. 1.3e+03;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
```

```
QY      2 EKNSPECTIG 11
| | | | |
Db      1 EVNTRCOLG 10

RESULT 86
US-10-621-363-344
/ Sequence 344, Application US/10621363
/ Publication No. US20040023283A1
/ GENERAL INFORMATION:
/ APPLICANT: Ruben et al.
/ TITLE OF INVENTION: 90 Human Secreted Proteins
/ FILE REFERENCE: P2013P2C1
/ CURRENT APPLICATION NUMBER: US/10/621,363
/ CURRENT FILING DATE: 2003-07-18
/ PRIOR APPLICATION NUMBER: 09/969,730
/ PRIOR FILING DATE: 2001-10-06
/ PRIOR APPLICATION NUMBER: 09/774,639
/ PRIOR FILING DATE: 2001-02-01
/ PRIOR APPLICATION NUMBER: 60/238,291
/ PRIOR FILING DATE: 2000-10-06
/ PRIOR APPLICATION NUMBER: 09/244,112
```

```
/ PRIOR FILING DATE: 1999-02-04
/ PRIOR APPLICATION NUMBER: PCT/US98/16235
/ PRIOR FILING DATE: 1998-08-04
/ PRIOR APPLICATION NUMBER: 60/056,371
/ PRIOR FILING DATE: 1997-08-19
/ PRIOR APPLICATION NUMBER: 60/056,732
/ PRIOR FILING DATE: 1997-08-19
/ PRIOR APPLICATION NUMBER: 60/056,366
/ PRIOR FILING DATE: 1997-08-19
/ PRIOR APPLICATION NUMBER: 60/056,364
/ PRIOR FILING DATE: 1997-08-19
/ PRIOR APPLICATION NUMBER: 60/056,370
/ PRIOR FILING DATE: 1997-08-19
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 373
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO: 344
/ LENGTH: 16
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-621-363-344

Query Match      38.8%; Score 26; DB 4; Length 16;
Best Local Similarity 50.0%; Pred. No. 1.3e+03;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
```

```
QY      3 KNSPECTIGP 12
| | | | |
Db      4 KTPAECLTYP 13

RESULT 87
US-10-471-346-15
/ Sequence 15, Application US/10471346
/ Publication No. US20040236090A1
/ GENERAL INFORMATION:
/ APPLICANT: Hyseq, Inc
/ APPLICANT: Godbole, Shubhada D
/ APPLICANT: Boyle, Bryan J
/ APPLICANT: Arterburn, Matthew C
/ APPLICANT: Liu, Chenghua
/ APPLICANT: Tang, Y Tom
/ APPLICANT: Drmanac, Radoje T
/ TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO FIBULIN-LIKE POLYPEPTIDES AND
/ FILE REFERENCE: 24059-040-061
/ CURRENT APPLICATION NUMBER: US/10/471,346
/ CURRENT FILING DATE: 2003-09-08
/ PRIOR APPLICATION NUMBER: US 09/802,704
/ PRIOR FILING DATE: 2001-03-08
/ PRIOR APPLICATION NUMBER: US 09/560,875
/ PRIOR FILING DATE: 2000-04-27
/ PRIOR APPLICATION NUMBER: US 09/496,914
/ PRIOR FILING DATE: 2000-02-03
/ NUMBER OF SEQ ID NOS: 22
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO: 15
/ LENGTH: 16
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-471-346-15

Query Match      38.8%; Score 26; DB 5; Length 16;
Best Local Similarity 44.4%; Pred. No. 1.3e+03;
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
```

```
QY      4 NSPECTIGP 12
| | | | |
Db      6 NOYRCLTYP 14

RESULT 88
US-10-352-786-1127
```

```

; Sequence 1127, Application US/10352786
; Publication No. US20030228353A1
; GENERAL INFORMATION:
; APPLICANT: Cowstar, Donald R.
; TITLE OF INVENTION: Bioactive Keratin Peptides
; FILE REFERENCE: KER020/4-024US
; CURRENT APPLICATION NUMBER: US/10/352,786
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: 630/352,396
; PRIOR FILING DATE: 2002-01-28
; NUMBER OF SEQ ID NOS: 4468
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 1127
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Consensus Peptide
US-10-352-786-1127

```

```

Query Match      38.8%; Score 26; DB 4; Length 17;
Best Local Similarity 50.0%; Pred. No. 1.4e+03;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

```

```

Qy      2 EKNSPCTIG 11
      ||:||||
Db      1 EVNTLRCQIG 10

```

```

RESULT 89
US-10-352-786-1128
; Sequence 1128, Application US/10352786
; Publication No. US20030228353A1
; GENERAL INFORMATION:
; APPLICANT: Cowstar, Donald R.
; TITLE OF INVENTION: Bioactive Keratin Peptides
; FILE REFERENCE: KER020/4-024US
; CURRENT APPLICATION NUMBER: US/10/352,786
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: 630/352,396
; PRIOR FILING DATE: 2002-01-28
; NUMBER OF SEQ ID NOS: 4468
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 1128
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Consensus Peptide
US-10-352-786-1128

```

```

Query Match      38.8%; Score 26; DB 4; Length 17;
Best Local Similarity 50.0%; Pred. No. 1.4e+03;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

```

```

Qy      2 EKNSPCTIG 11
      ||:||||
Db      1 EVNTLRCQIG 10

```

```

RESULT 90
US-09-858-935B-121
; Sequence 121, Application US/09858935B
; Publication No. US20030069177A1
; GENERAL INFORMATION:
; APPLICANT: Dubaigle, Yves
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Lowman, Henry B.
; TITLE OF INVENTION: METHOD FOR TREATING CARTILAGE DISORDERS
; FILE REFERENCE: P1794R1
; CURRENT APPLICATION NUMBER: US/09/858,935B
; CURRENT FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: US 60/248,985

```

```

; PRIOR FILING DATE: 2000-11-15
; PRIOR APPLICATION NUMBER: US 60/204,490
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 153
; SEQ ID NO 121
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized
US-09-858-935B-121

```

```

Query Match      38.8%; Score 26; DB 3; Length 18;
Best Local Similarity 66.7%; Pred. No. 1.4e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy      7 ECIIGP 12
      ||:||||
Db      4 ECIWGP 9

```

```

RESULT 91
US-10-271-869-121
; Sequence 121, Application US/10271869
; Publication No. US20030211992A1
; GENERAL INFORMATION:
; APPLICANT: Dubaigle, Yves
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Lowman, Henry B.
; TITLE OF INVENTION: METHOD FOR TREATING CARTILAGE DISORDERS
; FILE REFERENCE: P1794R1
; CURRENT APPLICATION NUMBER: US/10/271,869
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: US/09/858,935
; PRIOR FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: US 60/248,985
; PRIOR FILING DATE: 2000-11-15
; PRIOR APPLICATION NUMBER: US 60/204,490
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 153
; SEQ ID NO 121
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized
US-10-271-869-121

```

```

Query Match      38.8%; Score 26; DB 4; Length 18;
Best Local Similarity 66.7%; Pred. No. 1.4e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy      7 ECIIGP 12
      ||:||||
Db      4 ECIWGP 9

```

```

RESULT 92
US-10-352-786-1243
; Sequence 1243, Application US/10352786
; Publication No. US20030228353A1
; GENERAL INFORMATION:
; APPLICANT: Cowstar, Donald R.
; TITLE OF INVENTION: Bioactive Keratin Peptides
; FILE REFERENCE: KER020/4-024US
; CURRENT APPLICATION NUMBER: US/10/352,786
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: 630/352,396
; PRIOR FILING DATE: 2002-01-28
; NUMBER OF SEQ ID NOS: 4468
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 1243
; LENGTH: 18

```

/ TYPE: PRT  
/ ORGANISM: Artificial  
/ FEATURE:  
/ OTHER INFORMATION: Consensus Peptide  
US-10-352-786-1243

Query Match 38.8%; Score 26; DB 4; Length 18;  
Best Local Similarity 50.0%; Pred. No. 1.4e+03;  
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 EKNSPECILG 11  
| : |  
| : |  
Db 1 EVNLTLCQGL 10

RESULT 93  
US-10-352-786-1244  
/ Sequence 1244, Application US/10352786  
/ Publication No. US20030228353A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Cowart, Donald R.  
/ TITLE OF INVENTION: Bioactive Keratin Peptides  
/ FILE REFERENCE: KER020/4-024US  
/ CURRENT APPLICATION NUMBER: US/10/352,786  
/ PRIOR FILING DATE: 2003-06-06  
/ PRIOR APPLICATION NUMBER: 630/352,396  
/ PRIOR FILING DATE: 2002-01-28  
/ NUMBER OF SEQ ID NOS: 468  
/ SOFTWARE: PatentIn version 3.2  
/ SEQ ID NO 1244  
/ LENGTH: 18  
/ TYPE: PRT  
/ ORGANISM: Artificial  
/ FEATURE:  
/ OTHER INFORMATION: Consensus Peptide  
US-10-352-786-1244

Query Match 38.8%; Score 26; DB 4; Length 18;  
Best Local Similarity 50.0%; Pred. No. 1.4e+03;  
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 EKNSPECILG 11  
| : |  
| : |  
Db 1 EVNLTLCQGL 10

RESULT 94  
US-10-754-437-25  
/ Sequence 25, Application US/10754437  
/ Publication No. US20040146915A1  
/ GENERAL INFORMATION:  
/ APPLICANT: METAMORPHIX, INC.  
/ APPLICANT: Ferrite, Bonita J.M.  
/ APPLICANT: Johnston, Eric V.  
/ APPLICANT: Denise, Sue  
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETERMINING CANINE GENDER  
/ FILE REFERENCE: MM1130-1  
/ CURRENT APPLICATION NUMBER: US/10/754,437  
/ PRIOR FILING DATE: 2004-01-09  
/ PRIOR APPLICATION NUMBER: US 60/439,188  
/ NUMBER OF SEQ ID NOS: 99  
/ SOFTWARE: PatentIn version 3.1  
/ SEQ ID NO 25  
/ LENGTH: 18  
/ TYPE: PRT  
/ ORGANISM: Homo sapiens X  
US-10-754-437-25

Query Match 38.8%; Score 26; DB 4; Length 18;  
Best Local Similarity 66.7%; Pred. No. 1.4e+03;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 FECTILG 11  
| : |  
| : |  
Db 7 FACILG 12

RESULT 95  
US-10-754-437-29  
/ Sequence 29, Application US/10754437  
/ Publication No. US20040146915A1  
/ GENERAL INFORMATION:  
/ APPLICANT: METAMORPHIX, INC.  
/ APPLICANT: Ferrite, Bonita J.M.  
/ APPLICANT: Johnston, Eric V.  
/ APPLICANT: Denise, Sue  
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETERMINING CANINE GENDER  
/ FILE REFERENCE: MM1130-1  
/ CURRENT APPLICATION NUMBER: US/10/754,437  
/ PRIOR FILING DATE: 2004-01-09  
/ PRIOR APPLICATION NUMBER: US 60/439,188  
/ PRIOR FILING DATE: 2003-01-10  
/ NUMBER OF SEQ ID NOS: 99  
/ SOFTWARE: PatentIn version 3.1  
/ SEQ ID NO 29  
/ LENGTH: 18  
/ TYPE: PRT  
/ ORGANISM: Canis familiaris X  
US-10-754-437-29

Query Match 38.8%; Score 26; DB 4; Length 18;  
Best Local Similarity 66.7%; Pred. No. 1.4e+03;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 FECTILG 11  
| : |  
| : |  
Db 7 FACILG 12

RESULT 96  
US-10-754-437-31  
/ Sequence 31, Application US/10754437  
/ Publication No. US20040146915A1  
/ GENERAL INFORMATION:  
/ APPLICANT: METAMORPHIX, INC.  
/ APPLICANT: Ferrite, Bonita J.M.  
/ APPLICANT: Johnston, Eric V.  
/ APPLICANT: Denise, Sue  
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETERMINING CANINE GENDER  
/ FILE REFERENCE: MM1130-1  
/ CURRENT APPLICATION NUMBER: US/10/754,437  
/ PRIOR FILING DATE: 2004-01-09  
/ PRIOR APPLICATION NUMBER: US 60/439,188  
/ PRIOR FILING DATE: 2003-01-10  
/ NUMBER OF SEQ ID NOS: 99  
/ SOFTWARE: PatentIn version 3.1  
/ SEQ ID NO 31  
/ LENGTH: 18  
/ TYPE: PRT  
/ ORGANISM: Canis familiaris X  
US-10-754-437-31

Query Match 38.8%; Score 26; DB 4; Length 18;  
Best Local Similarity 66.7%; Pred. No. 1.4e+03;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 FECTILG 11  
| : |  
| : |  
Db 7 FACILG 12

RESULT 97  
US-09-864-761-43430  
/ Sequence 43430, Application US/09864761  
/ Patent No. US20020048763A1

```

; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aecmca-X-1
; CURRENT APPLICATION NUMBER: US/09/664,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263,6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 43430
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC008009.4
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 4.6
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.7
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.6
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.1
; OTHER INFORMATION: EST_HUMAN HIT: AV706204.1, EVALUE 3.70e-02
US-09-664-761-43430

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Query Match      38.8%; Score 26; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      2 BKNSP 6
      |||||
Db      1 BKNSP 5

RESULT 98
US-10-225-567A-1330

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; Sequence 1330, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: Lifespan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burner, Glenn C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTOR
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1330
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-1330

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Query Match      38.8%; Score 26; DB 4; Length 19;
Best Local Similarity 40.0%; Pred. No. 1.5e+03;
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY      1 DEKNSPFCIL 10
      ||:|:|
Db      4 DEQGRQCIVL 13

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RESULT 99
US-10-352-786-1365
; Sequence 1365, Application US/10352786
; Publication No. US20030228353A1
; GENERAL INFORMATION:
; APPLICANT: Cowart, Donald R.
; TITLE OF INVENTION: Bioactive Keratin Peptides
; FILE REFERENCE: KER020/4-024US
; CURRENT FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: 630/352,396
; PRIOR FILING DATE: 2002-01-28
; NUMBER OF SEQ ID NOS: 4468
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1365
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Consensus Peptide
US-10-352-786-1365

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Query Match      38.8%; Score 26; DB 4; Length 19;
Best Local Similarity 50.0%; Pred. No. 1.5e+03;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY      2 BKNSPFCILG 11
      ||:|:|
Db      1 EYNTLRQCLG 10

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RESULT 100
US-10-352-786-1366
; Sequence 1366, Application US/10352786
; Publication No. US20030228353A1
; GENERAL INFORMATION:
; APPLICANT: Cowart, Donald R.
; TITLE OF INVENTION: Bioactive Keratin Peptides
; FILE REFERENCE: KER020/4-024US
; CURRENT APPLICATION NUMBER: US/10/352,786
; CURRENT FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: 630/352,396
; PRIOR FILING DATE: 2002-01-28

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NUMBER OF SEQ ID NOS: 4468  
SOFTWARE: Patencin version 3.2  
SEQ ID NO: 1366  
LENGTH: 19  
TYPE: PRT  
ORGANISM: Artificial  
FEATURE:  
OTHER INFORMATION: Consensus Peptide  
US-10-352-786-1366

Query Match 38.8%; Score 26; DB 4; Length 19;  
Best Local Similarity 50.0%; Pred. No. 1.5e+03;  
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 EKRSPECTIG 11  
| | | | |  
| | | | |  
Db 1 EYVTLRCQLG 10

Search completed: January 20, 2006, 19:45:41  
Job time : 44.2692 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2006 CompuGen Ltd.

OW protein - protein search, using sw model

Run on: January 20, 2006, 19:12:21 : Search time 4.84615 Seconds  
(without alignments)  
25.093 Million cell updates/sec

Title: US-09-662-293-5  
Perfect score: 67  
Sequence: 1 DEKNSPFCILGP 12

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 70606 seqs, 10133881 residues

Total number of hits satisfying chosen parameters: 34662

Minimum DB seq length: 0  
Maximum DB seq length: 20

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : Published Applications AA New:\*  
1: /cgn2\_6/prodata/1/pubppa/US08\_NEW\_PUB.pep:\*  
2: /cgn2\_6/prodata/1/pubppa/US06\_NEW\_PUB.pep:\*  
3: /cgn2\_6/prodata/1/pubppa/US07\_NEW\_PUB.pep:\*  
4: /cgn2\_6/prodata/1/pubppa/PCT\_NEW\_PUB.pep:\*  
5: /cgn2\_6/prodata/1/pubppa/US09\_NEW\_PUB.pep:\*  
6: /cgn2\_6/prodata/1/pubppa/US10\_NEW\_PUB.pep:\*  
7: /cgn2\_6/prodata/1/pubppa/US11\_NEW\_PUB.pep:\*  
8: /cgn2\_6/prodata/1/pubppa/US60\_NEW\_PUB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30	44.8	19	6	US-10-939-890-220
2	28	41.8	9	6	US-10-517-784-11
3	28	41.8	14	6	US-10-866-501-340
4	27	40.3	19	6	US-10-503-575-200
5	26	38.8	16	6	US-10-986-501-344
6	26	38.8	18	7	US-11-033-039-1313
7	26	38.8	19	6	US-10-503-575-163
8	24	35.8	13	6	US-10-511-559-965
9	24	35.8	13	6	US-10-511-559-966
10	24	35.8	13	6	US-10-511-559-967
11	24	35.8	13	6	US-10-511-559-968
12	24	35.8	16	6	US-10-467-657-8750
13	23.5	35.1	17	7	US-11-090-497-22
14	23	34.3	9	6	US-10-517-784-37
15	23	34.3	9	7	US-11-208-541-1
16	23	34.3	10	6	US-10-859-643-533
17	23	34.3	10	6	US-10-859-643-533
18	23	34.3	10	7	US-11-097-864-635
19	23	34.3	10	7	US-11-097-864-635
20	23	34.3	10	7	US-11-097-864-635
21	23	34.3	10	7	US-11-097-864-635
22	23	34.3	13	6	US-10-511-559-883
23	23	34.3	13	6	US-10-511-559-884
24	23	34.3	14	6	US-10-939-890-79
25	23	34.3	15	7	US-11-054-515-2765

26	23	34.3	16	6	US-10-939-890-349	Sequence 349, App
27	23	34.3	16	6	US-10-939-890-825	Sequence 825, App
28	23	34.3	17	6	US-10-834-397-207	Sequence 207, App
29	23	34.3	19	6	US-10-939-890-218	Sequence 218, App
30	23	34.3	19	6	US-10-939-890-221	Sequence 221, App
31	23	34.3	19	6	US-10-939-890-348	Sequence 348, App
32	23	34.3	19	6	US-10-939-890-824	Sequence 824, App
33	23	34.3	20	7	US-11-022-562-188	Sequence 188, App
34	23	34.3	20	7	US-11-022-562-189	Sequence 189, App
35	22	32.8	9	6	US-10-982-145-30	Sequence 50, App1
36	22	32.8	9	6	US-10-982-145-50	Sequence 57, App1
37	22	32.8	9	6	US-10-982-145-57	Sequence 58, App1
38	22	32.8	9	6	US-10-982-145-63	Sequence 63, App1
39	22	32.8	9	6	US-10-982-145-64	Sequence 64, App1
40	22	32.8	11	6	US-10-873-427A-24	Sequence 24, App1
41	22	32.8	12	6	US-10-873-427A-23	Sequence 23, App1
42	22	32.8	13	6	US-10-511-559-892	Sequence 92, App1
43	22	32.8	13	6	US-10-873-427A-20	Sequence 20, App1
44	22	32.8	13	6	US-10-970-847-21	Sequence 21, App1
45	22	32.8	13	6	US-10-939-890-66	Sequence 66, App1
46	22	32.8	14	6	US-10-873-427A-19	Sequence 19, App1
47	22	32.8	14	7	US-11-198-847-278	Sequence 278, App1
48	22	32.8	14	7	US-11-112-784-79	Sequence 79, App1
49	22	32.8	15	6	US-10-939-890-199	Sequence 199, App
50	22	32.8	15	6	US-10-467-657-8630	Sequence 8690, App
51	22	32.8	15	6	US-10-467-657-8789	Sequence 8789, App
52	22	32.8	15	6	US-10-873-427A-14	Sequence 14, App1
53	22	32.8	16	6	US-10-873-427A-13	Sequence 13, App1
54	22	32.8	16	6	US-10-969-314-28	Sequence 28, App1
55	22	32.8	17	6	US-10-873-427A-12	Sequence 12, App1
56	22	32.8	17	6	US-11-106-415-221	Sequence 221, App1
57	22	32.8	18	7	US-11-106-415-238	Sequence 238, App1
58	22	32.8	20	7	US-10-962-145C-9	Sequence 9, App11
59	22	32.8	20	7	US-11-106-415-188	Sequence 188, App
60	22	32.8	20	7	US-11-106-415-214	Sequence 214, App
61	22	32.8	20	7	US-11-106-415-288	Sequence 288, App
62	22	32.8	20	7	US-10-467-657-8643	Sequence 8643, App
63	21	31.3	9	6	US-10-859-643-570	Sequence 570, App1
64	21	31.3	9	7	US-11-097-912-570	Sequence 570, App1
65	21	31.3	9	7	US-11-097-912-570	Sequence 570, App1
66	21	31.3	10	6	US-10-859-643-167	Sequence 167, App
67	21	31.3	10	7	US-11-097-912-167	Sequence 167, App
68	21	31.3	10	7	US-11-119-098-38	Sequence 38, App1
69	21	31.3	12	7	US-11-016-706-45	Sequence 45, App1
70	21	31.3	13	6	US-10-511-559-272	Sequence 272, App
71	21	31.3	13	6	US-10-511-559-272	Sequence 272, App
72	21	31.3	13	6	US-10-511-559-273	Sequence 273, App
73	21	31.3	13	6	US-10-511-559-274	Sequence 274, App
74	21	31.3	13	6	US-10-511-559-845	Sequence 845, App
75	21	31.3	13	7	US-11-016-706-7	Sequence 7, App11
76	21	31.3	14	6	US-10-929-988-451	Sequence 451, App1
77	21	31.3	15	7	US-11-106-932-45	Sequence 45, App1
78	21	31.3	15	7	US-11-145-703-234	Sequence 234, App
79	21	31.3	15	7	US-11-041-893-275	Sequence 275, App
80	21	31.3	15	7	US-11-041-893-275	Sequence 275, App
81	21	31.3	15	7	US-10-939-890-99	Sequence 99, App1
82	21	31.3	19	6	US-10-939-890-217	Sequence 217, App
83	21	31.3	19	6	US-11-054-515-2956	Sequence 2956, App
84	21	31.3	20	6	US-10-997-201A-31	Sequence 31, App1
85	21	31.3	20	7	US-11-041-893-264	Sequence 264, App
86	20	29.9	8	7	US-11-045-024-2757	Sequence 2757, App
87	20	29.9	8	7	US-11-045-024-8435	Sequence 8435, App
88	20	29.9	8	7	US-11-045-024-10862	Sequence 10862, App
89	20	29.9	9	6	US-10-986-501-241	Sequence 241, App
90	20	29.9	9	7	US-11-010-748A-260	Sequence 260, App
91	20	29.9	9	7	US-11-045-024-37	Sequence 37, App1
92	20	29.9	9	7	US-11-045-024-38	Sequence 38, App1

99 20 29.9 9 7 US-11-045-024-2802  
100 20 29.9 9 7 US-11-045-024-6167

Sequence 2802, Ap  
Sequence 6167, Ap

## ALIGNMENTS

## RESULT 1

US-10-939-890-220  
Sequence 220, Application US/10939890  
Publication No. US20050250700A1

GENERAL INFORMATION:

APPLICANT: Sato, Aaron K.

APPLICANT: Sexton, Daniel J.

APPLICANT: Dransfield, Daniel T.

APPLICANT: Lachner, Robert C.

APPLICANT: Arbogast, Christophe

APPLICANT: Bussat, Philippe

APPLICANT: Fan, Hong

APPLICANT: Khurana, Sudha

APPLICANT: Linder, Karen E.

APPLICANT: Marinelli, Edmund R.

APPLICANT: Nanjappan, Palaniasappa

APPLICANT: Nunn, Adrian D.

APPLICANT: Pillai, Radhakrishna

APPLICANT: Pochon, Sibylle

APPLICANT: Ramalingam, Kondaredthar

APPLICANT: Shrivastava, Ajay

APPLICANT: Song, Bo

APPLICANT: Swenson, Rolf E.

APPLICANT: Von Wronski, Mathew A.

FILE REFERENCE: D0617.70014US00

CURRENT APPLICATION NUMBER: US/10/939,890

CURRENT FILING DATE: 2004-09-13

PRIOR APPLICATION NUMBER: US 10/661,156

PRIOR FILING DATE: 2003-09-11

PRIOR APPLICATION NUMBER: US 10/382,082

PRIOR FILING DATE: 2003-03-03

PRIOR APPLICATION NUMBER: PCT/US03/06731

PRIOR FILING DATE: 2003-03-03

PRIOR APPLICATION NUMBER: US 60/440,411

PRIOR FILING DATE: 2003-01-15

PRIOR APPLICATION NUMBER: US 60/360,851

PRIOR FILING DATE: 2002-03-01

NUMBER OF SEQ ID NOS: 883

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 220

LENGTH: 19

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Library Isolate

US-10-939-890-220

Query Match

Best Local Similarity 44.8%; Score 30; DB 6; Length 19;

Matches 5; Conservativity 100.0%; Pred. No. 7.9; 0; Indels 0; Gaps 0;

Qy 4 NSPEC 8

Db 12 NSPEC 16

RESULT 2

US-10-517-784-11

Sequence 11, Application US/10517784

Publication No. US20060003315A1

GENERAL INFORMATION:

APPLICANT: GROSS, Gideon

APPLICANT: MARGALIT, Alon

FILE REFERENCE: D0617.70014US00

CURRENT APPLICATION NUMBER: US/10/939,890

CURRENT FILING DATE: 2004-09-13

PRIOR APPLICATION NUMBER: US 10/661,156

PRIOR FILING DATE: 2003-09-11

PRIOR APPLICATION NUMBER: US 10/382,082

PRIOR FILING DATE: 2003-03-03

PRIOR APPLICATION NUMBER: PCT/US03/06731

PRIOR FILING DATE: 2003-03-03

PRIOR APPLICATION NUMBER: US 60/440,411

PRIOR FILING DATE: 2003-01-15

PRIOR APPLICATION NUMBER: US 60/360,851

PRIOR FILING DATE: 2002-03-01

NUMBER OF SEQ ID NOS: 883

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 220

LENGTH: 19

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Library Isolate

US-10-939-890-220

Query Match

Best Local Similarity 44.8%; Score 30; DB 6; Length 19;

Matches 5; Conservativity 100.0%; Pred. No. 7.9; 0; Indels 0; Gaps 0;

Qy 4 NSPEC 8

Db 12 NSPEC 16

RESULT 3

US-10-986-501-340

Sequence 340, Application US/10986501

Publication No. US20050244845A1

GENERAL INFORMATION:

APPLICANT: Ruben et al.

FILE REFERENCE: P2013P2C1

CURRENT APPLICATION NUMBER: US/10/986,501

CURRENT FILING DATE: 2004-11-12

PRIOR APPLICATION NUMBER: US/10/621,363

PRIOR FILING DATE: 2003-07-18

PRIOR APPLICATION NUMBER: 09/969,730

PRIOR FILING DATE: 2001-10-06

PRIOR APPLICATION NUMBER: 09/774,639

PRIOR FILING DATE: 2001-02-01

PRIOR APPLICATION NUMBER: 60/238,291

PRIOR FILING DATE: 2000-10-06

PRIOR APPLICATION NUMBER: 09/244,112

PRIOR FILING DATE: 1999-02-04

PRIOR APPLICATION NUMBER: PCT/US98/16235

PRIOR FILING DATE: 1998-08-04

PRIOR APPLICATION NUMBER: 60/056,371

PRIOR FILING DATE: 1997-08-19

PRIOR APPLICATION NUMBER: 60/056,732

PRIOR FILING DATE: 1997-08-19

PRIOR APPLICATION NUMBER: 60/056,366

PRIOR FILING DATE: 1997-08-19

PRIOR APPLICATION NUMBER: 60/056,364

PRIOR FILING DATE: 1997-08-19

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 373

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 340

LENGTH: 14

TYPE: PRT

ORGANISM: Homo sapiens

US-10-986-501-340

Query Match

Best Local Similarity 41.8%; Score 28; DB 6; Length 14;

Matches 5; Conservativity 55.6%; Pred. No. 14; 0; Indels 0; Gaps 0;

Qy 3 KNSPEC 11

Db 3 KNSPEC 11

RESULT 4

US-10-517-784-11

Sequence 11, Application US/10517784

Publication No. US20060003315A1

GENERAL INFORMATION:

APPLICANT: GROSS, Gideon

APPLICANT: MARGALIT, Alon

FILE REFERENCE: D0617.70014US00

CURRENT APPLICATION NUMBER: US/10/939,890

CURRENT FILING DATE: 2004-09-13

PRIOR APPLICATION NUMBER: US 10/661,156

PRIOR FILING DATE: 2003-09-11

PRIOR APPLICATION NUMBER: US 10/382,082

PRIOR FILING DATE: 2003-03-03

PRIOR APPLICATION NUMBER: PCT/US03/06731

PRIOR FILING DATE: 2003-03-03

PRIOR APPLICATION NUMBER: US 60/440,411

PRIOR FILING DATE: 2003-01-15

PRIOR APPLICATION NUMBER: US 60/360,851

PRIOR FILING DATE: 2002-03-01

NUMBER OF SEQ ID NOS: 883

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 220

LENGTH: 19

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Library Isolate

US-10-939-890-220

Query Match

Best Local Similarity 44.8%; Score 30; DB 6; Length 19;

Matches 5; Conservativity 100.0%; Pred. No. 7.9; 0; Indels 0; Gaps 0;

Qy 4 NSPEC 8

Db 12 NSPEC 16



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RESULT 4
US-10-503-575-200
; Sequence 200, Application US/10503575
; Publication No. US20050244823A1
; GENERAL INFORMATION:
; APPLICANT: Drifffhout, Jan Wouter
; APPLICANT: van Veele, Petrus Antonius
; APPLICANT: Koning, Frits
; TITLE OF INVENTION: NOVEL EPITOPES FOR CELIAC DISEASE AND AUTOIMMUNE DISEASES, METHOD
; FILE REFERENCE: 2799/72843-PCT-US
; CURRENT APPLICATION NUMBER: US/10/503,575
; CURRENT FILING DATE: 2004-08-04
; PRIOR APPLICATION NUMBER: PCT/NL03/00077
; PRIOR FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: EP 02075456.0
; PRIOR FILING DATE: 2002-02-04
; NUMBER OF SEQ ID NOS: 340
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 200
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-503-575-200

Query Match      40.3%; Score 27; DB 6; Length 19;
Best Local Similarity 50.0%; Pred. No. 29;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      5 SPECIFICP 12
DB      12 SYECLCKP 19

RESULT 5
US-10-986-501-344
; Sequence 344, Application US/10986501
; Publication No. US20050244845A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 90 Human Secreted Proteins
; FILE REFERENCE: P2013P2C1
; CURRENT APPLICATION NUMBER: US/10/986,501
; CURRENT FILING DATE: 2004-11-12
; PRIOR APPLICATION NUMBER: US/10/621,363
; PRIOR FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: 09/969,730
; PRIOR FILING DATE: 2001-10-06
; PRIOR APPLICATION NUMBER: 09/774,639
; PRIOR FILING DATE: 2001-02-01
; PRIOR APPLICATION NUMBER: 60/238,291
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 09/244,112
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: PCT/US98/16235
; PRIOR FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: 60/056,371
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,732
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,366
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,364
; Remaining Prior Application data removed - See file Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 373
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 344
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-986-501-344
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Query Match      38.8%; Score 26; DB 6; Length 16;
Best Local Similarity 50.0%; Pred. No. 38;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY      3 KNSPECILGP 12
DB      4 KTRPACILVP 13

RESULT 6
US-11-033-039-1313
; Sequence 1313, Application US/11033039
; Publication No. US20060002947A1
; GENERAL INFORMATION:
; APPLICANT: HUMPHREYS, ROBERT
; APPLICANT: XU, MINZHEN
; TITLE OF INVENTION: LI-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
; FILE REFERENCE: RH-2017U501
; CURRENT APPLICATION NUMBER: US/11/033,039
; CURRENT FILING DATE: 2005-01-11
; PRIOR APPLICATION NUMBER: 10/245,871
; PRIOR FILING DATE: 2002-09-17
; PRIOR APPLICATION NUMBER: 10/197,000
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: 09/396,813
; PRIOR FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 1452
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1313
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; NAME/KEY: MOD_RES
; LOCATION: (5)..(5)
; OTHER INFORMATION: Ava
US-11-033-039-1313

Query Match      38.8%; Score 26; DB 7; Length 18;
Best Local Similarity 33.3%; Pred. No. 43;
Matches 4; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY      1 DEKNSPECILGP 12
DB      6 DIARTFKPVIGP 17

RESULT 7
US-10-503-575-163
; Sequence 163, Application US/10503575
; Publication No. US20050244823A1
; GENERAL INFORMATION:
; APPLICANT: Drifffhout, Jan Wouter
; APPLICANT: van Veele, Petrus Antonius
; APPLICANT: Koning, Frits
; TITLE OF INVENTION: NOVEL EPITOPES FOR CELIAC DISEASE AND AUTOIMMUNE DISEASES, METHOD
; FILE REFERENCE: 2799/72843-PCT-US
; CURRENT APPLICATION NUMBER: US/10/503,575
; CURRENT FILING DATE: 2004-08-04
; PRIOR APPLICATION NUMBER: PCT/NL03/00077
; PRIOR FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: EP 02075456.0
; PRIOR FILING DATE: 2002-02-04
; NUMBER OF SEQ ID NOS: 340
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 163
; LENGTH: 19
; TYPE: PRT
```

/ ORGANISM: Homo sapiens  
US-10-503-575-163

Query Match 38.8%; Score 26; DB 6; Length 19;  
Best Local Similarity 33.3%; Pred. No. 45;  
Matches 4; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 DEKNSPECILGP 12  
| : : : :  
Db 4 DDINGQSLXGP 15

RESULT 8  
US-10-511-559-965

/ Sequence 965, Application US/10511559  
/ Publication No. US20050256304A1  
/ GENERAL INFORMATION:

/ APPLICANT: JONES, Tim

/ APPLICANT: BAKER, Matthew

/ APPLICANT: CARR, Francis, J.

/ TITLE OF INVENTION: MODIFIED FACTOR VIII

/ FILE REFERENCE: MER-133

/ CURRENT APPLICATION NUMBER: US/10/511,559

/ CURRENT FILING DATE: 2004-10-15

/ PRIOR APPLICATION NUMBER: PCT/EP03/04063

/ PRIOR FILING DATE: 2003-04-17

/ PRIOR APPLICATION NUMBER: EP 02008712.8

/ PRIOR FILING DATE: 2002-04-18

/ PRIOR APPLICATION NUMBER: EP 03006554.4

/ PRIOR FILING DATE: 2003-03-24

/ NUMBER OF SEQ ID NOS: 1147

/ SOFTWARE: FastSeq for Windows Version 4.0

/ SEQ ID NO 965

/ LENGTH: 13

/ TYPE: PRT

/ ORGANISM: Artificial Sequence

/ FEATURE:

/ OTHER INFORMATION: Potential Epitope of human Factor VIII

US-10-511-559-965

Query Match 35.8%; Score 24; DB 6; Length 13;  
Best Local Similarity 60.0%; Pred. No. 74;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 7 ECLIG 11  
| : : : :  
Db 7 ECLIG 11

RESULT 9  
US-10-511-559-966

/ Sequence 966, Application US/10511559  
/ Publication No. US20050256304A1  
/ GENERAL INFORMATION:

/ APPLICANT: JONES, Tim

/ APPLICANT: BAKER, Matthew

/ APPLICANT: CARR, Francis, J.

/ TITLE OF INVENTION: MODIFIED FACTOR VIII

/ FILE REFERENCE: MER-133

/ CURRENT APPLICATION NUMBER: US/10/511,559

/ CURRENT FILING DATE: 2004-10-15

/ PRIOR APPLICATION NUMBER: PCT/EP03/04063

/ PRIOR FILING DATE: 2003-04-17

/ PRIOR APPLICATION NUMBER: EP 02008712.8

/ PRIOR FILING DATE: 2002-04-18

/ PRIOR APPLICATION NUMBER: EP 03006554.4

/ PRIOR FILING DATE: 2003-03-24

/ NUMBER OF SEQ ID NOS: 1147

/ SOFTWARE: FastSeq for Windows Version 4.0

/ SEQ ID NO 966

/ LENGTH: 13

/ TYPE: PRT

/ ORGANISM: Artificial Sequence

/ FEATURE:  
/ OTHER INFORMATION: Potential Epitope of human Factor VIII  
US-10-511-559-966

Query Match 35.8%; Score 24; DB 6; Length 13;  
Best Local Similarity 60.0%; Pred. No. 74;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 7 ECLIG 11  
| : : : :  
Db 6 ECLIG 10

RESULT 10  
US-10-511-559-967

/ Sequence 967, Application US/10511559  
/ Publication No. US20050256304A1  
/ GENERAL INFORMATION:

/ APPLICANT: JONES, Tim

/ APPLICANT: BAKER, Matthew

/ APPLICANT: CARR, Francis, J.

/ TITLE OF INVENTION: MODIFIED FACTOR VIII

/ FILE REFERENCE: MER-133

/ CURRENT APPLICATION NUMBER: US/10/511,559

/ CURRENT FILING DATE: 2004-10-15

/ PRIOR APPLICATION NUMBER: PCT/EP03/04063

/ PRIOR FILING DATE: 2003-04-17

/ PRIOR APPLICATION NUMBER: EP 02008712.8

/ PRIOR FILING DATE: 2002-04-18

/ PRIOR APPLICATION NUMBER: EP 03006554.4

/ PRIOR FILING DATE: 2003-03-24

/ NUMBER OF SEQ ID NOS: 1147

/ SOFTWARE: FastSeq for Windows Version 4.0

/ SEQ ID NO 967

/ LENGTH: 13

/ TYPE: PRT

/ ORGANISM: Artificial Sequence

/ FEATURE:

/ OTHER INFORMATION: Potential Epitope of human Factor VIII

US-10-511-559-967

Query Match 35.8%; Score 24; DB 6; Length 13;  
Best Local Similarity 60.0%; Pred. No. 74;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 7 ECLIG 11  
| : : : :  
Db 4 ECLIG 8

RESULT 11  
US-10-511-559-968

/ Sequence 968, Application US/10511559  
/ Publication No. US20050256304A1  
/ GENERAL INFORMATION:

/ APPLICANT: JONES, Tim

/ APPLICANT: BAKER, Matthew

/ APPLICANT: CARR, Francis, J.

/ TITLE OF INVENTION: MODIFIED FACTOR VIII

/ FILE REFERENCE: MER-133

/ CURRENT APPLICATION NUMBER: US/10/511,559

/ CURRENT FILING DATE: 2004-10-15

/ PRIOR APPLICATION NUMBER: PCT/EP03/04063

/ PRIOR FILING DATE: 2003-04-17

/ PRIOR APPLICATION NUMBER: EP 02008712.8

/ PRIOR FILING DATE: 2002-04-18

/ PRIOR APPLICATION NUMBER: EP 03006554.4

/ PRIOR FILING DATE: 2003-03-24

/ NUMBER OF SEQ ID NOS: 1147

/ SOFTWARE: FastSeq for Windows Version 4.0

/ SEQ ID NO 968

/ LENGTH: 13

/ TYPE: PRT

/ ORGANISM: Artificial Sequence

ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Potential Epitope of human Factor VIII  
US-10-511-559-968

Query Match 35.8%; Score 24; DB 6; Length 13;  
Best Local Similarity 60.0%; Pred. No. 74;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 7 ECLIG 11  
DB 1 ECLIG 5

RESULT 12  
US-10-467-657-8750  
Sequence 8750, Application US/10467657  
Publication No. US20050260581A1  
GENERAL INFORMATION:  
APPLICANT: CHIRON SPA  
APPLICANT: FONTANA Maria Rita  
APPLICANT: PIZZA Mariagrazia  
APPLICANT: MONACI Elisabetta  
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS  
FILE REFERENCE:  
CURRENT APPLICATION NUMBER: US/10/467,657  
CURRENT FILING DATE: 2003-08-11  
PRIOR APPLICATION NUMBER: GB-0103424.8  
PRIOR FILING DATE: 2001-02-12  
NUMBER OF SEQ ID NOS: 9218  
SOFTWARE: SeqMn99, version 1.04  
SEQ ID NO 8750  
LENGTH: 16  
TYPE: PRT  
ORGANISM: Neisseria gonorrhoeae  
US-10-467-657-8750

Query Match 35.8%; Score 24; DB 6; Length 16;  
Best Local Similarity 42.9%; Pred. No. 91;  
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 NSPECIL 10  
DB 1 NDFACLI 7

RESULT 13  
US-11-090-497-22  
Sequence 22, Application US/11090497  
Publication No. US2005028263A1  
GENERAL INFORMATION:  
APPLICANT: Large Scale Biology Corporation  
TITLE OF INVENTION: FLEXIBLE VACCINE ASSEMBLY AND VACCINE DELIVERY PLATFORM  
FILE REFERENCE: N8630  
CURRENT APPLICATION NUMBER: US/11/090,497  
CURRENT FILING DATE: 2005-03-25  
PRIOR APPLICATION NUMBER: 60/386,921  
PRIOR FILING DATE: 2002-06-07  
PRIOR APPLICATION NUMBER: 60/407,795  
PRIOR FILING DATE: 2002-09-03  
NUMBER OF SEQ ID NOS: 22  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 22  
LENGTH: 17  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Created from Seq ID No: 10 inserted into TMV  
US-11-090-497-22

Query Match 35.1%; Score 23.5; DB 7; Length 17;  
Best Local Similarity 46.2%; Pred. No. 1.2e+02;

Matches 6; Conservative 2; Mismatches 4; Indels 1; Gaps 1;

QY 1 DERNS-FECLIGP 12  
DB 3 DERNSPFTTLGAP 15

RESULT 14  
US-10-517-784-37  
Sequence 37, Application US/10517784  
Publication No. US20060003315A1  
GENERAL INFORMATION:  
APPLICANT: GROSS, Gideon  
APPLICANT: MARGALIT, Alon  
TITLE OF INVENTION: MEMBRANE-ANCHORED BETA-2 MICROGLOBULIN COVALENTLY LINKED TO MHC  
FILE REFERENCE: GAVISH-004 US  
CURRENT APPLICATION NUMBER: US/10/517,784  
CURRENT FILING DATE: 2004-12-13  
PRIOR APPLICATION NUMBER: US 60/388,273  
PRIOR FILING DATE: 2002-06-12  
PRIOR APPLICATION NUMBER: PCT/IL03/00501  
PRIOR FILING DATE: 2003-06-12  
NUMBER OF SEQ ID NOS: 64  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 37  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic  
US-10-517-784-37

Query Match 34.3%; Score 23; DB 6; Length 9;  
Best Local Similarity 80.0%; Pred. No. 5.5e+04;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 KNSPF 7  
DB 4 RNSPF 8

RESULT 15  
US-11-208-541-1  
Sequence 1, Application US/11208541  
Publication No. US20050287160A1  
GENERAL INFORMATION:  
APPLICANT: ITOH, Kyogo  
APPLICANT: HARADA, Mamoru  
TITLE OF INVENTION: HLA-A\*24 Binding Peptides of Enhancer of Zeste Homolog 2  
FILE REFERENCE: 541818  
CURRENT APPLICATION NUMBER: US/11/208,541  
CURRENT FILING DATE: 2005-08-23  
NUMBER OF SEQ ID NOS: 18  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 1  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Artificial  
FEATURE:  
OTHER INFORMATION: EZH2 291-299  
US-11-208-541-1

Query Match 34.3%; Score 23; DB 7; Length 9;  
Best Local Similarity 42.9%; Pred. No. 5.5e+04;  
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 6 FECLIGP 12  
DB 2 YDCFLHP 8

RESULT 16

US-10-859-643-533  
; Sequence 533, Application US/10859643  
; Publication No. US2006000293A1  
; GENERAL INFORMATION:  
; APPLICANT: Chaillita-Eld, Pia M.  
; APPLICANT: Raitano, Arthur B.  
; APPLICANT: Paris, Mary  
; APPLICANT: Hubert, Rene S.  
; APPLICANT: Morrison, Karen Jane Meyrick  
; APPLICANT: Jakobovits, Aya  
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein  
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of  
; FILE REFERENCE: 511582006203  
; CURRENT APPLICATION NUMBER: US/10/859,643  
; PRIOR FILING DATE: 2004-06-02  
; PRIOR APPLICATION NUMBER: US 10/005,480  
; NUMBER OF SEQ ID NOS: 765  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 533  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-859-643-533

Query Match 34.3% Score 23; DB 6; Length 10;  
Best Local Similarity 44.4% Pred. No. 88;  
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 EKNSPECIL 10  
DB 2 QKNVDHCLL 10

RESULT 17  
US-10-859-643-635  
; Sequence 635, Application US/10859643  
; Publication No. US2006000293A1  
; GENERAL INFORMATION:  
; APPLICANT: Chaillita-Eld, Pia M.  
; APPLICANT: Raitano, Arthur B.  
; APPLICANT: Paris, Mary  
; APPLICANT: Hubert, Rene S.  
; APPLICANT: Morrison, Karen Jane Meyrick  
; APPLICANT: Jakobovits, Aya  
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein  
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of  
; FILE REFERENCE: 511582006203  
; CURRENT APPLICATION NUMBER: US/10/859,643  
; PRIOR FILING DATE: 2004-06-02  
; PRIOR APPLICATION NUMBER: US 10/005,480  
; NUMBER OF SEQ ID NOS: 765  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 635  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-859-643-635

Query Match 34.3% Score 23; DB 6; Length 10;  
Best Local Similarity 44.4% Pred. No. 88;  
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 EKNSPECIL 10  
DB 2 QKNVDHCLL 10

RESULT 18  
US-11-097-864-533

; Sequence 533, Application US/11097864  
; Publication No. US20050265924A1  
; GENERAL INFORMATION:  
; APPLICANT: Chaillita-Eld, Pia M.  
; APPLICANT: Raitano, Arthur B.  
; APPLICANT: Paris, Mary  
; APPLICANT: Hubert, Rene S.  
; APPLICANT: Morrison, Karen Jane Meyrick  
; APPLICANT: Jakobovits, Aya  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 161P2F10B  
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF CANCER  
; FILE REFERENCE: 511582006205  
; CURRENT APPLICATION NUMBER: US/11/097,864  
; PRIOR FILING DATE: 2005-04-01  
; PRIOR APPLICATION NUMBER: US 10/062,109  
; PRIOR FILING DATE: 2002-01-31  
; PRIOR APPLICATION NUMBER: US 10/005,480  
; NUMBER OF SEQ ID NOS: 765  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 533  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-11-097-864-533

Query Match 34.3% Score 23; DB 7; Length 10;  
Best Local Similarity 44.4% Pred. No. 88;  
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 EKNSPECIL 10  
DB 2 QKNVDHCLL 10

RESULT 19  
US-11-097-864-635  
; Sequence 635, Application US/11097864  
; Publication No. US20050265924A1  
; GENERAL INFORMATION:  
; APPLICANT: Chaillita-Eld, Pia M.  
; APPLICANT: Raitano, Arthur B.  
; APPLICANT: Paris, Mary  
; APPLICANT: Hubert, Rene S.  
; APPLICANT: Morrison, Karen Jane Meyrick  
; APPLICANT: Jakobovits, Aya  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 161P2F10B  
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF CANCER  
; FILE REFERENCE: 511582006205  
; CURRENT APPLICATION NUMBER: US/11/097,864  
; PRIOR FILING DATE: 2005-04-01  
; PRIOR APPLICATION NUMBER: US 10/062,109  
; PRIOR FILING DATE: 2002-01-31  
; PRIOR APPLICATION NUMBER: US 10/005,480  
; NUMBER OF SEQ ID NOS: 765  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 635  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-11-097-864-635

Query Match 34.3% Score 23; DB 7; Length 10;  
Best Local Similarity 44.4% Pred. No. 88;  
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 EKNSPECIL 10  
DB 2 QKNVDHCLL 10

RESULT 20

US-11-097-912-533  
 / Sequence 533, Application US/11097912  
 / Publication No. US20050265921A1  
 / GENERAL INFORMATION:  
 / APPLICANT: Chailita-Bld, Pia M.  
 / APPLICANT: Raitano, Arthur B.  
 / APPLICANT: Paris, Mary  
 / APPLICANT: Hubert, Rene S.  
 / APPLICANT: Morrison, Karen Jane Meyrick  
 / APPLICANT: Jakobovits, Aya  
 / TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 161P2P10B  
 / FILE REFERENCE: US/11/097,912  
 / CURRENT FILING DATE: 2005-04-01  
 / PRIOR APPLICATION NUMBER: US 10/062,109  
 / PRIOR FILING DATE: 2002-01-31  
 / PRIOR APPLICATION NUMBER: US 10/005,480  
 / PRIOR FILING DATE: 2001-11-07  
 / NUMBER OF SEQ ID NOS: 765  
 / SOFTWARE: FastSeq for Windows Version 4.0  
 / SEQ ID NO 533  
 / LENGTH: 10  
 / TYPE: PRT  
 / ORGANISM: Homo Sapien  
 / OTHER INFORMATION: Potential Epitope of human Factor VIII

Query Match 34.3%; Score 23; DB 7; Length 10;  
 Best Local Similarity 44.4%; Pred. No. 88;  
 Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 EKNSPECIL 10  
 Db 2 QKNVDHCLL 10

RESULT 21  
 US-11-097-912-635  
 / Sequence 635, Application US/11097912  
 / Publication No. US20050265921A1  
 / GENERAL INFORMATION:  
 / APPLICANT: Chailita-Bld, Pia M.  
 / APPLICANT: Raitano, Arthur B.  
 / APPLICANT: Paris, Mary  
 / APPLICANT: Hubert, Rene S.  
 / APPLICANT: Morrison, Karen Jane Meyrick  
 / APPLICANT: Jakobovits, Aya  
 / TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 161P2P10B  
 / FILE REFERENCE: US/11/097,912  
 / CURRENT FILING DATE: 2005-04-01  
 / PRIOR APPLICATION NUMBER: US 10/062,109  
 / PRIOR FILING DATE: 2002-01-31  
 / PRIOR APPLICATION NUMBER: US 10/005,480  
 / PRIOR FILING DATE: 2001-11-07  
 / NUMBER OF SEQ ID NOS: 765  
 / SOFTWARE: FastSeq for Windows Version 4.0  
 / SEQ ID NO 635  
 / LENGTH: 10  
 / TYPE: PRT  
 / ORGANISM: Homo Sapien  
 / OTHER INFORMATION: Potential Epitope of human Factor VIII

Query Match 34.3%; Score 23; DB 7; Length 10;  
 Best Local Similarity 44.4%; Pred. No. 88;  
 Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 EKNSPECIL 10  
 Db 2 QKNVDHCLL 10

RESULT 22  
 US-10-511-559-883  
 / Sequence 883, Application US/10511559  
 / Publication No. US20050256304A1  
 / GENERAL INFORMATION:  
 / APPLICANT: JONES, Tim  
 / APPLICANT: BAKER, Matthew  
 / APPLICANT: Carr, Francis, J.  
 / TITLE OF INVENTION: MODIFIED FACTOR VIII  
 / FILE REFERENCE: MER-133  
 / CURRENT APPLICATION NUMBER: US/10/511,559  
 / CURRENT FILING DATE: 2004-10-15  
 / PRIOR APPLICATION NUMBER: PCT/EP03/04063  
 / PRIOR FILING DATE: 2003-04-17  
 / PRIOR APPLICATION NUMBER: EP 02008712.8  
 / PRIOR FILING DATE: 2002-04-18  
 / PRIOR APPLICATION NUMBER: EP 03006554.4  
 / PRIOR FILING DATE: 2003-03-24  
 / NUMBER OF SEQ ID NOS: 1147  
 / SOFTWARE: FastSeq for Windows Version 4.0  
 / SEQ ID NO 883  
 / LENGTH: 13  
 / TYPE: PRT  
 / ORGANISM: Artificial Sequence  
 / FEATURE:  
 / OTHER INFORMATION: Potential Epitope of human Factor VIII

Query Match 34.3%; Score 23; DB 6; Length 13;  
 Best Local Similarity 50.0%; Pred. No. 11e+02;  
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 KNSFEC 8  
 Db 7 KDEPDC 12

RESULT 23  
 US-10-511-559-884  
 / Sequence 884, Application US/10511559  
 / Publication No. US20050256304A1  
 / GENERAL INFORMATION:  
 / APPLICANT: JONES, Tim  
 / APPLICANT: BAKER, Matthew  
 / APPLICANT: Carr, Francis, J.  
 / TITLE OF INVENTION: MODIFIED FACTOR VIII  
 / FILE REFERENCE: MER-133  
 / CURRENT APPLICATION NUMBER: US/10/511,559  
 / CURRENT FILING DATE: 2004-10-15  
 / PRIOR APPLICATION NUMBER: PCT/EP03/04063  
 / PRIOR FILING DATE: 2003-04-17  
 / PRIOR APPLICATION NUMBER: EP 02008712.8  
 / PRIOR FILING DATE: 2002-04-18  
 / PRIOR APPLICATION NUMBER: EP 03006554.4  
 / PRIOR FILING DATE: 2003-03-24  
 / NUMBER OF SEQ ID NOS: 1147  
 / SOFTWARE: FastSeq for Windows Version 4.0  
 / SEQ ID NO 884  
 / LENGTH: 13  
 / TYPE: PRT  
 / ORGANISM: Artificial Sequence  
 / FEATURE:  
 / OTHER INFORMATION: Potential Epitope of human Factor VIII

Query Match 34.3%; Score 23; DB 6; Length 13;  
 Best Local Similarity 50.0%; Pred. No. 1.1e+02;  
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 KNSFEC 8  
 Db 7 KDEPDC 12

```
RESULT 24
US-10-939-890-79
; Sequence 79, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussac, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappa, Palanappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylla
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
; FILE REFERENCE: D0617.70014US00
; CURRENT APPLICATION NUMBER: US/10/939,890
; CURRENT FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: US 10/661,156
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 10/382,082
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 79
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Library Isolate
; US-10-939-890-79

Query Match      34.3% Score 23; DB 6; Length 14;
Best Local Similarity 42.9%; Pred. No. 1.2e+02;
Matches 3; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY      4 NSPECIL 10
       :::|||:
DB      7 DAMECIM 13

RESULT 25
US-11-054-515-2765
; Sequence 2765, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS23P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
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; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2765
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-054-515-2765

Query Match      34.3% Score 23; DB 7; Length 15;
Best Local Similarity 80.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      3 KNSPE 7
       :::||:
DB      10 KNAPE 14

RESULT 26
US-10-939-890-349
; Sequence 349, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussac, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappa, Palanappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylla
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
; FILE REFERENCE: D0617.70014US00
; CURRENT APPLICATION NUMBER: US/10/939,890
; CURRENT FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: US 10/661,156
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 10/382,082
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 349
```

LENGTH: 16  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURES:  
OTHER INFORMATION: KDR or KDR/VEGF Complex Binding Polypeptide  
US-10-939-890-349

Query Match 34.3%; Score 23; DB 6; Length 16;  
Best Local Similarity 30.0%; Pred. No. 1.4e+02;  
Matches 3; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 2 EKNSFCLIG 11  
|::|::|  
Db 4 EEDWYCMIG 13

RESULT 27  
US-10-939-890-825  
Sequence 825, Application US/10939890  
Publication No. US20050250700A1  
GENERAL INFORMATION:  
APPLICANT: Sato, Aaron K.  
APPLICANT: Sexton, Daniel J.  
APPLICANT: Dransfield, Daniel T.  
APPLICANT: Ladner, Robert C.  
APPLICANT: Arbogast, Christophe  
APPLICANT: Bueset, Philippe  
APPLICANT: Fan, Hong  
APPLICANT: Khurana, Sucha  
APPLICANT: Linder, Karen B.  
APPLICANT: Marinelli, Edmund R.  
APPLICANT: Nanjappa, Palaniappa  
APPLICANT: Nunn, Adrian D.  
APPLICANT: Pillai, Radhakrishna  
APPLICANT: Pochon, Sibylla  
APPLICANT: Ramalingam, Kondaredtalar  
APPLICANT: Shrivastava, Ajay  
APPLICANT: Song, Bo  
APPLICANT: Swenson, Rolf E.  
APPLICANT: Von Wronski, Mathew A.  
TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES  
FILE REFERENCE: D0617.70014US00  
CURRENT APPLICATION NUMBER: US/10/939,890  
FILING DATE: 2004-09-13  
PRIOR APPLICATION NUMBER: US 10/661,156  
PRIOR FILING DATE: 2003-09-11  
PRIOR APPLICATION NUMBER: US 10/382,082  
PRIOR FILING DATE: 2003-03-03  
PRIOR APPLICATION NUMBER: PCT/US03/06731  
PRIOR FILING DATE: 2003-03-03  
PRIOR APPLICATION NUMBER: US 60/440,411  
PRIOR FILING DATE: 2003-01-15  
PRIOR APPLICATION NUMBER: US 60/360,851  
PRIOR FILING DATE: 2002-03-01  
NUMBER OF SEQ ID NOS: 883  
SOFTWARE: PasteSeq for Windows Version 4.0  
SEQ ID NO 825  
LENGTH: 16  
TYPE: PRT  
ORGANISM: Artificial sequence  
FEATURES:  
OTHER INFORMATION: Synthetic peptide  
NAME/KEY: MOD\_RES  
LOCATION: (1)-(1)  
OTHER INFORMATION: ACETYLATION  
FEATURES:  
NAME/KEY: MOD\_RES  
LOCATION: (16)-(16)  
OTHER INFORMATION: Lys residue modified with Biotin JJ spacer linker  
US-10-939-890-825  
Query Match 34.3%; Score 23; DB 6; Length 16;

Best Local Similarity 30.0%; Pred. No. 1.4e+02;  
Matches 3; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 2 EKNSFCLIG 11  
|::|::|  
Db 4 EEDWYCMIG 13

RESULT 28  
US-10-834-397-207  
Sequence 207, Application US/10834397  
Publication No. US20060003334A1  
GENERAL INFORMATION:  
APPLICANT: Knappik, Achim  
APPLICANT: Pack, Peter  
APPLICANT: Ilag, VJC  
APPLICANT: Ge, Laming  
APPLICANT: Moroney, Simon  
APPLICANT: Plueckhuhn, Andreas  
TITLE OF INVENTION: Protein/(poly)peptide libraries  
NUMBER OF SEQUENCES: 373  
CORRESPONDENCE ADDRESS:  
ADDRESSER: James F. Haley, Jr., Esq. c/o Fish & Neave  
STREET: 1251 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10021  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
OPERATING SYSTEM: IBM PC compatible  
SOFTWARE: Patent Release #1.0, Version #1.30 (BPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/834,397  
FILING DATE: 29-Apr-2004  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/490,324  
FILING DATE: 24-Jan-2000  
APPLICATION NUMBER: US/09/025,769  
FILING DATE: 18-FEB-1998  
APPLICATION NUMBER: EP 95 11 3021.0  
FILING DATE: 18-AUG-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: James F. Haley, Jr., Esq.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: MORPHO/5  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)596-9000  
TELEFAX: (212)596-9090  
INFORMATION FOR SEQ ID NO: 207:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: internal  
SEQUENCE DESCRIPTION: SEQ ID NO: 207:  
US-10-834-397-207  
Query Match 34.3%; Score 23; DB 6; Length 17;  
Best Local Similarity 80.0%; Pred. No. 1.5e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 KNSFE 7  
|::|::|  
Db 11 KNSFD 15

RESULT 29  
US-10-939-890-218  
Sequence 218, Application US/10939890

```
/ Publication No. US20050250700A1
/ GENERAL INFORMATION:
/ APPLICANT: Sato, Aaron K.
/ APPLICANT: Sexton, Daniel J.
/ APPLICANT: Dransfield, Daniel T.
/ APPLICANT: Ladhner, Robert C.
/ APPLICANT: Arbogast, Christophe
/ APPLICANT: Buseat, Philippe
/ APPLICANT: Fan, Hong
/ APPLICANT: Khurana, Sudha
/ APPLICANT: Linder, Karen E.
/ APPLICANT: Marinelli, Edmund R.
/ APPLICANT: Nanjappan, Palanlappa
/ APPLICANT: Nunn, Adrian D.
/ APPLICANT: Pillai, Radhakrishna
/ APPLICANT: Pochon, Sibylle
/ APPLICANT: Ramalingam, Kondareddiar
/ APPLICANT: Shrivastava, Ajay
/ APPLICANT: Swenson, Rolf E.
/ APPLICANT: Von Wronski, Mathew A.
/ TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
/ FILE REFERENCE: D0617.70014US00
/ CURRENT FILING DATE: 2004-09-13
/ PRIOR FILING DATE: 2003-09-11
/ PRIOR APPLICATION NUMBER: US 10/661,156
/ PRIOR FILING DATE: 2003-09-11
/ PRIOR APPLICATION NUMBER: US 10/382,082
/ PRIOR FILING DATE: 2003-03-03
/ PRIOR APPLICATION NUMBER: PCT/US03/06731
/ PRIOR FILING DATE: 2003-03-03
/ PRIOR APPLICATION NUMBER: US 60/440,411
/ PRIOR FILING DATE: 2003-01-15
/ PRIOR APPLICATION NUMBER: US 60/360,851
/ PRIOR FILING DATE: 2002-03-01
/ NUMBER OF SEQ ID NOS: 883
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 218
/ LENGTH: 19
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ OTHER INFORMATION: Library Isolate
US-10-939-890-221
Query Match 34.3%; Score 23; DB 6; Length 19;
Best Local Similarity 50.0%; Pred. No. 1.7e+02;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 6 PCTIG 11
DB 14 PSCVYG 19

RESULT 30
US-10-939-890-221
/ Sequence 221, Application US/10939890
/ Publication No. US20050250700A1
/ GENERAL INFORMATION:
/ APPLICANT: Sato, Aaron K.
/ APPLICANT: Sexton, Daniel J.
/ APPLICANT: Dransfield, Daniel T.
/ APPLICANT: Ladhner, Robert C.
/ APPLICANT: Arbogast, Christophe
/ APPLICANT: Buseat, Philippe
/ APPLICANT: Fan, Hong
/ APPLICANT: Khurana, Sudha
/ APPLICANT: Linder, Karen E.
/ APPLICANT: Marinelli, Edmund R.
/ APPLICANT: Nanjappan, Palanlappa
/ APPLICANT: Nunn, Adrian D.
/ APPLICANT: Pillai, Radhakrishna
/ APPLICANT: Pochon, Sibylle
```

```
/ APPLICANT: Ramalingam, Kondareddiar
/ APPLICANT: Shrivastava, Ajay
/ APPLICANT: Song, Bo
/ APPLICANT: Swenson, Rolf E.
/ APPLICANT: Von Wronski, Mathew A.
/ TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
/ FILE REFERENCE: D0617.70014US00
/ CURRENT FILING DATE: 2004-09-13
/ PRIOR FILING DATE: 2003-09-11
/ PRIOR APPLICATION NUMBER: US 10/661,156
/ PRIOR FILING DATE: 2003-09-11
/ PRIOR APPLICATION NUMBER: US 10/382,082
/ PRIOR FILING DATE: 2003-03-03
/ PRIOR APPLICATION NUMBER: PCT/US03/06731
/ PRIOR FILING DATE: 2002-03-01
/ NUMBER OF SEQ ID NOS: 883
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 221
/ LENGTH: 19
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ OTHER INFORMATION: Library Isolate
US-10-939-890-221
Query Match 34.3%; Score 23; DB 6; Length 19;
Best Local Similarity 50.0%; Pred. No. 1.7e+02;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 6 PCTIG 11
DB 14 PSCVYG 19

RESULT 31
US-10-939-890-348
/ Sequence 348, Application US/10939890
/ Publication No. US20050250700A1
/ GENERAL INFORMATION:
/ APPLICANT: Sato, Aaron K.
/ APPLICANT: Sexton, Daniel J.
/ APPLICANT: Dransfield, Daniel T.
/ APPLICANT: Ladhner, Robert C.
/ APPLICANT: Arbogast, Christophe
/ APPLICANT: Buseat, Philippe
/ APPLICANT: Fan, Hong
/ APPLICANT: Khurana, Sudha
/ APPLICANT: Linder, Karen E.
/ APPLICANT: Marinelli, Edmund R.
/ APPLICANT: Nanjappan, Palanlappa
/ APPLICANT: Nunn, Adrian D.
/ APPLICANT: Pillai, Radhakrishna
/ APPLICANT: Pochon, Sibylle
/ APPLICANT: Ramalingam, Kondareddiar
/ APPLICANT: Shrivastava, Ajay
/ APPLICANT: Song, Bo
/ APPLICANT: Swenson, Rolf E.
/ APPLICANT: Von Wronski, Mathew A.
/ TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
/ FILE REFERENCE: D0617.70014US00
/ CURRENT FILING DATE: 2004-09-13
/ PRIOR FILING DATE: 2003-09-11
/ PRIOR APPLICATION NUMBER: US 10/661,156
/ PRIOR FILING DATE: 2003-09-11
/ PRIOR APPLICATION NUMBER: US 10/382,082
/ PRIOR FILING DATE: 2003-03-03
/ PRIOR APPLICATION NUMBER: PCT/US03/06731
/ PRIOR FILING DATE: 2003-03-03
/ PRIOR APPLICATION NUMBER: US 60/440,411
```



```
/ PRIOR FILING DATE: 2003-01-15
/ PRIOR APPLICATION NUMBER: US 60/360,851
/ PRIOR FILING DATE: 2002-03-01
/ NUMBER OF SEQ ID NOS: 883
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 348
/ LENGTH: 19
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: KDR or KDR/VEGF Complex Binding Polypeptide
US-10-939-890-348

Query Match          34.3%; Score 23; DB 6; Length 19;
Best Local Similarity 30.0%; Pred. No. 1.7e+02;
Matches 3; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY      2 EKNSPCTIG 11
Db      7 EBDWYCMIG 16

RESULT 32
US-10-939-890-824
/ Sequence 824, Application US/10939890
/ Publication No. US20050250700A1
/ GENERAL INFORMATION:
/ APPLICANT: Sato, Aaron K.
/ APPLICANT: Sexton, Daniel J.
/ APPLICANT: Dransfield, Daniel T.
/ APPLICANT: Ladner, Robert C.
/ APPLICANT: Arbogast, Christophe
/ APPLICANT: Bussat, Philippe
/ APPLICANT: Ren, Hong
/ APPLICANT: Knutana, Sudha
/ APPLICANT: Linder, Karen E.
/ APPLICANT: Marinelli, Edmund R.
/ APPLICANT: Nanjappa, Palaniappa
/ APPLICANT: Nunn, Adrian D.
/ APPLICANT: Pillai, Radhakrishna
/ APPLICANT: Pochoen, Sibylle
/ APPLICANT: Ramalingam, Kondaredtlar
/ APPLICANT: Shrivastava, Ajay
/ APPLICANT: Song, Bo
/ APPLICANT: Swenson, Rolf E.
/ APPLICANT: Von Wronski, Matthew A.
/ TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
/ FILE REFERENCE: D0617.70014US00
/ CURRENT APPLICATION NUMBER: US/10/939,890
/ CURRENT FILING DATE: 2004-09-13
/ PRIOR APPLICATION NUMBER: US 10/661,156
/ PRIOR FILING DATE: 2003-09-11
/ PRIOR APPLICATION NUMBER: US 10/382,082
/ PRIOR FILING DATE: 2003-03-03
/ PRIOR APPLICATION NUMBER: PCT/US03/06731
/ PRIOR FILING DATE: 2003-03-03
/ PRIOR APPLICATION NUMBER: US 60/440,411
/ PRIOR FILING DATE: 2003-01-15
/ PRIOR APPLICATION NUMBER: US 60/360,851
/ PRIOR FILING DATE: 2002-03-01
/ NUMBER OF SEQ ID NOS: 883
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 824
/ LENGTH: 19
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Synthetic peptide
/ NAME/KEY: MOD_RES
/ LOCATION: (1)-(1)
/ OTHER INFORMATION: ACETYLTATION
/ FEATURE:
```

```
/ NAME/KEY: MOD_RES
/ LOCATION: (19)-(19)
/ OTHER INFORMATION: Lys residue modified with Biotin JJ spacer linker
US-10-939-890-824

Query Match          34.3%; Score 23; DB 6; Length 19;
Best Local Similarity 30.0%; Pred. No. 1.7e+02;
Matches 3; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY      2 EKNSPCTIG 11
Db      7 EBDWYCMIG 16

RESULT 33
US-11-022-562-188
/ Sequence 188, Application US/11022562
/ Publication No. US20050249742A1
/ GENERAL INFORMATION:
/ APPLICANT: Ruprecht, Ruth M.
/ APPLICANT: Shisong, Jiang
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING
/ TITLE OF INVENTION: A CYTOTOXIC T LYMPHOCYTE IMMUNE RESPONSE
/ FILE REFERENCE: DFN-043CN
/ CURRENT APPLICATION NUMBER: US/11/022,562
/ CURRENT FILING DATE: 2004-12-22
/ PRIOR APPLICATION NUMBER: PCT/US03/20322
/ PRIOR FILING DATE: 2003-06-27
/ PRIOR APPLICATION NUMBER: 60/392718
/ PRIOR FILING DATE: 2002-06-27
/ NUMBER OF SEQ ID NOS: 340
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 188
/ LENGTH: 20
/ TYPE: PRT
/ ORGANISM: Simian Immunodeficiency Virus
US-11-022-562-188

Query Match          34.3%; Score 23; DB 7; Length 20;
Best Local Similarity 66.7%; Pred. No. 1.8e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      2 EKNSPCT 7
Db      13 EKNNYR 18

RESULT 34
US-11-022-562-189
/ Sequence 189, Application US/11022562
/ Publication No. US20050249742A1
/ GENERAL INFORMATION:
/ APPLICANT: Ruprecht, Ruth M.
/ APPLICANT: Shisong, Jiang
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING
/ TITLE OF INVENTION: A CYTOTOXIC T LYMPHOCYTE IMMUNE RESPONSE
/ FILE REFERENCE: DFN-043CN
/ CURRENT APPLICATION NUMBER: US/11/022,562
/ CURRENT FILING DATE: 2004-12-22
/ PRIOR APPLICATION NUMBER: PCT/US03/20322
/ PRIOR FILING DATE: 2003-06-27
/ PRIOR APPLICATION NUMBER: 60/392718
/ PRIOR FILING DATE: 2002-06-27
/ NUMBER OF SEQ ID NOS: 340
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 189
/ LENGTH: 20
/ TYPE: PRT
/ ORGANISM: Simian Immunodeficiency Virus
US-11-022-562-189

Query Match          34.3%; Score 23; DB 7; Length 20;
Best Local Similarity 66.7%; Pred. No. 1.8e+02;
```

Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 2 EKNSPE 7  
Db 3 EKNSMR 8

RESULT 35  
US-10-982-145-38

/ Sequence 38, Application US/10982145  
/ Publication No. US20050272645A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Robert Lehrer  
/ APPLICANT: Alan Maring  
/ APPLICANT: Alexander Cole  
/ APPLICANT: Teresa Hong  
/ TITLE OF INVENTION: Retrocyclins: Antiviral and  
/ FILE REFERENCE: UCLA-001CIP2  
/ CURRENT APPLICATION NUMBER: US/10/982,145  
/ PRIOR FILING DATE: 2004-11-05  
/ PRIOR APPLICATION NUMBER: US03/14106  
/ PRIOR FILING DATE: 2003-05-06  
/ PRIOR APPLICATION NUMBER: 10/141,645  
/ PRIOR FILING DATE: 2002-05-06  
/ PRIOR APPLICATION NUMBER: US02/12353  
/ PRIOR FILING DATE: 2002-04-18  
/ PRIOR APPLICATION NUMBER: 60/284,855  
/ NUMBER OF SEQ ID NOS: 135  
/ SOFTWARE: FastSeq for Windows Version 4.0  
/ SEQ ID NO 38  
/ LENGTH: 9  
/ TYPE: PRT  
/ ORGANISM: Artificial Sequence  
/ FEATURE:  
/ OTHER INFORMATION: generated by replacement of variants in consensus  
/ OTHER INFORMATION: sequence  
US-10-982-145-38

Query Match 32.8%; Score 22; DB 6; Length 9;  
Best Local Similarity 75.0%; Pred. No. 5.5e+04;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 CILG 11  
Db 4 CVLG 7

RESULT 36  
US-10-982-145-50

/ Sequence 50, Application US/10982145  
/ Publication No. US20050272645A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Robert Lehrer  
/ APPLICANT: Alan Maring  
/ APPLICANT: Alexander Cole  
/ APPLICANT: Teresa Hong  
/ TITLE OF INVENTION: Retrocyclins: Antiviral and  
/ FILE REFERENCE: UCLA-001CIP2  
/ CURRENT APPLICATION NUMBER: US/10/982,145  
/ PRIOR FILING DATE: 2004-11-05  
/ PRIOR APPLICATION NUMBER: US03/14106  
/ PRIOR FILING DATE: 2003-05-06  
/ PRIOR APPLICATION NUMBER: 10/141,645  
/ PRIOR FILING DATE: 2002-05-06  
/ PRIOR APPLICATION NUMBER: US02/12353  
/ PRIOR FILING DATE: 2002-04-18  
/ PRIOR APPLICATION NUMBER: 60/284,855  
/ NUMBER OF SEQ ID NOS: 135  
/ SOFTWARE: FastSeq for Windows Version 4.0

/ SEQ ID NO 50  
/ LENGTH: 9  
/ TYPE: PRT  
/ ORGANISM: Artificial Sequence  
/ FEATURE:  
/ OTHER INFORMATION: generated by replacement of variants in consensus  
/ OTHER INFORMATION: sequence  
US-10-982-145-50

Query Match 32.8%; Score 22; DB 6; Length 9;  
Best Local Similarity 75.0%; Pred. No. 5.5e+04;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 CILG 11  
Db 4 CVLG 7

RESULT 37  
US-10-982-145-57

/ Sequence 57, Application US/10982145  
/ Publication No. US20050272645A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Robert Lehrer  
/ APPLICANT: Alan Maring  
/ APPLICANT: Alexander Cole  
/ APPLICANT: Teresa Hong  
/ TITLE OF INVENTION: Retrocyclins: Antiviral and  
/ FILE REFERENCE: UCLA-001CIP2  
/ CURRENT APPLICATION NUMBER: US/10/982,145  
/ PRIOR FILING DATE: 2004-11-05  
/ PRIOR APPLICATION NUMBER: US03/14106  
/ PRIOR FILING DATE: 2003-05-06  
/ PRIOR APPLICATION NUMBER: 10/141,645  
/ PRIOR FILING DATE: 2002-05-06  
/ PRIOR APPLICATION NUMBER: US02/12353  
/ PRIOR FILING DATE: 2002-04-18  
/ PRIOR APPLICATION NUMBER: 60/284,855  
/ NUMBER OF SEQ ID NOS: 135  
/ SOFTWARE: FastSeq for Windows Version 4.0  
/ SEQ ID NO 57  
/ LENGTH: 9  
/ TYPE: PRT  
/ ORGANISM: Artificial Sequence  
/ FEATURE:  
/ OTHER INFORMATION: generated by replacement of variants in consensus  
/ OTHER INFORMATION: sequence  
US-10-982-145-57

Query Match 32.8%; Score 22; DB 6; Length 9;  
Best Local Similarity 75.0%; Pred. No. 5.5e+04;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 CILG 11  
Db 4 CVLG 7

RESULT 38  
US-10-982-145-58

/ Sequence 58, Application US/10982145  
/ Publication No. US20050272645A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Robert Lehrer  
/ APPLICANT: Alan Maring  
/ APPLICANT: Alexander Cole  
/ APPLICANT: Teresa Hong  
/ TITLE OF INVENTION: Retrocyclins: Antiviral and  
/ FILE REFERENCE: UCLA-001CIP2  
/ CURRENT APPLICATION NUMBER: US/10/982,145

```
/ CURRENT FILING DATE: 2004-11-05
/ PRIOR APPLICATION NUMBER: US03/14106
/ PRIOR FILING DATE: 2003-05-06
/ PRIOR APPLICATION NUMBER: 10/141,645
/ PRIOR FILING DATE: 2002-05-06
/ PRIOR APPLICATION NUMBER: US02/12353
/ PRIOR FILING DATE: 2002-04-18
/ PRIOR APPLICATION NUMBER: 60/284,855
/ PRIOR FILING DATE: 2001-04-18
/ NUMBER OF SEQ ID NOS: 135
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 58
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: generated by replacement of variants in consensus
/ OTHER INFORMATION: sequence
US-10-982-145-58
```

```
Query Match          32.8%; Score 22; DB 6; Length 9;
Best Local Similarity 75.0%; Pred. No. 5.5e+04;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      8 CILG 11
      |||
Db      4 CVLG 7
```

```
RESULT 39
US-10-982-145-63
/ Sequence 63, Application US/10982145
/ Publication No. US20050272645A1
/ GENERAL INFORMATION:
/ APPLICANT: Robert Lehrer
/ APPLICANT: Alan Waring
/ APPLICANT: Alexander Cole
/ APPLICANT: Teresa Hong
/ TITLE OF INVENTION: Retrocyclins: Antiviral and
/ TITLE OF INVENTION: Antimicrobial Peptides
/ FILE REFERENCE: UCLA-001CIP2
/ CURRENT APPLICATION NUMBER: US/10/982,145
/ CURRENT FILING DATE: 2004-11-05
/ PRIOR APPLICATION NUMBER: US03/14106
/ PRIOR FILING DATE: 2003-05-06
/ PRIOR APPLICATION NUMBER: 10/141,645
/ PRIOR FILING DATE: 2002-05-06
/ PRIOR APPLICATION NUMBER: US02/12353
/ PRIOR FILING DATE: 2002-04-18
/ PRIOR APPLICATION NUMBER: 60/284,855
/ PRIOR FILING DATE: 2001-04-18
/ NUMBER OF SEQ ID NOS: 135
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 63
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: generated by replacement of variants in consensus
/ OTHER INFORMATION: sequence
US-10-982-145-63
```

```
Query Match          32.8%; Score 22; DB 6; Length 9;
Best Local Similarity 75.0%; Pred. No. 5.5e+04;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      8 CILG 11
      |||
Db      4 CVLG 7
```

```
RESULT 40
US-10-982-145-64
```

```
/ Sequence 64, Application US/10982145
/ Publication No. US20050272645A1
/ GENERAL INFORMATION:
/ APPLICANT: Robert Lehrer
/ APPLICANT: Alan Waring
/ APPLICANT: Alexander Cole
/ APPLICANT: Teresa Hong
/ TITLE OF INVENTION: Retrocyclins: Antiviral and
/ TITLE OF INVENTION: Antimicrobial Peptides
/ FILE REFERENCE: UCLA-001CIP2
/ CURRENT APPLICATION NUMBER: US/10/982,145
/ CURRENT FILING DATE: 2004-11-05
/ PRIOR APPLICATION NUMBER: US03/14106
/ PRIOR FILING DATE: 2003-05-06
/ PRIOR APPLICATION NUMBER: 10/141,645
/ PRIOR FILING DATE: 2002-05-06
/ PRIOR APPLICATION NUMBER: US02/12353
/ PRIOR FILING DATE: 2002-04-18
/ PRIOR APPLICATION NUMBER: 60/284,855
/ PRIOR FILING DATE: 2001-04-18
/ NUMBER OF SEQ ID NOS: 135
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 64
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: generated by replacement of variants in consensus
/ OTHER INFORMATION: sequence
US-10-982-145-64
```

```
Query Match          32.8%; Score 22; DB 6; Length 9;
Best Local Similarity 75.0%; Pred. No. 5.5e+04;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      8 CILG 11
      |||
Db      4 CVLG 7
```

```
RESULT 41
US-10-873-427A-24
/ Sequence 24, Application US/10873427A
/ Publication No. US20050281914A1
/ GENERAL INFORMATION:
/ APPLICANT: STEELE, JAMES L.
/ APPLICANT: BRODBENT, JEFFREY R.
/ APPLICANT: SRIDHAR, VIDYA R.
/ TITLE OF INVENTION: METHODS AND COMPOSITIONS INVOLVING ENDOPEPTIDASES PEPO2
/ TITLE OF INVENTION: AND PEPO3
/ FILE REFERENCE: WARP:009US
/ CURRENT APPLICATION NUMBER: US/10/873,427A
/ CURRENT FILING DATE: 2004-06-21
/ PRIOR APPLICATION NUMBER: 60/452,257
/ PRIOR FILING DATE: 2003-06-20
/ NUMBER OF SEQ ID NOS: 33
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 24
/ LENGTH: 11
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic
/ OTHER INFORMATION: Peptide
US-10-873-427A-24
```

```
Query Match          32.8%; Score 22; DB 6; Length 11;
Best Local Similarity 66.7%; Pred. No. 1.5e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      7 ECIAG 12
      |||
Db      2 ECVLGP 7
```

RESULT 42  
US-10-873-427A-23  
; Sequence 23, Application US/10873427A  
; Publication No. US20050281914A1  
; GENERAL INFORMATION:  
; APPLICANT: STEELE, JAMES L.  
; APPLICANT: BROADBENT, JEFFREY R.  
; APPLICANT: SRIDHAR, VIDYA R.  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS INVOLVING ENDOPEPTIDASES PEPO2  
; TITLE OF INVENTION: AND PEPO3  
; FILE REFERENCE: WARP:009US  
; CURRENT APPLICATION NUMBER: US/10/873,427A  
; CURRENT FILING DATE: 2004-06-21  
; PRIOR APPLICATION NUMBER: 60/452,257  
; PRIOR FILING DATE: 2003-06-20  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 23  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-10-873-427A-23

Query Match 32.8%; Score 22; DB 6; Length 12;  
Best Local Similarity 66.7%; Pred. No. 1.8e+02;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 ECIIGP 12  
|:|:|  
DB 3 EPIVIGP 8

RESULT 43  
US-10-511-559-892  
; Sequence 892, Application US/10511559  
; Publication No. US20050256304A1  
; GENERAL INFORMATION:  
; APPLICANT: JONES, Tim  
; APPLICANT: BAKER, Matthew  
; APPLICANT: CARR, Francis, J.  
; TITLE OF INVENTION: MODIFIED FACTOR VIII  
; FILE REFERENCE: MER-133  
; CURRENT APPLICATION NUMBER: US/10/511,559  
; CURRENT FILING DATE: 2004-10-15  
; PRIOR APPLICATION NUMBER: PCT/EP03/04063  
; PRIOR FILING DATE: 2003-04-17  
; PRIOR APPLICATION NUMBER: EP 02008712.8  
; PRIOR FILING DATE: 2002-04-18  
; PRIOR APPLICATION NUMBER: EP 03006554.4  
; NUMBER OF SEQ ID NOS: 1147  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 892  
; LENGTH: 13  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Potential Epitope of human Factor VIII  
US-10-511-559-892

Query Match 32.8%; Score 22; DB 6; Length 13;  
Best Local Similarity 36.4%; Pred. No. 1.8e+02;  
Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 EKNSPECTIGP 12  
|:|:|  
DB 2 EKDVHSGIIGP 12

RESULT 44  
US-10-873-427A-20  
; Sequence 20, Application US/10873427A  
; Publication No. US20050281914A1  
; GENERAL INFORMATION:  
; APPLICANT: STEELE, JAMES L.  
; APPLICANT: BROADBENT, JEFFREY R.  
; APPLICANT: SRIDHAR, VIDYA R.  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS INVOLVING ENDOPEPTIDASES PEPO2  
; TITLE OF INVENTION: AND PEPO3  
; FILE REFERENCE: WARP:009US  
; CURRENT APPLICATION NUMBER: US/10/873,427A  
; CURRENT FILING DATE: 2004-06-21  
; PRIOR APPLICATION NUMBER: 60/452,257  
; PRIOR FILING DATE: 2003-06-20  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 20  
; LENGTH: 13  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-10-873-427A-20

Query Match 32.8%; Score 22; DB 6; Length 13;  
Best Local Similarity 66.7%; Pred. No. 1.8e+02;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 ECIIGP 12  
|:|:|  
DB 2 EPIVIGP 7

RESULT 45  
US-10-970-847-21  
; Sequence 21, Application US/10970847  
; Publication No. US2006002854A1  
; GENERAL INFORMATION:  
; APPLICANT: Hanahan, Douglas  
; APPLICANT: Rucslant, Erkki  
; TITLE OF INVENTION: MOLECULES THAT SELECTIVELY HOME TO  
; TITLE OF INVENTION: VASCULATURE OF PRE-MALIGNANT DYSPLASTIC LESIONS OR  
; FILE REFERENCE: 66821-311  
; CURRENT APPLICATION NUMBER: US/10/970,847  
; CURRENT FILING DATE: 2004-10-20  
; PRIOR APPLICATION NUMBER: 60/513,407  
; PRIOR FILING DATE: 2003-10-21  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 21  
; LENGTH: 13  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic construct  
US-10-970-847-21

Query Match 32.8%; Score 22; DB 6; Length 13;  
Best Local Similarity 75.0%; Pred. No. 1.8e+02;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 CIIIG 11  
|:|:|  
DB 5 CIIIG 8

RESULT 46  
US-10-939-890-66  
; Sequence 66, Application US/10939890

```
/ Publication No. US20050250700A1
/ GENERAL INFORMATION:
/ APPLICANT: Sato, Aaron K.
/ APPLICANT: Sexton, Daniel J.
/ APPLICANT: Dransfield, Daniel T.
/ APPLICANT: Ladner, Robert C.
/ APPLICANT: Arbogast, Christophe
/ APPLICANT: Bussac, Philippe
/ APPLICANT: Pan, Hong
/ APPLICANT: Kourana, Sudha
/ APPLICANT: Linder, Karen E.
/ APPLICANT: Marinelli, Edmund R.
/ APPLICANT: Nanjappa, Palaniappa
/ APPLICANT: Nunn, Adrian D.
/ APPLICANT: Pillai, Radhakrishna
/ APPLICANT: Pochon, Sibylle
/ APPLICANT: Ramalingam, Kondareddi
/ APPLICANT: Shrivastava, Ajay
/ APPLICANT: Song, Bo
/ APPLICANT: Swenson, Rolf E.
/ APPLICANT: Von Wronski, Matthew A.
/ TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
/ FILE REFERENCE: D0617.70014US00
/ CURRENT APPLICATION NUMBER: US/10/939,890
/ PRIOR FILING DATE: 2004-09-13
/ PRIOR APPLICATION NUMBER: US 10/661,156
/ PRIOR FILING DATE: 2003-09-11
/ PRIOR APPLICATION NUMBER: US 10/382,082
/ PRIOR FILING DATE: 2003-03-03
/ PRIOR APPLICATION NUMBER: PCT/US03/06731
/ PRIOR FILING DATE: 2003-03-03
/ PRIOR APPLICATION NUMBER: US 60/440,411
/ PRIOR FILING DATE: 2003-01-15
/ PRIOR APPLICATION NUMBER: US 60/360,851
/ PRIOR FILING DATE: 2002-03-01
/ NUMBER OF SEQ ID NOS: 883
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 66
/ LENGTH: 14
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Library Isolate
/ US-10-939-890-66

Query Match          32.8%; Score 22; DB 6; Length 14;
Best Local Similarity 60.0%; Pred. No. 1.9e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 7 ECIIG 11
DB 10 KCIIG 14

RESULT 47
US-10-873-427A-19
/ Sequence 19, Application US/10873427A
/ Publication No. US2005028194A1
/ GENERAL INFORMATION:
/ APPLICANT: STEELE, JAMES L.
/ APPLICANT: BROADBENT, JEFFREY R.
/ APPLICANT: SRIDHAR, VIDYA R.
/ TITLE OF INVENTION: METHODS AND COMPOSITIONS INVOLVING ENDOPEPTIDASES PEPO2
/ TITLE OF INVENTION: AND PEPO3
/ FILE REFERENCE: WARF.009US
/ CURRENT APPLICATION NUMBER: US/10/873,427A
/ PRIOR FILING DATE: 2004-06-21
/ PRIOR APPLICATION NUMBER: 60/452,257
/ PRIOR FILING DATE: 2003-06-20
/ NUMBER OF SEQ ID NOS: 33
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 19
/ LENGTH: 14
```

```
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic
/ OTHER INFORMATION: Peptide
/ US-10-873-427A-19
```

```
Query Match          32.8%; Score 22; DB 6; Length 14;
Best Local Similarity 66.7%; Pred. No. 1.9e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 7 ECIIGP 12
DB 3 ECIIGP 8
```

```
RESULT 48
US-11-198-847-278
/ Sequence 278, Application US/11198847
/ Publication No. US20050271589A1
/ GENERAL INFORMATION:
/ APPLICANT: University of Utah Research Foundation
/ APPLICANT: Cognetix, Inc.
/ APPLICANT: Jones, Robert M.
/ APPLICANT: Garrett, James E.
/ APPLICANT: Watkins, Maren
/ APPLICANT: Olivera, Baldomero M.
/ TITLE OF INVENTION: B-Superfamily Conotoxins
/ FILE REFERENCE: 2314-296
/ CURRENT APPLICATION NUMBER: US/11/198,847
/ PRIOR FILING DATE: 2005-08-08
/ PRIOR APPLICATION NUMBER: US 10/838,226
/ PRIOR FILING DATE: 2004-05-05
/ PRIOR APPLICATION NUMBER: US 10/058,053
/ PRIOR FILING DATE: 2000-01-29
/ PRIOR APPLICATION NUMBER: US 60/264323
/ PRIOR FILING DATE: 2001-01-29
/ NUMBER OF SEQ ID NOS: 340
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 278
/ LENGTH: 14
/ TYPE: PRT
/ ORGANISM: Conus vexillum
/ US-11-198-847-278
```

```
Query Match          32.8%; Score 22; DB 7; Length 14;
Best Local Similarity 57.1%; Pred. No. 1.9e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 6 ECIIGP 12
DB 1 FCCIFAP 7
```

```
RESULT 49
US-11-112-784-79
/ Sequence 79, Application US/11112784
/ Publication No. US20050287554A1
/ GENERAL INFORMATION:
/ APPLICANT: Archambault, Jacques
/ TITLE OF INVENTION: Regions of Papilloma Virus E1 Helicase Involved in E1
/ TITLE OF INVENTION: Oligomerization
/ FILE REFERENCE: 13/069-1-D1
/ CURRENT APPLICATION NUMBER: US/11/112,784
/ PRIOR FILING DATE: 2005-04-22
/ PRIOR APPLICATION NUMBER: US/10/339,268
/ PRIOR FILING DATE: 2003-01-09
/ PRIOR APPLICATION NUMBER: US 60/093,626
/ PRIOR FILING DATE: 1998-07-21
/ NUMBER OF SEQ ID NOS: 79
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 79
/ LENGTH: 14
```

```
/ TYPE: PRT
/ ORGANISM: C-terminal B1
US-11-112-784-79

Query Match          32.8%; Score 22; DB 7; Length 14;
Best Local Similarity 42.9%; Pred. No. 1.9e+02;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      5 SPECIOLG 11
      |||:|
Db      2 AFRCPVG 8

RESULT 50
US-10-939-890-199
/ Sequence 199, Application US/10939890
/ Publication No. US20050250700A1
/ GENERAL INFORMATION:
/ APPLICANT: Sato, Aaron K.
/ APPLICANT: Sexton, Daniel J.
/ APPLICANT: Dransfield, Daniel T.
/ APPLICANT: Ladner, Robert C.
/ APPLICANT: Arbogast, Christophe
/ APPLICANT: Bussat, Philippe
/ APPLICANT: Fan, Hong
/ APPLICANT: Khurana, Sudha
/ APPLICANT: Linder, Karen B.
/ APPLICANT: Marinelli, Edmund R.
/ APPLICANT: Nanjappan, Palanisappa
/ APPLICANT: Nunn, Adrian D.
/ APPLICANT: Pillai, Radhakrishna
/ APPLICANT: Pochon, Sibylle
/ APPLICANT: Ramalingam, Kondareddiar
/ APPLICANT: Shrivastava, Ajay
/ APPLICANT: Song, Bo
/ APPLICANT: Swenson, Rolf E.
/ APPLICANT: Von Wronski, Mathew A.
/ TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
/ FILE REFERENCE: D0617.70014US00
/ CURRENT APPLICATION NUMBER: US/10/939,890
/ CURRENT FILING DATE: 2004-09-13
/ PRIOR APPLICATION NUMBER: US 10/661,156
/ PRIOR FILING DATE: 2003-09-11
/ PRIOR APPLICATION NUMBER: US 10/382,082
/ PRIOR FILING DATE: 2003-03-03
/ PRIOR APPLICATION NUMBER: PCT/US03/06731
/ PRIOR FILING DATE: 2003-03-03
/ PRIOR APPLICATION NUMBER: US 60/440,411
/ PRIOR FILING DATE: 2003-01-15
/ PRIOR APPLICATION NUMBER: US 60/360,851
/ PRIOR FILING DATE: 2002-03-01
/ NUMBER OF SEQ ID NOS: 883
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 199
/ LENGTH: 15
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Library Isolate
US-10-939-890-199

Query Match          32.8%; Score 22; DB 6; Length 15;
Best Local Similarity 42.9%; Pred. No. 2e+02;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
```

```
/ Publication No. US20050260581A1
/ GENERAL INFORMATION:
/ APPLICANT: CHIRON SPA
/ APPLICANT: PONTANA Maria Rita
/ APPLICANT: PIZZA Mariagrazia
/ APPLICANT: MASIGNANI Vega
/ APPLICANT: MONACI Elisabetta
/ TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
/ FILE REFERENCE:
/ CURRENT APPLICATION NUMBER: US/10/467,657
/ CURRENT FILING DATE: 2003-08-11
/ PRIOR APPLICATION NUMBER: GB-0103424.8
/ PRIOR FILING DATE: 2001-02-12
/ NUMBER OF SEQ ID NOS: 9218
/ SOFTWARE: Seqwin99, version 1.04
/ SEQ ID NO 8690
/ LENGTH: 15
/ TYPE: PRT
/ ORGANISM: Neisseria gonorrhoeae
US-10-467-657-8690

Query Match          32.8%; Score 22; DB 6; Length 15;
Best Local Similarity 44.4%; Pred. No. 2e+02;
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY      3 KNSPECIOLG 11
      |||:|
Db      1 KNRACCPNG 9

RESULT 52
US-10-467-657-8789
/ Sequence 8789, Application US/10467657
/ Publication No. US20050260581A1
/ GENERAL INFORMATION:
/ APPLICANT: CHIRON SPA
/ APPLICANT: FONTANA Maria Rita
/ APPLICANT: PIZZA Mariagrazia
/ APPLICANT: MASIGNANI Vega
/ APPLICANT: MONACI Elisabetta
/ TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
/ FILE REFERENCE:
/ CURRENT APPLICATION NUMBER: US/10/467,657
/ CURRENT FILING DATE: 2003-08-11
/ PRIOR APPLICATION NUMBER: GB-0103424.8
/ PRIOR FILING DATE: 2001-02-12
/ NUMBER OF SEQ ID NOS: 9218
/ SOFTWARE: Seqwin99, version 1.04
/ SEQ ID NO 8789
/ LENGTH: 15
/ TYPE: PRT
/ ORGANISM: Neisseria gonorrhoeae
US-10-467-657-8789

Query Match          32.8%; Score 22; DB 6; Length 15;
Best Local Similarity 66.7%; Pred. No. 2e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      3 KNSPEC 8
      |||:|
Db      1 KNSGRC 6

RESULT 53
US-10-873-427A-14
/ Sequence 14, Application US/10873427A
/ Publication No. US20050281914A1
/ GENERAL INFORMATION:
/ APPLICANT: STEELE, JAMES L.
/ APPLICANT: BROADBENT, JEFFREY R.
/ APPLICANT: SRIDHAR, VIDYA R.
/ TITLE OF INVENTION: METHODS AND COMPOSITIONS INVOLVING ENDOPEPTIDASES PEP02
/ TITLE OF INVENTION: AND PEP03
```

/ FILE REFERENCE: WARP:009US  
/ CURRENT APPLICATION NUMBER: US/10/873,427A  
/ CURRENT FILING DATE: 2004-06-21  
/ PRIOR APPLICATION NUMBER: 60/452,257  
/ PRIOR FILING DATE: 2003-06-20  
/ NUMBER OF SEQ ID NOS: 33  
/ SOFTWARE: PatentIn Ver. 2.1  
/ SEQ ID NO 14  
/ LENGTH: 15  
/ TYPE: PRT  
/ ORGANISM: Artificial Sequence  
/ FEATURE:  
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-10-873-427A-14

Query Match 32.8%; Score 22; DB 6; Length 15;  
Best Local Similarity 66.7%; Pred. No. 2e+02;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 ECIIGP 12  
|:||||  
DB 1 BPVLGP 6

RESULT 54  
US-10-873-427A-13  
/ Sequence 13, Application US/10873427A  
/ Publication No. US20050281914A1  
/ GENERAL INFORMATION:  
/ APPLICANT: STEELE, JAMES L.  
/ APPLICANT: BROADBENT, JEFFREY R.  
/ APPLICANT: SRIDHAR, VIDYA R.  
/ TITLE OF INVENTION: METHODS AND COMPOSITIONS INVOLVING ENDOPEPTIDASES PEP02  
/ FILE REFERENCE: WARP:009US  
/ CURRENT APPLICATION NUMBER: US/10/873,427A  
/ CURRENT FILING DATE: 2004-06-21  
/ PRIOR FILING DATE: 2003-06-20  
/ PRIOR APPLICATION NUMBER: 60/452,257  
/ NUMBER OF SEQ ID NOS: 33  
/ SOFTWARE: PatentIn Ver. 2.1  
/ SEQ ID NO 13  
/ LENGTH: 16  
/ TYPE: PRT  
/ ORGANISM: Artificial Sequence  
/ FEATURE:  
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-10-873-427A-13

Query Match 32.8%; Score 22; DB 6; Length 16;  
Best Local Similarity 66.7%; Pred. No. 2.2e+02;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 ECIIGP 12  
|:||||  
DB 2 BPVLGP 7

RESULT 55  
US-10-873-427A-18  
/ Sequence 18, Application US/10873427A  
/ Publication No. US20050281914A1  
/ GENERAL INFORMATION:  
/ APPLICANT: STEELE, JAMES L.  
/ APPLICANT: BROADBENT, JEFFREY R.  
/ APPLICANT: SRIDHAR, VIDYA R.  
/ TITLE OF INVENTION: METHODS AND COMPOSITIONS INVOLVING ENDOPEPTIDASES PEP02  
/ FILE REFERENCE: WARP:009US  
/ CURRENT APPLICATION NUMBER: US/10/873,427A  
/ CURRENT FILING DATE: 2004-06-21

/ PRIOR APPLICATION NUMBER: 60/452,257  
/ PRIOR FILING DATE: 2003-06-20  
/ NUMBER OF SEQ ID NOS: 33  
/ SOFTWARE: PatentIn Ver. 2.1  
/ SEQ ID NO 18  
/ LENGTH: 16  
/ TYPE: PRT  
/ ORGANISM: Artificial Sequence  
/ FEATURE:  
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-10-873-427A-18

Query Match 32.8%; Score 22; DB 6; Length 16;  
Best Local Similarity 66.7%; Pred. No. 2.2e+02;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 ECIIGP 12  
|:||||  
DB 3 BPVLGP 8

RESULT 56  
US-10-969-314-28  
/ Sequence 28, Application US/10969314  
/ Publication No. US20050249719A1  
/ GENERAL INFORMATION:  
/ APPLICANT: SHAN, LU  
/ APPLICANT: BETHUNE, MICHAEL  
/ APPLICANT: KHOSLA, CHAITAN  
/ APPLICANT: GASS, JONATHAN  
/ APPLICANT: FYLE, GAIL G.  
/ APPLICANT: GRAY, GARY  
/ APPLICANT: STROMBERGER, GREGG  
/ TITLE OF INVENTION: ENZYME TREATMENT OF FOODSTUFFS FOR  
/ FILE REFERENCE: STAN-361  
/ CURRENT APPLICATION NUMBER: US/10/969,314  
/ CURRENT FILING DATE: 2004-10-19  
/ PRIOR APPLICATION NUMBER: 60/565,668  
/ PRIOR FILING DATE: 2004-04-26  
/ PRIOR APPLICATION NUMBER: 10/367,405  
/ PRIOR FILING DATE: 2003-02-14  
/ PRIOR APPLICATION NUMBER: 60/357,238  
/ PRIOR FILING DATE: 2002-02-14  
/ PRIOR APPLICATION NUMBER: 60/380,761  
/ PRIOR FILING DATE: 2002-05-14  
/ PRIOR APPLICATION NUMBER: 60/392,782  
/ PRIOR FILING DATE: 2002-06-28  
/ PRIOR APPLICATION NUMBER: 60/422,933  
/ PRIOR FILING DATE: 2002-10-31  
/ NUMBER OF SEQ ID NOS: 46  
/ SOFTWARE: FastSeq for Windows Version 4.0  
/ SEQ ID NO 28  
/ LENGTH: 17  
/ TYPE: PRT  
/ ORGANISM: Triticum aestivum  
US-10-969-314-28

Query Match 32.8%; Score 22; DB 6; Length 17;  
Best Local Similarity 66.7%; Pred. No. 2.3e+02;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 ECIIGP 12  
|:||||  
DB 3 BPVLGP 8

RESULT 57  
US-10-873-427A-12  
/ Sequence 12, Application US/10873427A  
/ Publication No. US20050281914A1

```
/ GENERAL INFORMATION:
/ APPLICANT: STEELE, JAMES L.
/ APPLICANT: BROADBENT, JEFFREY R.
/ APPLICANT: SRIDHAR, VIDYA R.
/ TITLE OF INVENTION: METHODS AND COMPOSITIONS INVOLVING ENDOPEPTIDASES PEPO2
/ TITLE OF INVENTION: AND PEPO3
/ FILE REFERENCE: WARP:009US
/ CURRENT APPLICATION NUMBER: US/10/873,427A
/ CURRENT FILING DATE: 2004-06-21
/ PRIOR APPLICATION NUMBER: 60/452,257
/ PRIOR FILING DATE: 2003-06-20
/ NUMBER OF SEQ ID NOS: 33
/ SOFTWARE: Patentin Ver. 2.1
/ SEQ ID NO 12
/ LENGTH: 17
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-873-427A-12

Query Match      32.8%; Score 22; DB 6; Length 17;
Best Local Similarity 66.7%; Pred. No. 2.3e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      7 ECILGP 12
      |||||
Db      3 EYVLGP 8

RESULT 58
US-11-106-415-221
/ Sequence 221, Application US/11106415
/ Publication No. US20050287153A1
/ GENERAL INFORMATION:
/ APPLICANT: MARK S. DENNIS
/ TITLE OF INVENTION: Serum Albumin Binding Peptides for Tumor Targeting
/ FILE REFERENCE: P1774R1P2
/ CURRENT APPLICATION NUMBER: US/11/106,415
/ CURRENT FILING DATE: 2005-04-13
/ PRIOR APPLICATION NUMBER: US 10/186,229
/ PRIOR FILING DATE: 2002-06-28
/ NUMBER OF SEQ ID NOS: 425
/ SEQ ID NO 221
/ LENGTH: 18
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: sequence is synthesized
US-11-106-415-221

Query Match      32.8%; Score 22; DB 7; Length 18;
Best Local Similarity 60.0%; Pred. No. 2.5e+02;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      8 CILGP 12
      |||||
Db      13 CLWGP 17

RESULT 59
US-11-106-415-238
/ Sequence 238, Application US/11106415
/ Publication No. US20050287153A1
/ GENERAL INFORMATION:
/ APPLICANT: MARK S. DENNIS
/ TITLE OF INVENTION: Serum Albumin Binding Peptides for Tumor Targeting
/ FILE REFERENCE: P1774R1P2
/ CURRENT APPLICATION NUMBER: US/11/106,415
/ CURRENT FILING DATE: 2005-04-13
/ PRIOR APPLICATION NUMBER: US 10/186,229
/ PRIOR FILING DATE: 2002-06-28
```

```
/ NUMBER OF SEQ ID NOS: 425
/ SEQ ID NO 238
/ LENGTH: 18
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: sequence is synthesized
US-11-106-415-238

Query Match      32.8%; Score 22; DB 7; Length 18;
Best Local Similarity 60.0%; Pred. No. 2.5e+02;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      8 CILGP 12
      |||||
Db      13 CLWGP 17

RESULT 60
US-10-962-145C-9
/ Sequence 9, Application US/10962145C
/ Publication No. US20050249754A1
/ GENERAL INFORMATION:
/ APPLICANT: DIEPOLDER, HELMUT
/ APPLICANT: JUNG, MARIA-CHRISTINA
/ TITLE OF INVENTION: CD4+ T-LYMPHOCYTE-SPECIFIC HEPATITIS C VIRUS EPITOPES
/ FILE REFERENCE: 085449-0167
/ CURRENT APPLICATION NUMBER: US/10/962,145C
/ CURRENT FILING DATE: 2004-10-07
/ PRIOR APPLICATION NUMBER: PCT/EP03/03732
/ PRIOR FILING DATE: 2003-04-10
/ PRIOR APPLICATION NUMBER: EP 02008033.9
/ PRIOR FILING DATE: 2002-04-10
/ NUMBER OF SEQ ID NOS: 17
/ SOFTWARE: Patentin Ver. 3.3
/ SEQ ID NO 9
/ LENGTH: 20
/ TYPE: PRT
/ ORGANISM: Hepatitis C virus
US-10-962-145C-9

Query Match      32.8%; Score 22; DB 6; Length 20;
Best Local Similarity 50.0%; Pred. No. 2.7e+02;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY      3 KNSPECILGP 12
      |||||
Db      9 KNGSMRIYGP 18

RESULT 61
US-11-106-415-188
/ Sequence 188, Application US/11106415
/ Publication No. US20050287153A1
/ GENERAL INFORMATION:
/ APPLICANT: MARK S. DENNIS
/ TITLE OF INVENTION: Serum Albumin Binding Peptides for Tumor Targeting
/ FILE REFERENCE: P1774R1P2
/ CURRENT APPLICATION NUMBER: US/11/106,415
/ CURRENT FILING DATE: 2005-04-13
/ PRIOR APPLICATION NUMBER: US 10/186,229
/ PRIOR FILING DATE: 2002-06-28
/ NUMBER OF SEQ ID NOS: 425
/ SEQ ID NO 188
/ LENGTH: 20
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: sequence is synthesized
US-11-106-415-188

Query Match      32.8%; Score 22; DB 7; Length 20;
Best Local Similarity 60.0%; Pred. No. 2.7e+02;
```



Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 8 CILGP 12  
 DB 14 CLWGP 18

RESULT 62  
 US-11-106-415-214  
 ; Sequence 214, Application US/11106415  
 ; Publication No. US20050287153A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: MARK S. DENNIS  
 ; TITLE OF INVENTION: Serum Albumin Binding Peptides for Tumor Targeting  
 ; FILE REFERENCE: P1774R12  
 ; CURRENT APPLICATION NUMBER: US/11/106,415  
 ; CURRENT FILING DATE: 2005-04-13  
 ; PRIOR APPLICATION NUMBER: US 10/186,229  
 ; PRIOR FILING DATE: 2002-06-28  
 ; NUMBER OF SEQ ID NOS: 425  
 ; SEQ ID NO 214  
 ; LENGTH: 20  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: sequence is synthesized  
 US-11-106-415-214

Query Match 32.8%; Score 22; DB 7; Length 20;  
 Best Local Similarity 60.0%; Pred. No. 2.7e+02;  
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 CILGP 12  
 DB 14 CLWGP 18

RESULT 63  
 US-11-106-415-288  
 ; Sequence 288, Application US/11106415  
 ; Publication No. US20050287153A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: MARK S. DENNIS  
 ; TITLE OF INVENTION: Serum Albumin Binding Peptides for Tumor Targeting  
 ; FILE REFERENCE: P1774R12  
 ; CURRENT APPLICATION NUMBER: US/11/106,415  
 ; CURRENT FILING DATE: 2005-04-13  
 ; PRIOR APPLICATION NUMBER: US 10/186,229  
 ; PRIOR FILING DATE: 2002-06-28  
 ; NUMBER OF SEQ ID NOS: 425  
 ; SEQ ID NO 288  
 ; LENGTH: 20  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: sequence is synthesized  
 US-11-106-415-288

Query Match 32.8%; Score 22; DB 7; Length 20;  
 Best Local Similarity 60.0%; Pred. No. 2.7e+02;  
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 CILGP 12  
 DB 14 CLWGP 18

RESULT 64  
 US-10-467-657-8643  
 ; Sequence 8643, Application US/10467657  
 ; Publication No. US20050260581A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: CHIRON SpA

; APPLICANT: FONTANA Maria Rita  
 ; APPLICANT: PIZZA Mariagrazia  
 ; APPLICANT: MASTIGNANI Vega  
 ; APPLICANT: MONACI Elisabetta  
 ; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS  
 ; FILE REFERENCE:  
 ; CURRENT APPLICATION NUMBER: US/10/467,657  
 ; CURRENT FILING DATE: 2003-08-11  
 ; PRIOR APPLICATION NUMBER: GB-0103424.8  
 ; PRIOR FILING DATE: 2001-02-12  
 ; NUMBER OF SEQ ID NOS: 9218  
 ; SOFTWARE: Seqwin99, version 1.04  
 ; SEQ ID NO 8643  
 ; LENGTH: 7  
 ; TYPE: PRT  
 ; ORGANISM: Neisseria gonorrhoeae  
 US-10-467-657-8643

Query Match 31.3%; Score 21; DB 6; Length 7;  
 Best Local Similarity 60.0%; Pred. No. 5.5e+04;  
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 FNCIL 10  
 DB 3 FNCIL 7

RESULT 65  
 US-10-859-643-50  
 ; Sequence 50, Application US/10859643  
 ; Publication No. US20060002993A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Chailita-Eld, Pia M.  
 ; APPLICANT: Raitano, Arthur B.  
 ; APPLICANT: Paris, Mary  
 ; APPLICANT: Hubert, Rene S.  
 ; APPLICANT: Morrison, Karen Jane Meyrick  
 ; APPLICANT: Jakobovits, Aya  
 ; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein  
 ; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of  
 ; FILE REFERENCE: 511582006203  
 ; CURRENT APPLICATION NUMBER: US/10/859,643  
 ; CURRENT FILING DATE: 2004-06-02  
 ; PRIOR APPLICATION NUMBER: US 10/005,480  
 ; PRIOR FILING DATE: 2001-11-07  
 ; NUMBER OF SEQ ID NOS: 765  
 ; SOFTWARE: FaastSeq for Windows Version 4.0  
 ; SEQ ID NO 50  
 ; LENGTH: 9  
 ; TYPE: PRT  
 ; ORGANISM: Homo Sapien  
 US-10-859-643-50

Query Match 31.3%; Score 21; DB 6; Length 9;  
 Best Local Similarity 50.0%; Pred. No. 5.5e+04;  
 Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 KNSPECIL 10  
 DB 1 KNSPECIL 8

RESULT 66  
 US-10-859-643-570  
 ; Sequence 570, Application US/10859643  
 ; Publication No. US20060002993A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Chailita-Eld, Pia M.  
 ; APPLICANT: Raitano, Arthur B.  
 ; APPLICANT: Paris, Mary  
 ; APPLICANT: Hubert, Rene S.  
 ; APPLICANT: Morrison, Karen Jane Meyrick

```
/ APPLICANT: Jakobovits, Aya
/ TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
/ TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
/ TITLE OF INVENTION: Cancer
/ FILE REFERENCE: 511582006203
/ CURRENT APPLICATION NUMBER: US/10/859,643
/ CURRENT FILING DATE: 2004-06-02
/ PRIOR APPLICATION NUMBER: US 10/005,480
/ PRIOR FILING DATE: 2001-11-07
/ NUMBER OF SEQ ID NOS: 765
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 570
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Homo Sapien
US-10-859-643-570
```

```
Query Match          31.3%; Score 21; DB 6; Length 9;
Best Local Similarity 50.0%; Pred. No. 5.5e+04;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      3 KNSPECIL 10
      |||
      1 KNVDRCLL 8
```

```
RESULT 67
US-11-097-864-50
/ Sequence 50, Application US/11097864
/ Publication No. US20050265924A1
/ GENERAL INFORMATION:
/ APPLICANT: Challita-Bid, Pia M.
/ APPLICANT: Raitano, Arthur B.
/ APPLICANT: Paris, Mary
/ APPLICANT: Hubert, Rene S.
/ APPLICANT: Morrison, Karen Jane Meyrick
/ APPLICANT: Jakobovits, Aya
/ TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 161P2F10B
/ TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF CANCER
/ FILE REFERENCE: 511582006205
/ CURRENT APPLICATION NUMBER: US/11/097,864
/ CURRENT FILING DATE: 2005-04-01
/ PRIOR APPLICATION NUMBER: US 10/062,109
/ PRIOR FILING DATE: 2002-01-31
/ PRIOR APPLICATION NUMBER: US 10/005,480
/ PRIOR FILING DATE: 2001-11-07
/ NUMBER OF SEQ ID NOS: 765
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 50
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Homo Sapien
US-11-097-864-50
```

```
Query Match          31.3%; Score 21; DB 7; Length 9;
Best Local Similarity 50.0%; Pred. No. 5.5e+04;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      3 KNSPECIL 10
      |||
      1 KNVDRCLL 8
```

```
RESULT 68
US-11-097-864-570
/ Sequence 570, Application US/11097864
/ Publication No. US20050265924A1
/ GENERAL INFORMATION:
/ APPLICANT: Challita-Bid, Pia M.
/ APPLICANT: Raitano, Arthur B.
/ APPLICANT: Paris, Mary
/ APPLICANT: Hubert, Rene S.
/ APPLICANT: Morrison, Karen Jane Meyrick
```

```
/ APPLICANT: Jakobovits, Aya
/ TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 161P2F10B
/ TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF CANCER
/ FILE REFERENCE: 511582006205
/ CURRENT APPLICATION NUMBER: US/11/097,864
/ CURRENT FILING DATE: 2005-04-01
/ PRIOR APPLICATION NUMBER: US 10/062,109
/ PRIOR FILING DATE: 2002-01-31
/ PRIOR APPLICATION NUMBER: US 10/005,480
/ PRIOR FILING DATE: 2001-11-07
/ NUMBER OF SEQ ID NOS: 765
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 570
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Homo Sapien
US-11-097-864-570
```

```
Query Match          31.3%; Score 21; DB 7; Length 9;
Best Local Similarity 50.0%; Pred. No. 5.5e+04;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      3 KNSPECIL 10
      |||
      1 KNVDRCLL 8
```

```
RESULT 69
US-11-097-912-50
/ Sequence 50, Application US/11097912
/ Publication No. US20050265921A1
/ GENERAL INFORMATION:
/ APPLICANT: Challita-Bid, Pia M.
/ APPLICANT: Raitano, Arthur B.
/ APPLICANT: Paris, Mary
/ APPLICANT: Hubert, Rene S.
/ APPLICANT: Morrison, Karen Jane Meyrick
/ APPLICANT: Jakobovits, Aya
/ TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 161P2F10B
/ TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF CANCER
/ FILE REFERENCE: 511582006204
/ CURRENT APPLICATION NUMBER: US/11/097,912
/ CURRENT FILING DATE: 2005-04-01
/ PRIOR APPLICATION NUMBER: US 10/062,109
/ PRIOR FILING DATE: 2002-01-31
/ PRIOR APPLICATION NUMBER: US 10/005,480
/ PRIOR FILING DATE: 2001-11-07
/ NUMBER OF SEQ ID NOS: 765
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 50
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Homo Sapien
US-11-097-912-50
```

```
Query Match          31.3%; Score 21; DB 7; Length 9;
Best Local Similarity 50.0%; Pred. No. 5.5e+04;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      3 KNSPECIL 10
      |||
      1 KNVDRCLL 8
```

```
RESULT 70
US-11-097-912-570
/ Sequence 570, Application US/11097912
/ Publication No. US20050265921A1
/ GENERAL INFORMATION:
/ APPLICANT: Challita-Bid, Pia M.
/ APPLICANT: Raitano, Arthur B.
/ APPLICANT: Paris, Mary
/ APPLICANT: Hubert, Rene S.
```

```

; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 161P2P10B
; TITLE OF INVENTION: USEFUL IN TREATMENT AND DETECTION OF CANCER
; FILE REFERENCE: 511582006204
; CURRENT APPLICATION NUMBER: US/11/097,912
; PRIOR FILING DATE: 2005-04-01
; PRIOR APPLICATION NUMBER: US 10/062,109
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 570
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapien
US-11-097-912-570

```

```

Query Match          31.3%; Score 21; DB 7; Length 9;
Best Local Similarity 50.0%; Pred. No. 5.Se+04;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

```

```

QY      3  KNSPECIL 10
      |||
      1  KQVYDHCLL 8

```

## RESULT 71

```

US-10-859-643-167
; Sequence 167, Application US/10859643
; Publication No. US20060002993A1
; GENERAL INFORMATION:
; APPLICANT: Chailita-Bid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Fairle, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161P2P10B Useful in Treatment and Detection of
; FILE REFERENCE: 511582006203
; CURRENT APPLICATION NUMBER: US/10/859,643
; CURRENT FILING DATE: 2004-06-02
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 167
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-859-643-167

```

```

Query Match          31.3%; Score 21; DB 6; Length 10;
Best Local Similarity 60.0%; Pred. No. 2.1e+02;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

QY      4  NSPEC 8
      |||
      6  NKFRFC 10

```

## RESULT 72

```

US-11-097-864-167
; Sequence 167, Application US/11097864
; Publication No. US20050265924A1
; GENERAL INFORMATION:
; APPLICANT: Chailita-Bid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Fairle, Mary
; APPLICANT: Hubert, Rene S.

```

```

; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 161P2P10B
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF CANCER
; FILE REFERENCE: 511582006205
; CURRENT APPLICATION NUMBER: US/11/097,864
; PRIOR FILING DATE: 2005-04-01
; PRIOR APPLICATION NUMBER: US 10/062,109
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 167
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapien
US-11-097-864-167

```

```

Query Match          31.3%; Score 21; DB 7; Length 10;
Best Local Similarity 60.0%; Pred. No. 2.1e+02;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

QY      4  NSPEC 8
      |||
      6  NKFRFC 10

```

## RESULT 73

```

US-11-097-912-167
; Sequence 167, Application US/11097912
; Publication No. US20050265921A1
; GENERAL INFORMATION:
; APPLICANT: Chailita-Bid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Fairle, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 161P2P10B
; TITLE OF INVENTION: USEFUL IN TREATMENT AND DETECTION OF CANCER
; FILE REFERENCE: 511582006204
; CURRENT APPLICATION NUMBER: US/11/097,912
; CURRENT FILING DATE: 2005-04-01
; PRIOR APPLICATION NUMBER: US 10/062,109
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 167
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapien
US-11-097-912-167

```

```

Query Match          31.3%; Score 21; DB 7; Length 10;
Best Local Similarity 60.0%; Pred. No. 2.1e+02;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

QY      4  NSPEC 8
      |||
      6  NKFRFC 10

```

## RESULT 74

```

US-11-119-098-38
; Sequence 38, Application US/1119098
; Publication No. US20050267030A1
; GENERAL INFORMATION:
; APPLICANT: Tsao, Philip S.
; APPLICANT: Mochly-Rosen, David
; TITLE OF INVENTION: Use of deltaPKC Peptides for Modulation of Reactive Oxygen Specie

```

```
/ FILE REFERENCE: 58600-8213.US00
/ CURRENT APPLICATION NUMBER: US/11/119,098
/ CURRENT FILING DATE: 2005-04-29
/ PRIOR APPLICATION NUMBER: US 60/567,315
/ PRIOR FILING DATE: 2004-04-30
/ NUMBER OF SEQ ID NOS: 71
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 38
/ LENGTH: 10
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: modified delta VL-1 peptide
US-11-119-098-38

Query Match      31.3%; Score 21; DB 7; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4 NSFE 7
      ||||
Db      3 NSFE 6

RESULT 75
US-11-016-706-45
/ Sequence 45, Application US/11016706
/ Publication No. US2005024344A1
/ GENERAL INFORMATION:
/ APPLICANT: CASTILLO, GERARDO
/ APPLICANT: LAKE, THOMAS P.
/ APPLICANT: NGUYEN, BETH P.
/ APPLICANT: SANDERS, VIRGINIA J.
/ APPLICANT: SNOW, ALAN D.
/ TITLE OF INVENTION: SMALL PEPTIDES FOR THE TREATMENT OF ALZHEIMER'S DISEASE AND
/ TITLE OF INVENTION: OTHER BETA-AMYLOID PROTEIN FIBRILLOGENESIS DISORDERS
/ FILE REFERENCE: PROTEO.P03C13
/ CURRENT APPLICATION NUMBER: US/11/016,706
/ CURRENT FILING DATE: 2004-12-16
/ PRIOR APPLICATION NUMBER: 09/962,955
/ PRIOR FILING DATE: 2001-09-24
/ PRIOR APPLICATION NUMBER: 09/938,275
/ PRIOR FILING DATE: 2001-08-22
/ PRIOR APPLICATION NUMBER: 08/947,057
/ PRIOR FILING DATE: 1997-10-08
/ NUMBER OF SEQ ID NOS: 89
/ SOFTWARE: PatentIn Ver. 3.2
/ SEQ ID NO 45
/ LENGTH: 12
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-016-706-45

Query Match      31.3%; Score 21; DB 7; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3 KNSF 6
      ||||
Db      1 KNSF 4

RESULT 76
US-10-511-559-271
/ Sequence 271, Application US/10511559
/ Publication No. US20050256304A1
/ GENERAL INFORMATION:
/ APPLICANT: JONES, Tim
/ APPLICANT: BAKER, Matthew
/ APPLICANT: CARR, Francis, J.
/ TITLE OF INVENTION: MODIFIED FACTOR VIII
/ FILE REFERENCE: MER-133
/ CURRENT APPLICATION NUMBER: US/10/511,559
```

```
/ CURRENT FILING DATE: 2004-10-15
/ PRIOR APPLICATION NUMBER: PCT/EP03/04063
/ PRIOR FILING DATE: 2003-04-17
/ PRIOR APPLICATION NUMBER: EP 02008712.8
/ PRIOR FILING DATE: 2002-04-18
/ PRIOR APPLICATION NUMBER: EP 03006554.4
/ PRIOR FILING DATE: 2003-03-24
/ NUMBER OF SEQ ID NOS: 1147
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 271
/ LENGTH: 13
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Potential Epitope of human Factor VIII
US-10-511-559-271

Query Match      31.3%; Score 21; DB 6; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      9 ILGP 12
      ||||
Db      9 ILGP 12

RESULT 77
US-10-511-559-272
/ Sequence 272, Application US/10511559
/ Publication No. US20050256304A1
/ GENERAL INFORMATION:
/ APPLICANT: JONES, Tim
/ APPLICANT: BAKER, Matthew
/ APPLICANT: CARR, Francis, J.
/ TITLE OF INVENTION: MODIFIED FACTOR VIII
/ FILE REFERENCE: MER-133
/ CURRENT APPLICATION NUMBER: US/10/511,559
/ CURRENT FILING DATE: 2004-10-15
/ PRIOR APPLICATION NUMBER: PCT/EP03/04063
/ PRIOR FILING DATE: 2003-04-17
/ PRIOR APPLICATION NUMBER: EP 02008712.8
/ PRIOR FILING DATE: 2002-04-18
/ PRIOR APPLICATION NUMBER: EP 03006554.4
/ PRIOR FILING DATE: 2003-03-24
/ NUMBER OF SEQ ID NOS: 1147
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 272
/ LENGTH: 13
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Potential Epitope of human Factor VIII
US-10-511-559-272

Query Match      31.3%; Score 21; DB 6; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      9 ILGP 12
      ||||
Db      6 ILGP 9

RESULT 78
US-10-511-559-273
/ Sequence 273, Application US/10511559
/ Publication No. US20050256304A1
/ GENERAL INFORMATION:
/ APPLICANT: JONES, Tim
/ APPLICANT: BAKER, Matthew
/ APPLICANT: CARR, Francis, J.
/ TITLE OF INVENTION: MODIFIED FACTOR VIII
/ FILE REFERENCE: MER-133
```

```

/ CURRENT APPLICATION NUMBER: US-10/511,559
/ CURRENT FILING DATE: 2004-10-15
/ PRIOR APPLICATION NUMBER: PCT/EP03/04063
/ PRIOR FILING DATE: 2003-04-17
/ PRIOR APPLICATION NUMBER: EP 02008712.8
/ PRIOR FILING DATE: 2002-04-18
/ PRIOR APPLICATION NUMBER: EP 03006554.4
/ PRIOR FILING DATE: 2003-03-24
/ NUMBER OF SEQ ID NOS: 1147
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 273
/ LENGTH: 13
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Potential Epitope of human Factor VIII
US-10-511-559-273

```

Query Match	31.3%	Score 21	DB 6	Length 13
Best Local Similarity	100.0%	Pred. No. 2.7e+02		
Matches 4	Conservative 0	Mismatches 0	Indels 0	Gaps 0

Oy	9 ILGP 12
Db	3 ILGP 6

```

RESULT 79
US-10-511-559-274
Sequence 274, Application US/10511559
Publication No. US20050256304v1
GENERAL INFORMATION:
APPLICANT: JONES, Tim
APPLICANT: BAKER, Matthew
TITLE OF INVENTION: MODIFIED FACTOR VIII
FILE REFERENCE: MER-133
CURRENT APPLICATION NUMBER: US/10/511,559
CURRENT FILING DATE: 2004-10-15
PRIORITY APPLICATION NUMBER: PCT/EP03/04063
PRIORITY FILING DATE: 2003-04-17
PRIORITY APPLICATION NUMBER: EP 02008712.8
PRIORITY FILING DATE: 2002-04-18
PRIORITY APPLICATION NUMBER: EP 03006554.4
PRIORITY FILING DATE: 2003-03-24
NUMBER OF SEQ ID NOS: 1147
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 274
LENGTH: 13
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
US-10-511-559-274
OTHER INFORMATION: Potential Epitope of human Factor VIII

```

Query Match 31.3%; Score 21; DB 6; Length 13;  
Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	9 ILGP 12
Db	2 ILGP 5

RESULT 80  
 US-10-511-559-849  
 / Sequence 849, Application US/10511559  
 / Publication No. US20050256304A1  
 / GENERAL INFORMATION:  
 / APPLICANT: JONES, Tim  
 / APPLICANT: BAKER, Matthew  
 / APPLICANT: CARR, Francis, J.  
 / TITLE OF INVENTION: MODIFIED FACTOR VIII

```

? FILE REFERENCE: MER-133
? CURRENT APPLICATION NUMBER: US/10/511,559
? CURRENT FILING DATE: 2004-10-15
? PRIOR APPLICATION NUMBER: PCT/EP03/04063
? PRIOR FILING DATE: 2003-04-17
? PRIOR APPLICATION NUMBER: EP 02008712.8
? PRIOR FILING DATE: 2002-04-18
? PRIOR APPLICATION NUMBER: EP 03006554.4
? PRIOR FILING DATE: 2003-03-24
? NUMBER OF SEQ ID NOS: 1147
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 849
? LENGTH: 13
? TYPE: PRT
? ORGANISM: Artificial Sequence
? FEATURE:
? OTHER INFORMATION: Potential Epitope of human Factor VIII
US-10-511-559-849

```

Query Match	31.3%	Score 21;	DB 6;	Length 13;
Best Local Similarity	45.5%	Pred. No. 2.7e+02;		
Matches	5;	Conservative	1;	Mismatches 5;
			Indels	0;
			Gaps	0;

Qy 2 EKNSPFCITLGP 12  
| | : ||  
Db 2 ELNENHGLTGLGP 12

```

RESULT 81
US-11-016-706-7
; Sequence 7, Application US/11016706
; Publication No. US20050244334A1
; GENERAL INFORMATION:
; APPLICANT: CASTILLO, GERRARDO
; APPLICANT: NGUYEN, BETH P.
; APPLICANT: SANDERS, VIRGINIA J.
; APPLICANT: SNOW, ALAN D.
; TITLE OF INVENTION: SMALL PEPTIDES FOR THE TREATMENT OF ALZHEIMER'S DISEASE AND
; FILE REFERENCE: OTHER BETA-AMYLOID PROTEIN FIBRILLOGENESIS DISORDERS
; CURRENT APPLICATION NUMBER: US/11/016,706
; CURRENT FILING DATE: 2004-12-16
; PRIOR APPLICATION NUMBER: 09/962,955
; PRIOR FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: 09/938,275
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 08/947,057
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 7
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-016-706-7

```

Query Match	31.3%;	Score 21;	DB 7;	Length 13;
Best Local Similarity	100.0%;	Pred. No. 2.7e+02;		
Matches	4;	Conservative	0;	Mismatches 0;
				Indels 0;
				Gaps 0;

Qy	3	KNSP	6
nb	10	KNSP	13

RESULT 82  
US-10-929-988-451  
; Sequence 451, Application US/10929988  
; Publication No. US20050277588A1  
; GENERAL INFORMATION:  
; APPLICANT: CWRILA, STEVEN E.  
; APPLICANT: BALU, PALANI

```
/ APPLICANT: DUFFIN, DAVID J.
/ APPLICANT: EPIPLANT, SUNILA
/ APPLICANT: MERRILL, BARBARA MCEOWEN
/ APPLICANT: SCHATZ, PETER JOSEPH
/ TITLE OF INVENTION: COMPOUNDS HAVING AFFINITY FOR THE GRANULOCYTE-COLONY
/ TITLE OF INVENTION: STIMULATING FACTOR RECEPTOR (G-CSFR) AND ASSOCIATED
/ FILE REFERENCE: 0300-0014
/ CURRENT APPLICATION NUMBER: US/10/929,988
/ PRIOR FILING DATE: 2004-08-30
/ PRIOR APPLICATION NUMBER: US/09/620,091
/ NUMBER OF SEQ ID NOS: 491
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 451
/ LENGTH: 14
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-929-988-451
```

```
Query Match      31.3%; Score 21; DB 6; Length 14;
Best Local Similarity 40.0%; Pred. No. 3e+02;
Matches 4; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
```

```
QY      2 EKNSPFCILG 11
DB      5 KKRKECAAG 14
```

```
RESULT 83
US-11-106-932-45
/ Sequence 45, Application US/11106932
/ Publication No. US20050260697A1
/ GENERAL INFORMATION:
/ APPLICANT: WANG, KA-RONALD
/ APPLICANT: HAYES, RONALD
/ APPLICANT: LIU, MING CHEN
/ APPLICANT: OLI, MONIKA
/ TITLE OF INVENTION: PROTEOLYTIC MARKERS AS DIAGNOSTIC BIOMARKERS FOR CANCER, ORGAN
/ TITLE OF INVENTION: INJURY AND MUSCLE REHABILITATION/EXERCISE OVERTRAINING
/ FILE REFERENCE: 5853-549-1
/ CURRENT APPLICATION NUMBER: US/11/106,932
/ CURRENT FILING DATE: 2005-04-15
/ NUMBER OF SEQ ID NOS: 147
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 45
/ LENGTH: 14
/ TYPE: PRT
/ ORGANISM: Bos taurus
US-11-106-932-45
```

```
Query Match      31.3%; Score 21; DB 7; Length 14;
Best Local Similarity 80.0%; Pred. No. 3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 DEKNS 5
DB      4 DEKSS 8
```

```
RESULT 84
US-11-145-703-234
/ Sequence 234, Application US/11145703
/ Publication No. US2005026067A1
/ GENERAL INFORMATION:
/ APPLICANT: Cohen, Daniel
/ APPLICANT: Blumenfeld, Marta
/ APPLICANT: Chumakov, Ilya
/ APPLICANT: Bougueterec, Lydie
/ APPLICANT: Bihain, Bernard
```

```
/ APPLICANT: Essioux, Laurent
/ TITLE OF INVENTION: SCHIZOPHRENIA ASSOCIATED GENES, PROTEINS AND BIALLERIC MARKERS
/ FILE REFERENCE: 53 US16 DIV
/ CURRENT APPLICATION NUMBER: US/11/145,703
/ CURRENT FILING DATE: 2000-03-30
/ PRIOR APPLICATION NUMBER: US/10/147,603
/ PRIOR FILING DATE: 2000-03-30
/ PRIOR APPLICATION NUMBER: 09/539,333
/ PRIOR FILING DATE: 2000-03-30
/ PRIOR APPLICATION NUMBER: US 60/126,903
/ PRIOR FILING DATE: 1999-03-30
/ PRIOR APPLICATION NUMBER: US 60/131,971
/ PRIOR FILING DATE: 1999-04-30
/ PRIOR APPLICATION NUMBER: US 60/132,065
/ PRIOR FILING DATE: 1999-04-30
/ PRIOR APPLICATION NUMBER: US 60/143,928
/ PRIOR FILING DATE: 1999-07-14
/ PRIOR APPLICATION NUMBER: US 60/145,915
/ PRIOR FILING DATE: 1999-07-27
/ PRIOR APPLICATION NUMBER: US 60/146,453
/ PRIOR FILING DATE: 1999-07-29
/ PRIOR APPLICATION NUMBER: US 60/146,452
/ PRIOR FILING DATE: 1999-07-29
/ PRIOR APPLICATION NUMBER: US 60/162,288
/ PRIOR FILING DATE: 1999-10-28
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 234
/ SOFTWARE: Patent.pm
/ SEQ ID NO 234
/ LENGTH: 15
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-145-703-234
```

```
Query Match      31.3%; Score 21; DB 7; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      9 ILGP 12
DB      6 ILGP 9
```

```
RESULT 85
US-11-041-893-274
/ Sequence 274, Application US/11041893
/ Publication No. US20060002941A1
/ GENERAL INFORMATION:
/ APPLICANT: Mahalirae, Gregory G.
/ TITLE OF INVENTION: COMPOSITIONS COMPRISING IMMUNE RESPONSE
/ TITLE OF INVENTION: ALTERING AGENTS AND METHODS OF USE
/ FILE REFERENCE: 100123.401
/ CURRENT APPLICATION NUMBER: US/11/041,893
/ CURRENT FILING DATE: 2005-01-24
/ PRIOR APPLICATION NUMBER: US 60/616,855
/ PRIOR FILING DATE: 2004-10-06
/ PRIOR APPLICATION NUMBER: US 60/538,713
/ PRIOR FILING DATE: 2004-01-23
/ NUMBER OF SEQ ID NOS: 295
/ SOFTWARE: FaetsSeq for Windows version 4.0
/ SEQ ID NO 274
/ LENGTH: 15
/ TYPE: PRT
/ ORGANISM: Mycobacteria tuberculosis
US-11-041-893-274
```

```
Query Match      31.3%; Score 21; DB 7; Length 15;
Best Local Similarity 50.0%; Pred. No. 3.2e+02;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
```

```
QY      2 EKNSPFCILG 11
DB      6 EAGNPFIRISG 15
```

```
RESULT 86
US-11-041-893-275
; Sequence 275, Application US/11041893
; Publication No. US20060002941A1
; GENERAL INFORMATION:
; APPLICANT: Mahatras, Gregory G.
; TITLE OF INVENTION: COMPOSITIONS COMPRISING IMMUNE RESPONSE
; FILE REFERENCE: 100123.401
; CURRENT APPLICATION NUMBER: US/11/041,893
; PRIOR FILING DATE: 2005-01-24
; PRIOR APPLICATION NUMBER: US 60/616,855
; PRIOR FILING DATE: 2004-10-06
; PRIOR APPLICATION NUMBER: US 60/538,713
; PRIOR FILING DATE: 2004-01-23
; NUMBER OF SEQ ID NOS: 295
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 275
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Mycobacteria tuberculosis
US-11-041-893-275

Query Match          31.3%; Score 21; DB 7; Length 15;
Best Local Similarity 50.0%; Pred. No. 3.2e+02;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
```

```
QY      2 EKNSPFCILQ 11
DB      2 EAGNFERISG 11
```

```
RESULT 87
US-10-939-890-99
; Sequence 99, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussac, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappan, Palaniappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
; FILE REFERENCE: D0617.70014US00
; CURRENT APPLICATION NUMBER: US/10/939,890
; PRIOR FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: US 10/661,156
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 10/382,082
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 883
```

```
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 99
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Library Isolate
US-10-939-890-99
```

```
Query Match          31.3%; Score 21; DB 6; Length 17;
Best Local Similarity 40.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
```

```
QY      1 DEKSNPFCIL 10
DB      7 NEKGMWNCYL 16
```

```
RESULT 88
US-10-939-890-217
; Sequence 217, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussac, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappan, Palaniappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
; FILE REFERENCE: D0617.70014US00
; CURRENT APPLICATION NUMBER: US/10/939,890
; PRIOR FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: US 10/661,156
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 10/382,082
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 217
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Library Isolate
US-10-939-890-217

Query Match          31.3%; Score 21; DB 6; Length 19;
Best Local Similarity 75.0%; Pred. No. 4e+02;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      5 SPFC 8
DB      13 TRFC 16
```

```
RESULT 89
US-11-054-515-2956
; Sequence 2956, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: P55393
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR FILING DATE: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See file Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2956
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-2956

Query Match      31.3%; Score 21; DB 7; Length 19;
Best Local Similarity 30.0%; Pred. No. 4e+02;
Matches 3; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy      2 EKNSPECTIG 11
Db      1 ERSQDFPLTG 10

RESULT 90
US-10-997-201A-31
; Sequence 31, Application US/10997201A
; Publication No. US20050249739A1
; GENERAL INFORMATION:
; APPLICANT: Marasco, Wayne
; APPLICANT: Sui, Jinhua
; TITLE OF INVENTION: Antibodies Against SARS-CoV and Methods of Use Thereof
; FILE REFERENCE: 20563-026
; CURRENT APPLICATION NUMBER: US/10/997,201A
; CURRENT FILING DATE: 2004-11-24
; PRIOR APPLICATION NUMBER: 60/524,840
; PRIOR FILING DATE: 2003-11-25
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-997-201A-31

Query Match      31.3%; Score 21; DB 6; Length 20;
Best Local Similarity 75.0%; Pred. No. 4.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 2; Gaps 1;
```

```
Qy      5 SPECIIGP 12
Db      6 SFE--LGP 11

RESULT 91
US-11-041-893-264
; Sequence 264, Application US/11041893
; Publication No. US20060002841A1
; GENERAL INFORMATION:
; APPLICANT: Mahalirae, Gregory G.
; TITLE OF INVENTION: COMPOSITIONS COMPRISING IMMUNE RESPONSES
; FILE REFERENCE: 100123.401
; CURRENT APPLICATION NUMBER: US/11/041,893
; CURRENT FILING DATE: 2005-01-24
; PRIOR APPLICATION NUMBER: US 60/616,855
; PRIOR FILING DATE: 2004-10-06
; PRIOR APPLICATION NUMBER: US 60/538,713
; PRIOR FILING DATE: 2004-01-23
; NUMBER OF SEQ ID NOS: 295
; SOFTWARE: fastSeq for Windows Version 4.0
; SEQ ID NO 264
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-11-041-893-264

Query Match      31.3%; Score 21; DB 7; Length 20;
Best Local Similarity 50.0%; Pred. No. 4.2e+02;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy      2 EKNSPECTIG 11
Db      4 EAGNFERISG 13

RESULT 92
US-11-045-024-2757
; Sequence 2757, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Celis, Esreban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
```





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/ PRIOR APPLICATION NUMBER: 60/056,371
/ PRIOR FILING DATE: 1997-08-19
/ PRIOR APPLICATION NUMBER: 60/056,732
/ PRIOR FILING DATE: 1997-08-19
/ PRIOR APPLICATION NUMBER: 60/056,366
/ PRIOR FILING DATE: 1997-08-19
/ PRIOR APPLICATION NUMBER: 60/056,364
/ PRIOR FILING DATE: 1997-08-19
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 373
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 241
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-986-501-241

Query Match          29.9%; Score 20; DB 6; Length 9;
Best Local Similarity 57.1%; Pred. No. 5.5e+04;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 NSPECIL 10
DB 2 NSSDCOL 8

RESULT 96
US-11-010-748A-260
/ Sequence 260, Application US/11010748A
/ Publication No. US20050244421A1
/ GENERAL INFORMATION:
/ APPLICANT: Merck Patent GmbH
/ APPLICANT: STRITTMAYER, Wolfgang
/ APPLICANT: MOLL, Heidrun
/ APPLICANT: SCHAM, Burkhard
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING IMMUNE RESPONSE
/ FILE REFERENCE: MER-136
/ CURRENT APPLICATION NUMBER: US/11/010,748A
/ PRIOR FILING DATE: 2004-12-13
/ PRIOR APPLICATION NUMBER: PCT/EP03/06251
/ PRIOR FILING DATE: 2003-06-13
/ PRIOR APPLICATION NUMBER: EP02013423.5
/ PRIOR FILING DATE: 2002-06-13
/ NUMBER OF SEQ ID NOS: 926
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 260
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: HLA-binding peptide of Seq. No. 259
US-11-010-748A-260

Query Match          29.9%; Score 20; DB 7; Length 9;
Best Local Similarity 25.0%; Pred. No. 5.5e+04;
Matches 2; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 DEKNSEFC 8
DB 2 DDSGEYRC 9

RESULT 97
US-11-045-024-37
/ Sequence 37, Application US/11045024
/ Publication No. US20050271676A1
/ GENERAL INFORMATION:
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Livingston, Brian
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Baker, Denise Marie
```

```
/ APPLICANT: Celis, Esteban
/ APPLICANT: Kubo, Ralph
/ APPLICANT: Grey, Howard M.
/ APPLICANT: EpiImmune Inc.
/ TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
/ FILE REFERENCE: 2060.0040007
/ CURRENT APPLICATION NUMBER: US/11/045,024
/ PRIOR FILING DATE: 2005-01-28
/ PRIOR APPLICATION NUMBER: US 09/412,863
/ PRIOR FILING DATE: 1999-10-05
/ PRIOR APPLICATION NUMBER: US 08/027,146
/ PRIOR FILING DATE: 1993-03-05
/ PRIOR APPLICATION NUMBER: US 08/073,205
/ PRIOR FILING DATE: 1993-06-04
/ PRIOR APPLICATION NUMBER: US 08/103,396
/ PRIOR FILING DATE: 1993-06-06
/ PRIOR APPLICATION NUMBER: US 08/159,184
/ PRIOR FILING DATE: 1994-12-01
/ NUMBER OF SEQ ID NOS: 14528
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 37
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-37

Query Match          29.9%; Score 20; DB 7; Length 9;
Best Local Similarity 60.0%; Pred. No. 5.5e+04;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 NSPEC 8
DB 1 HSFNC 5

RESULT 98
US-11-045-024-38
/ Sequence 38, Application US/11045024
/ Publication No. US20050271676A1
/ GENERAL INFORMATION:
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Livingston, Brian
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Baker, Denise Marie
/ APPLICANT: Celis, Esteban
/ APPLICANT: Kubo, Ralph
/ APPLICANT: Grey, Howard M.
/ APPLICANT: EpiImmune Inc.
/ TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
/ FILE REFERENCE: 2060.0040007
/ CURRENT APPLICATION NUMBER: US/11/045,024
/ PRIOR FILING DATE: 2005-01-28
/ PRIOR APPLICATION NUMBER: US 09/412,863
/ PRIOR FILING DATE: 1999-10-05
/ PRIOR APPLICATION NUMBER: US 08/027,146
/ PRIOR FILING DATE: 1993-03-05
/ PRIOR APPLICATION NUMBER: US 08/073,205
/ PRIOR FILING DATE: 1993-06-04
/ PRIOR APPLICATION NUMBER: US 08/103,396
/ PRIOR FILING DATE: 1993-06-06
/ PRIOR APPLICATION NUMBER: US 08/159,184
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/159,339
```

```
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/205,713
/ PRIOR FILING DATE: 1994-03-04
/ PRIOR APPLICATION NUMBER: US 08/347,610
/ PRIOR FILING DATE: 1994-12-01
/ NUMBER OF SEQ ID NOS: 14528
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 38
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-38
```

```
Query Match          29.9%; Score 20; DB 7; Length 9;
Best Local Similarity 60.0%; Pred. No. 5.5e+04;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      4 NSPEC 8
        :|||
Db       1 HSFNC 5
```

```
RESULT 99
US-11-045-024-2802
/ Sequence 2802, Application US/11045024
/ Publication No. US20050271676A1
/ GENERAL INFORMATION:
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Livingston, Brian
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Baker, Denise Marie
/ APPLICANT: Celis, Betsedan
/ APPLICANT: Kubo, Ralph
/ APPLICANT: Grey, Howard M.
/ APPLICANT: EpiImmune Inc.
/ TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
/ TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
/ FILE REFERENCE: 2060.0040007
/ CURRENT APPLICATION NUMBER: US/11/045,024
/ CURRENT FILING DATE: 2005-01-28
/ PRIOR APPLICATION NUMBER: US 09/412,863
/ PRIOR FILING DATE: 1999-10-05
/ PRIOR APPLICATION NUMBER: US 08/027,146
/ PRIOR FILING DATE: 1993-03-05
/ PRIOR APPLICATION NUMBER: US 08/073,205
/ PRIOR FILING DATE: 1993-06-04
/ PRIOR APPLICATION NUMBER: US 08/103,396
/ PRIOR FILING DATE: 1993-08-06
/ PRIOR APPLICATION NUMBER: US 08/159,184
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/159,339
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/205,713
/ PRIOR FILING DATE: 1994-03-04
/ PRIOR APPLICATION NUMBER: US 08/347,610
/ PRIOR FILING DATE: 1994-12-01
/ NUMBER OF SEQ ID NOS: 14528
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 2802
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-2802
```

```
Query Match          29.9%; Score 20; DB 7; Length 9;
Best Local Similarity 60.0%; Pred. No. 5.5e+04;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      4 NSPEC 8
        :|||
Db       4 HSFNC 8
```

```
RESULT 100
US-11-045-024-6167
/ Sequence 6167, Application US/11045024
/ Publication No. US20050271676A1
/ GENERAL INFORMATION:
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Livingston, Brian
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Baker, Denise Marie
/ APPLICANT: Celis, Betsedan
/ APPLICANT: Kubo, Ralph
/ APPLICANT: Grey, Howard M.
/ APPLICANT: EpiImmune Inc.
/ TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
/ TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
/ FILE REFERENCE: 2060.0040007
/ CURRENT APPLICATION NUMBER: US/11/045,024
/ CURRENT FILING DATE: 2005-01-28
/ PRIOR APPLICATION NUMBER: US 09/412,863
/ PRIOR FILING DATE: 1999-10-05
/ PRIOR APPLICATION NUMBER: US 08/027,146
/ PRIOR FILING DATE: 1993-03-05
/ PRIOR APPLICATION NUMBER: US 08/073,205
/ PRIOR FILING DATE: 1993-06-04
/ PRIOR APPLICATION NUMBER: US 08/103,396
/ PRIOR FILING DATE: 1993-08-06
/ PRIOR APPLICATION NUMBER: US 08/159,184
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/159,339
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/205,713
/ PRIOR FILING DATE: 1994-03-04
/ PRIOR APPLICATION NUMBER: US 08/347,610
/ PRIOR FILING DATE: 1994-12-01
/ NUMBER OF SEQ ID NOS: 14528
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 6167
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-6167
```

```
Query Match          29.9%; Score 20; DB 7; Length 9;
Best Local Similarity 60.0%; Pred. No. 5.5e+04;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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```
QY      4 NSPEC 8
        :|||
Db       1 HSFNC 5
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Search completed: January 20, 2006, 19:46:31  
Job time : 5.84615 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 20, 2006, 18:55:50 ; Search time 6.80769 Seconds

(without alignments)  
169.602 Million cell updates/sec

Title: US-09-662-293-5

Perfect score: 67

Sequence: 1 DEKNSPFCILGP 12

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 3886

Minimum DB seq length: 0

Maximum DB seq length: 20

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

1: PIR.80:\*  
2: PIR2:\*  
3: PIR3:\*  
4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	27	40.3	14	2	endothelial growth
2	27	40.3	19	2	gamma crystallin I
3	24	35.8	19	2	gamma crystallin I
4	23	34.3	13	2	gamma crystallin I
5	22	32.8	15	2	ig heavy chain DJ
6	22	32.8	16	2	fibronogen alpha c
7	22	32.8	18	2	ig heavy chain CDR
8	22	32.8	19	2	45k protein - pig
9	22	32.8	19	2	4K prothoracicpro
10	21	31.3	15	2	homeobox 4 protein
11	21	31.3	15	2	T-cell receptor be
12	21	31.3	15	2	urogenital tumor m
13	21	31.3	15	2	T-cell receptor be
14	21	31.3	16	2	phospholipase A2 (
15	20	30.6	16	2	gamma crystallin V
16	20	29.9	16	2	L-serine dehydrata
17	20	29.9	9	4	hypothetical E2 pr
18	20	29.9	16	2	amexin 36k chain
19	20	29.9	17	2	T-cell receptor al
20	20	29.9	18	2	T-cell receptor J-
21	20	29.9	18	2	heat-stable entero
22	20	29.9	18	2	heat-stable entero
23	20	29.9	18	2	hepatalin-degradi
24	20	29.9	19	1	ribosomal protein
25	20	29.9	19	1	ancovenin - Strept
26	20	29.9	20	2	cinamycin - Strept
27	20	29.9	20	2	bombaytin-IV chain
28	19.5	29.1	14	2	hypothetical prote
29	19	28.4	10	2	very late antigen-
					ig heavy chain DJ

30	19	28.4	15	2	A43839	beta-tubulin germ-
31	19	28.4	16	2	S57517	T cell receptor be
32	19	28.4	18	2	PH1350	ig heavy chain DJ
33	19	28.4	18	2	T13511	T-cell receptor de
34	19	28.4	20	2	B44581	bombinin H Met-8 -
35	19	28.4	20	2	C60894	gamma crystallin I
36	19	28.4	20	2	A48394	major fat-globule
37	19	28.4	20	2	A60100	fimbrial antigen C
38	19	28.4	20	2	S50743	proteinase inhibit
39	19	28.4	20	2	S71593	serine proteinase
40	19	28.4	20	2	S08605	hypothetical prote
41	18	26.9	12	2	PH1180	T-cell receptor al
42	18	26.9	12	2	PH1179	T-cell receptor al
43	18	26.9	12	2	PH1181	T-cell receptor al
44	18	26.9	13	1	NTKXNS	alpha-conotoxin SI
45	18	26.9	13	2	I49637	deoxynucleotidyltr
46	18	26.9	14	2	PH0795	T-cell receptor al
47	18	26.9	14	2	PH0804	T-cell receptor al
48	18	26.9	14	2	PH0776	T-cell receptor al
49	18	26.9	14	2	S21747	glutamate dehydrog
50	18	26.9	15	2	S26524	T-cell receptor al
51	18	26.9	15	2	S26523	T-cell receptor al
52	18	26.9	15	2	S26525	T-cell receptor al
53	18	26.9	15	2	PA0020	protein OAI00028 -
54	18	26.9	15	2	PH1762	T cell receptor al
55	18	26.9	15	2	PH0782	T-cell receptor al
56	18	26.9	16	2	F44908	chitinase (EC 3.2.
57	18	26.9	16	2	PH1778	T cell receptor al
58	18	26.9	16	2	A60839	neurokinin A homol
59	18	26.9	17	2	B49404	T-cell receptor be
60	18	26.9	17	2	B44873	caldesmon - rabbit
61	18	26.9	17	2	I49593	cystic fibrosis tr
62	18	26.9	17	2	I84733	gene CPTK protein
63	18	26.9	17	2	PH0809	ig heavy chain CRD
64	18	26.9	17	2	PH0809	T-cell receptor al
65	18	26.9	18	2	PH1794	T cell receptor al
66	18	26.9	18	2	S36121	lectin - spurge (B
67	18	26.9	18	2	B24867	ecyllorhizin II -
68	18	26.9	19	2	A21182	4K prothoracicpro
69	18	26.9	19	2	H61491	seed protein wa-24
70	18	26.9	20	2	S50175	kallikrein (PK-120
71	18	26.9	20	2	PH1783	T cell receptor al
72	18	26.9	20	2	A31516	lectin, galactose/
73	18	26.9	20	2	S29636	jaccalin beta-1 Cha
74	18	26.9	20	2	S03987	agglutinin beta-2
75	18	26.9	20	2	B61497	seed protein wa-20
76	18	26.9	20	2	AB0120	insertion element
77	17	25.4	7	2	A33098	244k exantigen -
78	17	25.4	8	4	I54017	granulocyte-colony
79	17	25.4	10	2	S65728	hemoglobin, extrac
80	17	25.4	11	2	PH1583	ig H chain V-D-J x
81	17	25.4	11	2	I41978	calli-FMRPamide 9 -
82	17	25.4	11	2	C37196	bradykinin-potent
83	17	25.4	12	2	C20907	ig kappa-l chain J
84	17	25.4	12	2	A49637	MHC class II histo
85	17	25.4	13	2	PH0305	ig heavy chain CRD
86	17	25.4	13	2	PH0787	T-cell receptor al
87	17	25.4	13	2	E42762	proteasome endope
88	17	25.4	14	2	PH1615	ig H chain V-D-J x
89	17	25.4	14	2	PT0210	T-cell receptor al
90	17	25.4	14	2	A41589	25k elastin-bindin
91	17	25.4	14	2	S33802	chaperone, TCP1-re
92	17	25.4	14	2	S68095	calcium-binding pr
93	17	25.4	14	2	B83836	hypothetical prote
94	17	25.4	15	2	S27140	hypothetical prote
95	17	25.4	15	2	PM0004	chlorophyll a/b-bl
96	17	25.4	15	2	PH1342	ig heavy chain DJ
97	17	25.4	15	2	PT0097	glutathione peroxi
98	17	25.4	15	2	PH1455	T-cell receptor al
99	17	25.4	15	2	PA0008	lectin B2 - pasopho
100	17	25.4	15	2	A61612	allatostatin - tob

## ALIGNMENTS

## RESULT 1

156493  
endothelial growth factor receptors flt [imported] - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 02-Jul-1996 #sequence\_rev1sion 02-Jul-1996 #text\_change 09-Jul-2004  
C/Accession: 156493  
R/Boocock, C.A.; Charnock-Jones, D.S.; Sharkey, A.M.; McLaren, J.; Barker, P.J.; Wright, J. Natl. Cancer Inst. 87, 506-516, 1995  
A/Title: Expression of vascular endothelial growth factor and its receptors flt and KDR  
A/Reference number: 156493; PMID:95222657; PMID:7707437  
A/Status: preliminary; translated from GB/EWBL/DBD  
A/Molecule type: mRNA  
A/Residues: 1-14 <RSS>  
A/Cross-references: UNIPROT:Q16332; UNIPARC:UPI000006EA07; GB:S77812; NID:9998564; PIND:  
C/Genetic: A;Gene: flt

Query Match 40.3%; Score 27; DB 2; Length 14;  
Best Local Similarity 50.0%; Pred. No. 1.3e+02;  
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 EKNSPEC 9  
| : : : : :  
Db 1 ELNSPECL 8

## RESULT 2

A60894  
gamma crystallin II - spectracted calman (fragment)  
C/Species: Calman crocodilus, Calman sclerops (spectracted calman)  
C/Date: 31-Dec-1993 #sequence\_rev1sion 31-Dec-1993 #text\_change 09-Jul-2004  
C/Accession: A60894  
R/Chlou, S.H.  
J. Protein Chem. 7, 527-534, 1988  
A/Title: The protein sequence homology of gamma-crystallins among major vertebrate class  
A/Reference number: A60894; PMID:89351593; PMID:3255376  
A/Accession: A60894  
A/Molecule type: protein  
A/Residues: 1-19 <CHI>  
A/Cross-references: UNIPROT:Q7LZ96; UNIPARC:UPI000017748P  
C/Superfamily: beta-crystallin  
C/Keywords: duplication; eye lens

Query Match 40.3%; Score 27; DB 2; Length 19;  
Best Local Similarity 50.0%; Pred. No. 1.7e+02;  
Matches 6; Conservative 2; Mismatches 0; Indels 4; Gaps 1;

QY 1 DEKN---SPEC 8  
: : : : :  
Db 7 EKNRFGGRSTEC 18

## RESULT 3

B60894  
gamma crystallin IV - spectracted calman (fragment)  
C/Species: Calman crocodilus, Calman sclerops (spectracted calman)  
C/Date: 31-Dec-1993 #sequence\_rev1sion 31-Dec-1993 #text\_change 09-Jul-2004  
C/Accession: B60894  
R/Chlou, S.H.  
J. Protein Chem. 7, 527-534, 1988  
A/Title: The protein sequence homology of gamma-crystallins among major vertebrate class  
A/Reference number: A60894; PMID:89351593; PMID:3255376  
A/Accession: B60894  
A/Molecule type: protein  
A/Residues: 1-19 <CHI>  
A/Cross-references: UNIPROT:Q7LZ99; UNIPARC:UPI000017748C  
C/Superfamily: beta-crystallin  
C/Keywords: duplication; eye lens

Query Match 35.8%; Score 24; DB 2; Length 19;  
Best Local Similarity 57.1%; Pred. No. 6.3e+02;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 EKNSPEC 8  
| : : : : :  
Db 12 EGRSYEC 18

## RESULT 4

PH1316  
Ig heavy chain DJ region (clone C388-107) - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 30-Sep-1993 #sequence\_rev1sion 30-Sep-1993 #text\_change 07-May-1999  
C/Accession: PH1316  
R/Wasserman, R.; Gallili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.  
J. Exp. Med. 176, 1577-1581, 1992  
A/Title: Predominance of fetal type DJH joining in young children with B precursor lymph  
A/Reference number: PH1302; PMID:93094761; PMID:1460419  
A/Accession: PH1316  
A/Molecule type: DNA  
A/Residues: 1-13 <WAS>  
A/Cross-references: UNIPARC:UPI000017C23E  
C/Keywords: heterotetramer; immunoglobulin

Query Match 34.3%; Score 23; DB 2; Length 13;  
Best Local Similarity 80.0%; Pred. No. 6.5e+02;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 CILGP 12  
| : : : : :  
Db 6 CDLGP 10

## RESULT 5

JP0101  
fibrinogen alpha chain - duck (fragment)  
N/Contains: fibrinopeptide A  
C/Species: Anas platyrhynchos (domestic duck)  
C/Date: 30-Jun-1987 #sequence\_rev1sion 28-Dec-1987 #text\_change 09-Jul-2004  
C/Accession: JP0101  
R/Min, Y.; Ping, Z.; Yaoshi, Z.  
Sci. Sin. B Chem. Biol. Agric. Med. Earth Sci. 28, 31-35, 1985  
A/Title: Purification and primary structures of duck fibrinopeptides A and B.  
A/Reference number: A94238  
A/Accession: JP0101  
A/Molecule type: protein  
A/Residues: 1-15 <MIN>  
A/Cross-references: UNIPROT:P12801; UNIPARC:UPI000012A74B  
C/Superfamily: fibrinogen alpha chain; fibrinogen disulfide ring homology  
C/Keywords: blood coagulation; plasma; pyroglutamic acid  
F1/Modified site: pyroglutamic acid (Gln) #status experimental

Query Match 32.8%; Score 22; DB 2; Length 15;  
Best Local Similarity 57.1%; Pred. No. 1.2e+03;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 DEKNSE 7  
| : : : : :  
Db 2 DEKSSFO 8

## RESULT 6

PT0224  
Ig heavy chain CDR3 region (clone I-91) - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 30-Sep-1993 #sequence\_rev1sion 30-Sep-1993 #text\_change 16-Aug-1996  
C/Accession: PT0224  
R/Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.  
J. Exp. Med. 173, 395-407, 1991  
A/Title: Preferential utilization of specific immunoglobulin heavy chain diversity and  
A/Reference number: PT0222; PMID:91108337; PMID:1899102  
A/Accession: PT0224

A/Molecule type: DNA  
 A/Residues: 1-16 <YAM>  
 A/Cross-references: UNIPARC:UPI000017C1D6  
 A/Title: Identification of differentially expressed members of tobacco homeobox familie  
 A/Reference number: JC2057; PMID:94161708; PMID:7509595  
 A/Accession: JC2059  
 A/Molecule type: DNA  
 A/Residues: 1-19 <FEN>  
 A/Cross-references: UNIPROT:Q95XV1; UNIPARC:UPI000017B0A8  
 A/Experimental source: Leaf  
 A/Genetics:  
 A/Gene: Hc4  
 C/Keywords: homeobox

Query Match 32.8%; Score 22; DB 2; Length 16;  
 Best Local Similarity 50.0%; Pred. No. 1.2e+03;  
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 SPECILGP 12  
 Db 6 SYGXILGP 13

## RESULT 7

45K protein - pig roundworm  
 C/Species: Ascaris suum (pig roundworm)  
 C/Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 24-Jul-1997  
 C/Accession: S23950  
 R/Komuniecki, R.; Rhee, R.; Bhat, D.; Duran, E.; Sidawy, E.; Song, H.  
 Arch. Biochem. Biophys. 296, 115-121, 1992  
 A/Title: The pyruvate dehydrogenase complex from the parasitic nematode Ascaris suum: nc  
 A/Reference number: S23950; PMID:92296744; PMID:1376597  
 A/Accession: S23950  
 A/Status: preliminary  
 A/Molecule type: Protein  
 A/Residues: 1-18 <KOM>  
 A/Cross-references: UNIPARC:UPI000017B698  
 A/Note: 13-Arg was also found

Query Match 33.8%; Score 22; DB 2; Length 18;  
 Best Local Similarity 55.6%; Pred. No. 1.4e+03;  
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 NSPECTILGP 12  
 Db 6 SSGHSILGP 14

## RESULT 8

4K prothoracicotropic hormone III - silkworm (fragment)  
 C/Species: Bombyx mori (silkworm)  
 C/Date: 03-Aug-1990 #sequence\_revision 03-Aug-1990 #text\_change 12-Apr-1995  
 C/Accession: C21182  
 R/Nagatawa, H.; Kataoka, H.; Isogai, A.; Tamura, S.; Suzuki, A.; Iehizaki, H.; Mizoguchi  
 Science 226, 1344-1345, 1984  
 A/Title: Amino-terminal amino acid sequence of the silkworm prothoracicotropic hormone:  
 A/Reference number: A21182  
 A/Accession: C21182  
 A/Status: preliminary  
 A/Molecule type: Protein  
 A/Residues: 1-19 <NAG>  
 A/Cross-references: UNIPARC:UPI000017665F  
 C/Superfamily: Insulin

Query Match 32.8%; Score 22; DB 2; Length 19;  
 Best Local Similarity 66.7%; Pred. No. 1.5e+03;  
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 ECTILGP 12  
 Db 5 ECTILGP 10

## RESULT 9

homeobox 4 protein - common tobacco (fragment)  
 C/Species: Nicotiana tabacum (common tobacco)  
 C/Date: 30-Sep-1993 #sequence\_revision 20-Aug-1994 #text\_change 09-Jul-2004

C/Accession: JC2059  
 R/Peng, X.H.; Kung, S.D.  
 Biochem. Biophys. Res. Commun. 198, 1012-1019, 1994

A/Title: Identification of differentially expressed members of tobacco homeobox familie  
 A/Reference number: JC2057; PMID:94161708; PMID:7509595  
 A/Accession: JC2059  
 A/Molecule type: DNA  
 A/Residues: 1-19 <FEN>  
 A/Cross-references: UNIPROT:Q95XV1; UNIPARC:UPI000017B0A8  
 A/Experimental source: Leaf  
 A/Genetics:  
 A/Gene: Hc4  
 C/Keywords: homeobox

Query Match 32.8%; Score 22; DB 2; Length 19;  
 Best Local Similarity 45.5%; Pred. No. 1.5e+03;  
 Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 DEKNSPECTILGP 11  
 Db 2 EKNRUSEITG 12

## RESULT 10

T-cell receptor beta-2 chain J-B2.7 segment - human (fragment)  
 C/Species: Homo sapiens (man)  
 C/Date: 16-Aug-1988 #sequence\_revision 16-Aug-1988 #text\_change 05-Nov-1999  
 C/Accession: F28587  
 R/Toyonaga, B.; Yoshikai, Y.; Vadasz, V.; Chin, B.; Mak, T.W.  
 Proc. Natl. Acad. Sci. U.S.A. 82, 8624-8628, 1985  
 A/Title: Organization and sequences of the diversity, joining, and constant region gene  
 A/Reference number: A94081; PMID:86094276; PMID:3866244  
 A/Accession: F28587  
 A/Molecule type: DNA  
 A/Residues: 1-15 <TOY>  
 A/Cross-references: UNIPARC:UPI0000113C7B; GB:M14159; NID:9338852; PIDN:AAA60681.1; PID  
 C/Keywords: T-cell receptor

Query Match 31.3%; Score 21; DB 2; Length 15;  
 Best Local Similarity 50.0%; Pred. No. 1.8e+03;  
 Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 5 SPECILGP 12  
 Db 1 SYEQYFGP 8

## RESULT 11

urogenital tumor maker protein - human (fragment)  
 N/Alternate names: p21 protein; replication initiation protein homolog  
 C/Species: Homo sapiens (man)  
 C/Date: 12-May-1994 #sequence\_revision 12-May-1994 #text\_change 27-Jun-1994  
 C/Accession: A61247  
 R/Smallitin, C.; Epelbaum, R.; Valensi, C.; Segal, R.; Mekori, T.; Lover, B.; Robinson,  
 Int. J. Cancer 49, 861-866, 1991  
 A/Title: A novel 21-kDa protein as a serum marker for benign and malignant urogenital t  
 A/Reference number: A61247; PMID:92071053; PMID:1959989  
 A/Accession: A61247  
 A/Molecule type: Protein  
 A/Residues: 1-15 <SHA>  
 A/Cross-references: UNIPARC:UPI000002D270  
 C/Keywords: plasma

Query Match 31.3%; Score 21; DB 2; Length 15;  
 Best Local Similarity 50.0%; Pred. No. 1.8e+03;  
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 EKNSEFP 7  
 Db 8 ERNRFQ 13

## RESULT 12

153284

T-cell receptor beta 2 chain J region, Jbeta2.7 - rabbit

C/Species: Oryctolagus cuniculus (domestic rabbit)

C/Date: 02-May-1994 #sequence\_revision 18-Nov-1994 #text\_change 05-Nov-1999

C/Accession: 153284

R/Harindranath, N.; Alexander, C.B.; Mage, R.G.

Mol. Immunol. 28, 881-888, 1991

A/Title: Evolutionarily conserved organization and sequences of germ-line diversity and

A/Reference number: A53284; MUID:91342655; PMID:1678859

A/Accession: 153284

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-15 &lt;HAR&gt;

A/Cross-references: UNIPARC:UPI0000115418; GB:S60737; NID:q233916; PIRN:AAH19525.1; PID:

A/Note: Sequence extracted from NCBI backbone (NCBIN:60737, NCBIPI:60747)

C/Keywords: T-cell receptor

## Query Match

Best Local Similarity 31.3%; Score 21; DB 2; Length 15;

Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 5 SFECLIGP 12

DB 1 SYEQYFGP 8

## RESULT 13

S65520

phospholipase A2 (EC 3.1.1.4) - Malayan splitting cobra (fragment)

N/Contains: muscarinic acetylcholine receptor inhibitor

C/Species: Naja naja sputatrix (Malayan splitting cobra)

C/Date: 19-Mar-1997 #sequence\_revision 29-Aug-1997 #text\_change 05-Oct-2004

C/Accession: S65520

R/Miyoshi, S.; Tu, A.T.

Arch. Biochem. Biophys. 328, 17-25, 1996

A/Title: Phospholipase A(2) from Naja naja sputatrix Venom is a muscarinic acetylcholine

A/Reference number: S65520; MUID:96195757; PMID:8638927

A/Accession: S65520

A/Molecule type: protein

A/Residues: 1-16 &lt;MTY&gt;

A/Cross-references: UNIPROT:Q10756; UNIPARC:UPI000013117A

C/Suprafamily: Phospholipase A2

C/Keywords: calcium; carboxylic ester hydrolase; lipid degradation; metalloprotein; pres

## Query Match

Best Local Similarity 31.3%; Score 21; DB 2; Length 16;

Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 KNSFEC 8

DB 6 KNMTQC 11

## RESULT 14

D60894

gamma crystallin V - bullfrog (fragment)

C/Species: Rana catesbeiana (bullfrog)

C/Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 09-Jul-2004

C/Accession: D60894

R/Chlou, S.H.

J. Protein Chem. 7, 527-534, 1988

A/Title: The protein sequence homology of gamma-crystallins among major vertebrate class

A/Reference number: A60894; MUID:89351593; PMID:3255376

A/Accession: D60894

A/Molecule type: protein

A/Residues: 1-20 &lt;CHI&gt;

A/Cross-references: UNIPROT:Q7LZ97; UNIPARC:UPI000017748E

C/Suprafamily: beta-crystallin

C/Keywords: duplication; eye lens

## Query Match

31.3%; Score 21; DB 2; Length 20;

Best Local Similarity 75.0%; Pred. No. 2.4e+03;

Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 SFECLIGP 8

DB 15 SYEQ 18

## RESULT 15

S16376

L-serine dehydratase beta chain - Peptostreptococcus asaccharolyticus

C/Species: Peptostreptococcus asaccharolyticus

C/Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 09-Jul-2004

C/Accession: S16376

R/Grabowski, R.; Buckel, W.

Eur. J. Biochem. 199, 89-94, 1991

A/Title: Purification and properties of an iron-sulfur-containing and pyridoxal-phosphat

A/Reference number: S16224; MUID:91293139; PMID:2065681

A/Accession: S16376

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-16 &lt;EUR&gt;

A/Cross-references: UNIPROT:P33074; UNIPARC:UPI000017ABE6

## Query Match

Best Local Similarity 30.6%; Score 20.5; DB 2; Length 16;

Matches 4; Conservative 4; Mismatches 0; Indels 1; Gaps 1;

QY 4 NSFECLIGP 12

DB 2 SAFE-VMGP 9

## RESULT 16

I73804

hypothetical E2 protein - human papillomavirus type 16 (fragment)

C/Species: human papillomavirus type 16

C/Date: 18-Feb-2000 #sequence\_revision 18-Feb-2000 #text\_change 09-Jul-2004

C/Accession: I73804

R/Schneider-Maunoury, S.; Croissant, O.; Orth, G.

J. Virol. 61, 3295-3298, 1987

A/Title: Integration of human papillomavirus type 16 DNA sequences: a possible early eve

A/Reference number: I56695; MUID:87311896; PMID:3041049

A/Accession: I73804

A/Status: translated from GB/BMBL/DBBJ

A/Molecule type: DNA

A/Residues: 1-9 &lt;SCH&gt;

A/Cross-references: UNIPROT:Q918T3; UNIPROT:Q9YV74; UNIPROT:Q9E841; UNIPROT:Q918T0; UNIP

PROT:Q9YV76; UNIPROT:Q9YV73; UNIPROT:Q9YV75; UNIPROT:Q918U5; UNIPROT:Q9E839; UNIPROT:Q91

96.1; PID:9553617

C/Comment: This is the hypothetical translation of a viral sequence integrated into the

## Query Match

Best Local Similarity 29.9%; Score 20; DB 4; Length 9;

Matches 2; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 2 EKNSFECT 9

DB 1 DNMTLKCL 8

## RESULT 17

A26393

amexin 36k chain - pig (fragment)

C/Species: Sus scrofa domestica (domestic pig)

C/Date: 02-Jun-1988 #sequence\_revision 02-Jun-1988 #text\_change 09-Jul-2004

C/Accession: A26393

R/Gelsow, M.J.; Fritzsche, U.; Hexham, J.M.; Dash, B.; Johnson, T.

Nature 320, 636-638, 1986

A/Title: A consensus amino-acid sequence repeat in Torpedo and mammalian Ca(2)+-depende

A/Reference number: A93379; MUID:86203621; PMID:2422556

A/Accession: A26393

A/Molecule type: protein



A/Residues: 1-16 <GRI>  
A/Cross-references: UNIPROT:Q7M2P4; UNIPARC:UPI000017C456

Query Match 29.9%; Score 20; DB 2; Length 16;  
Best Local Similarity 50.0%; Pred. No. 2.9e+03;  
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 DEKNSEFICL 10  
DB 7 DEKRLRITIL 16

## RESULT 18

PH1789  
T cell receptor alpha chain V region (clone 2PB1 V alpha 24-5) - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 16-Jul-1999  
C/Accession: PH1789  
R/Portelli, S.; Yockey, C.E.; Brenner, M.B.; Balik, S.P.  
J. Exp. Med. 178, 1-16, 1993  
A/Title: Analysis of T cell antigen receptor (TCR) expression by human peripheral blood

A/Reference number: PH1754; MUID:93301585; PMID:8391057  
A/Accession: PH1789  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-17 <POR>  
A/Cross-references: UNIPARC:UPI000017C378

Query Match 29.9%; Score 20; DB 2; Length 17;  
Best Local Similarity 40.0%; Pred. No. 3e+03;  
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 8 CILGP 12  
DB 3 CVVSP 7

## RESULT 19

S47201  
T-cell receptor J-alpha wntv.3 - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 06-Feb-1995 #sequence\_revision 06-Feb-1995 #text\_change 05-Nov-1999  
C/Accession: S47201  
R/Plaza, A.; Kono, D.H.; Theofilopoulos, A.N.  
Submitted to the EMBL Data Library, February 1993  
A/Reference number: S40133  
A/Accession: S47201  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-17 <FLA>  
A/Cross-references: UNIPARC:UPI0000116133; EMBL:X71048; NID:G506944; PIDN:CAA50365.1; PI  
C/Keywords: T-cell receptor

Query Match 29.9%; Score 20; DB 2; Length 17;  
Best Local Similarity 66.7%; Pred. No. 3e+03;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DEKNSEF 6  
DB 2 DEKLTTF 7

## RESULT 20

QHEC2  
heat-stable enterotoxin ST-2 - Escherichia coli  
C/Species: Escherichia coli  
C/Date: 06-Jul-1982 #sequence\_revision 06-Jul-1982 #text\_change 09-Jul-2004  
C/Accession: A01823  
R/Chan, S.K.; Giamella, R.A.  
J. Biol. Chem. 256, 7744-7746, 1981  
A/Title: Amino acid sequence of heat-stable enterotoxin produced by Escherichia coli pat  
A/Reference number: A01823; MUID:81264141; PMID:7021541

A/Accession: A01823  
A/Molecule type: protein

A/Residues: 1-18 <CHA>  
A/Cross-references: UNIPROT:P01560; UNIPARC:UPI000012CDB1  
A/Experimental source: strain 18D, serotype 0.42:K86:H37  
C/Comment: This enterotoxin is one of several, of differing molecular sizes, produced b  
idues of the heat-stable enterotoxin ST-1.  
C/Superfamily: heat-stable enterotoxin ST-1.  
C/Keywords: enterotoxin; heat-stable protein  
F/1-18/Product: heat-stable enterotoxin ST-2 #status experimental <MAT>  
F/5-10,6-14,9-17/Disulfide bonds: #status predicted

Query Match 29.9%; Score 20; DB 1; Length 18;  
Best Local Similarity 60.0%; Pred. No. 3.2e+03;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 NSPEC 8  
DB 1 NTFYC 5

## RESULT 21

A60103  
heat-stable enterotoxin ST-1a - Citrobacter freundii  
C/Species: Citrobacter freundii  
C/Date: 10-Nov-1992 #sequence\_revision 10-Nov-1992 #text\_change 09-Jul-2004  
C/Accession: A60103  
R/Guarino, A.; Giamella, R.; Thompson, M.R.  
Infect. Immun. 57, 649-652, 1989  
A/Title: Citrobacter freundii produces an 18-amino-acid, heat-stable enterotoxin identic  
A/Reference number: A60103; MUID:89108617; PMID:2512902  
A/Accession: A60103  
A/Molecule type: protein  
A/Residues: 1-18 <GUA>  
A/Cross-references: UNIPROT:Q7M0U3; UNIPARC:UPI000003112P  
C/Superfamily: heat-stable enterotoxin ST

Query Match 29.9%; Score 20; DB 2; Length 18;  
Best Local Similarity 60.0%; Pred. No. 3.2e+03;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 NSPEC 8  
DB 1 NTFYC 5

## RESULT 22

A60915  
enkephalin-degrading aminopeptidase (EC 3.4.-.-), puromycin-sensitive - rat (fragment)  
N/Alternate names: aminocephalinalase; aminopeptidase MII  
C/Species: Rattus norvegicus (Norway rat)  
C/Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 09-Jul-2004  
C/Accession: A60915  
R/Dyer, S.H.; Stauffer, C.A.; Orth, K.; Moosaw, C.R.; Hersh, L.B.  
J. Neurochem. 54, 547-554, 1990  
A/Title: Comparison of the soluble and membrane-bound forms of the puromycin-sensitive  
A/Reference number: A60915; MUID:90132681; PMID:2299352  
A/Accession: A60915  
A/Molecule type: protein  
A/Residues: 1-18 <DYR>  
A/Cross-references: UNIPROT:Q7M076; UNIPARC:UPI00001789A0  
A/Note: this sequence represents the N-terminus of both soluble and membrane-associated  
C/Superfamily: membrane alanyl aminopeptidase  
C/Keywords: hydrolase

Query Match 29.9%; Score 20; DB 2; Length 18;  
Best Local Similarity 66.7%; Pred. No. 3.2e+03;  
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 EKNSFE 7  
DB 2 EKRPPE 7

RESULT 23  
S49026  
ribosomal protein HS25 [validated] - *Halocarcula marimortui* (fragment)  
C/Species: *Halocarcula marimortui*  
C/Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 09-Jul-2004  
C/Accession: S49026; S63967  
R/Engemann, S.; Herfurth, E.; Briesemester, U.; Grell, G.; Wittmann-Liebold, B.  
Submitted to the Protein Sequence Database, November 1994  
A/Description: Cartography of ribosomal proteins of the 30S subunit from the halophilic  
A/Reference number: S49023  
A/Accession: S49026  
A/Molecule type: protein  
A/Residues: 1-18 <ENM>  
A/Cross-references: UNIPROT:Q7M532; UNIPARC:UPI000017AE43  
R/Engemann, S.; Noelle, R.; Herfurth, E.; Briesemester, U.; Grell, G.; Wittmann-Liebold, B.  
Eur. J. Biochem. 234, 24-31, 1995  
A/Title: Cartography of ribosomal proteins of the 30S subunit from the halophilic *Halocarcula marimortui*  
A/Reference number: S63964; PMID:96096717; PMID:8529646  
A/Accession: S63967  
A/Molecule type: protein  
A/Residues: 1-18 <ENM>  
A/Cross-references: UNIPARC:UPI000017AE43  
C/Keywords: blocked amino end; protein biosynthesis; ribosome

Query Match  
Best Local Similarity 29.9%; Score 20; DB 2; Length 18;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 9 ILGP 12  
|  
|  
|  
DB 12 VLGP 15

RESULT 24  
EWSMAN  
ancovenin - *Streptomyces* sp. (strain A647P-2)  
C/Species: *Streptomyces* sp.  
C/Date: 12-May-1994 #sequence\_revision 19-May-1994 #text\_change 09-Jul-2004  
C/Accession: A61284  
R/Makamiya, T.; Ueki, Y.; Shiba, T.; Kido, Y.; Moroki, Y.  
Tetrahedron Lett. 26, 665-668, 1985  
A/Title: The structure of ancovenin, a new peptide inhibitor of angiotensin I converting  
A/Reference number: A61284  
A/Accession: A61284  
A/Molecule type: protein  
A/Residues: 1-19 <MMK>  
A/Cross-references: UNIPROT:P38655; UNIPARC:UPI0000052CC3  
C/Suprafamily: cinnamycin precursor  
C/Keywords: antibiotic; lantibiotic  
F/1-18/Cross-link: (2S,3S,6R)-3-methyl-lanthionine (Cys-Thr) #status experimental  
F/4-14/Cross-link: an-(2S,6R)-lanthionine (Ser-Cys) #status experimental  
F/5-11/Cross-link: (2S,3S,6R)-3-methyl-lanthionine (Cys-Thr) #status experimental  
F/6/Modified site: dehydroalanine (Ser) #status experimental

Query Match  
Best Local Similarity 29.9%; Score 20; DB 1; Length 19;  
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 CILGP 12  
|  
|  
|  
DB 5 CSFGP 9

RESULT 25  
EWSMCN  
cinnamycin - *Streptococcicillium cinnamomeum*  
N/Alternate names: lantibiotic; lantibiotic Ro 09-0198  
C/Species: *Streptococcicillium cinnamomeum*  
C/Date: 30-Sep-1993 #sequence\_revision 12-May-1994 #text\_change 09-Jul-2004  
C/Accession: A45767  
R/Naruse, N.; Tenmyo, O.; Tomita, K.; Konishi, M.; Miyaki, T.; Kawaguchi, H.; Fukase, K.  
J. Antibiot. 42, 837-845, 1989

A/Title: Lantibiotic, a new peptide antibiotic. Production, isolation and properties  
A/Reference number: A45767; PMID:89291558; PMID:2544544  
A/Accession: A45767  
A/Molecule type: protein  
A/Residues: 1-19 <MMK>  
A/Cross-references: UNIPROT:P29827; UNIPARC:UPI0000052CC3  
R/Makamiya, T.; Fukase, K.; Naruse, N.; Konishi, M.; Shiba, T.  
Tetrahedron Lett. 29, 4771-4772, 1988  
A/Title: Lantibiotic, a new peptide effective against Herpes simplex virus: structural  
A/Reference number: A53359  
A/Contents: annotation; strain L337-2  
C/Suprafamily: cinnamycin precursor  
C/Keywords: antibiotic; beta-hydroxyaspartic acid; lantibiotic  
F/1-18/Cross-link: (2S,3S,6R)-3-methyl-lanthionine (Cys-Thr) #status experimental  
F/4-14/Cross-link: an-(2S,6R)-lanthionine (Ser-Cys) #status experimental  
F/5-11/Cross-link: (2S,3S,6R)-3-methyl-lanthionine (Cys-Thr) #status experimental  
F/6-13/Cross-link: (2X,5S)-lysinoalanine (Ser-Lys) #status experimental  
F/15/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental

Query Match  
Best Local Similarity 29.9%; Score 20; DB 1; Length 19;  
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 CILGP 12  
|  
|  
|  
DB 5 CSFGP 9

RESULT 26  
JTO410  
bombyxin-IV chain A - silkworm  
C/Species: *Bombyx mori* (silkworm)  
C/Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 20-Mar-1998  
C/Accession: JTO410  
R/Maruyama, K.; Hietler, H.; Nagasawa, H.; Isogai, A.; Tamura, S.; Suzuki, A.; Ishizaki, A.  
Agric. Biol. Chem. 52, 3035-3041, 1988  
A/Title: Isolation and primary structure of bombyxin-IV, a novel molecular species of bc  
A/Reference number: JTO410  
A/Accession: JTO410  
A/Molecule type: protein  
A/Residues: 1-20 <MMK>  
A/Cross-references: UNIPARC:UPI0000176661  
C/Suprafamily: insulin  
F/6-11/Diulfide bonds: #status predicted  
F/7/Diulfide bonds: interchain (to chain B-10) #status predicted  
F/20/Diulfide bonds: interchain (to chain B-22) #status predicted

Query Match  
Best Local Similarity 29.9%; Score 20; DB 2; Length 20;  
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 7 ECILGP 12  
|  
|  
|  
DB 5 ECILGP 10

RESULT 27  
T26748  
hypothetical protein Y39A1B.4 - *Caenorhabditis elegans*  
C/Species: *Caenorhabditis elegans*  
C/Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
C/Accession: T26748  
R/Wall, M.  
Submitted to the EMBL Data Library, January 1998  
A/Reference number: Z20258  
A/Accession: T26748  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-20 <MTL>  
A/Cross-references: UNIPARC:UPI000017B660; EMBL:AL021482; P1DN:CA854436.1; GSPDB:GN0002  
C/Genetic: clone Y39A1B  
A/Experimental source: clone Y39A1B  
A/Genes: CESP:Y39A1B.4

A:Map position: 3  
A:introns: 16/3

Query Match 29.9%; Score 20; DB 2; Length 20;  
Best Local Similarity 41.7%; Pred. No. 3.6e+03;  
Matches 5; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 DEKNSPFCILGP 12  
|:|:|  
Db 7 DKSISISFLVP 18

## RESULT 28

A28018

very late antigen-1 alpha chain - human (fragment)  
N/Alternate names: VLA-1 alpha chain

C/Species: Homo sapiens (man)  
C/Date: 30-Jun-1989 #sequence\_revision 30-Jun-1989 #text\_change 12-May-1994  
C/Accession: A28018  
R/Takada, Y.; Strominger, J.L.; Hemler, M.E.  
Proc. Natl. Acad. Sci. U.S.A. 84, 3239-3243, 1987  
A/Title: The very late antigen family of heterodimers is part of a superfamily of molecu  
A/Reference number: A9451; PMID:87204112; PMID:3033641  
A/Accession: A28018  
A/Molecule type: protein  
A/Residues: 1-14 <TAK>  
A/Cross-references: UNIPARC:UPI000017C41B  
C/Keywords: duplication; heterodimer; membrane protein

Query Match 29.1%; Score 19.5; DB 2; Length 14;  
Best Local Similarity 50.0%; Pred. No. 3.1e+03;  
Matches 6; Conservative 1; Mismatches 4; Indels 1; Gaps 1;

QY 1 DEKNSPFCILGP 12  
|:|:|  
Db 4 DVKDSM-TFLGP 14

## RESULT 29

PH1345

Ig heavy chain DJ region (clone C100-94) - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999  
C/Accession: PH1345

R/Wasserman, R.; Gallil, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.  
J. Exp. Med. 176, 1577-1581, 1992  
A/Title: Predominance of fetal type DJH joining in young children with B precursor lymph  
A/Reference number: PH1302; PMID:93094761; PMID:1460419  
A/Accession: PH1345  
A/Molecule type: DNA  
A/Residues: 1-10 <MAS>  
A/Cross-references: UNIPARC:UPI000017C226  
A/Title: the authors translated the stop codon for residue 4 as X  
C/Keywords: heterotetramer; immunoglobulin

Query Match 28.4%; Score 19; DB 2; Length 10;  
Best Local Similarity 75.0%; Pred. No. 2.7e+03;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 9 ILGP 12  
:|:|:  
Db 5 ILGP 8

## RESULT 30

A43839

beta-tubulin germ-cell isotype - African clawed frog (fragment)  
C/Species: Xenopus laevis (African clawed frog)  
C/Date: 10-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change 11-Apr-1995  
C/Accession: A43839

R/Bleker, J.J.; Yazdani-Bulcky, M.  
Differentiation 50, 15-23, 1992  
A/Title: The multiple beta-tubulin genes of Xenopus: isolation and developmental express

A/Reference number: A43839; PMID:92347627; PMID:1379202

A/Accession: A43839  
A/Status: preliminary; not compared with conceptual translation  
A/Molecule type: nucleic acid  
A/Residues: 1-15 <BIR>  
A/Cross-references: UNIPARC:UPI000017BF7D  
A/Experimental source: oocyte  
A/Note: sequence extracted from NCBI backbone (NCBIF:110252)

Query Match 28.4%; Score 19; DB 2; Length 15;  
Best Local Similarity 42.9%; Pred. No. 4.1e+03;  
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 DEKNSFE 7  
:|:|:  
Db 1 EERGSFE 7

## RESULT 31

S57517

T cell receptor beta chain V region - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 10-Oct-1995 #sequence\_revision 17-Nov-1995 #text\_change 05-Nov-1999  
C/Accession: S57517

R/Burrows, S.R.; Sling, S.L.; Moss, D.J.; Khanna, R.; Misko, I.S.; Argact, V.P.  
submitted to the EMBL Data Library, June 1995  
A/Description: T cell receptor repertoire for a viral epitope in humans is diversified  
A/Reference number: S57494  
A/Accession: S57517  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-16 <BUR>

A/Cross-references: UNIPARC:UPI0000116739; EMBL:Z49924; NID:9887480; PIDN:CA90170.1; P  
C/Keywords: T-cell receptor

Query Match 28.4%; Score 19; DB 2; Length 16;  
Best Local Similarity 60.0%; Pred. No. 4.4e+03;  
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 CILGP 12  
|:|:|  
Db 1 CASGP 5

## RESULT 32

PH1350

Ig heavy chain DJ region (clone C100-109R) - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999  
C/Accession: PH1350

R/Wasserman, R.; Gallil, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.  
J. Exp. Med. 176, 1577-1581, 1992  
A/Title: Predominance of fetal type DJH joining in young children with B precursor lymph  
A/Reference number: PH1302; PMID:93094761; PMID:1460419  
A/Accession: PH1350  
A/Molecule type: DNA  
A/Residues: 1-18 <MAS>  
A/Cross-references: UNIPARC:UPI000017C220  
A/Note: the authors translated the stop codons for residues 2 and 11 as X  
C/Keywords: heterotetramer; immunoglobulin

Query Match 28.4%; Score 19; DB 2; Length 18;  
Best Local Similarity 75.0%; Pred. No. 4.9e+03;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 9 ILGP 12  
:|:|:  
Db 12 ILGP 15

## RESULT 33

I35141

T-cell receptor delta chain V region (105.28) - mouse (fragment)

C/Species: Mus musculus (house mouse)  
 C/Date: 31-Aug-1990 #sequence\_revision 31-Aug-1990 #text\_change 30-May-1997  
 C/Accession: J35141  
 R/Stm, G.K.; Augustin, A.  
 C/Title: 61, 397-405, 1990  
 A/Title: Dominantly inherited expression of BID, an invariant undiversified T cell receptor  
 A/Reference number: A35141, PMID:90242386; PMID:2110506  
 A/Accession: J35141  
 A/Status: preliminary; not compared with conceptual translation  
 A/Residues: 1-18 <STM>  
 A/Cross-references: UNIPARC:UPI000017C85A  
 C/Keywords: T-cell receptor

Query Match 28.4%; Score 19; DB 2; Length 18;  
 Best Local Similarity 60.0%; Pred. No. 4.9e+03;  
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 CIGP 12  
 DB 1 CAGP 5

RESULT 34  
 B44581  
 bombinin H Met-8 - yellow-bellied toad  
 C/Species: Bombina variegata (yellow-bellied toad)  
 C/Date: 27-Jun-1994 #sequence\_revision 27-Jun-1994 #text\_change 09-Jul-2004  
 C/Accession: B44581  
 R/Mgnogna, G.; Simmaco, M.; Kreil, G.; Barra, D.  
 EMBD J. 12, 4829-4832, 1993  
 A/Title: Antibacterial and haemolytic peptides containing D-alloisoleucine from the skin  
 A/Reference number: S39612; PMID:9403896; PMID:8223491  
 A/Accession: B44581  
 A/Status: preliminary  
 A/Molecule type: protein  
 A/Residues: 1-20 <MIG>  
 A/Cross-references: UNIPROT:P82282; UNIPARC:UPI00001766D2  
 C/Suprafamily: bombinin H precursor  
 C/Keywords: amidated carboxyl end; D-amino acid  
 F/2/Modified site: D-allo-isoleucine (ile) #status experimental  
 F/2/Modified site: amidated carboxyl end (ile) #status predicted

Query Match 28.4%; Score 19; DB 2; Length 20;  
 Best Local Similarity 75.0%; Pred. No. 5.5e+03;  
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 9 ILGP 12  
 DB 1 ILGP 4

RESULT 35  
 C60894  
 gamma crystallin III - bullfrog (fragment)  
 C/Species: Rana catesbeiana (bullfrog)  
 C/Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 09-Jul-2004  
 C/Accession: C60894  
 R/Chlou, S.H.  
 J. Protein Chem. 7, 527-534, 1988  
 A/Title: The protein sequence homology of gamma-crystallins among major vertebrate class  
 A/Reference number: A60894; PMID:89351593; PMID:3255376  
 A/Accession: C60894  
 A/Molecule type: protein  
 A/Residues: 1-20 <CHI>  
 A/Cross-references: UNIPROT:Q7L298; UNIPARC:UPI000017748D  
 C/Suprafamily: beta-crystallin  
 C/Keywords: duplication; eye lens

Query Match 28.4%; Score 19; DB 2; Length 20;  
 Best Local Similarity 33.3%; Pred. No. 5.5e+03;  
 Matches 4; Conservative 3; Mismatches 1; Indels 4; Gaps 1;

QY 1 DEKN---SFEC 8  
 DB 7 EDKNFGRCRYEC 18

RESULT 36  
 A48394  
 major fat-globule membrane protein/MGF-E8 homolog - guinea pig (fragment)  
 C/Species: Cavia porcellus (guinea pig)  
 C/Date: 19-Nov-1993 #sequence\_revision 18-Nov-1994 #text\_change 31-Oct-1997  
 C/Accession: A48394  
 R/Mather, I.H.; Banghart, L.R.; Lane, W.S.  
 Biochem. Mol. Biol. Int. 29, 545-554, 1993  
 A/Title: The major fat-globule membrane proteins, bovine components 15/16 and guinea-pig  
 II-like sequences.  
 A/Reference number: A48394; PMID:93250576; PMID:8485470  
 A/Accession: A48394  
 A/Status: preliminary  
 A/Molecule type: protein  
 A/Residues: 1-20 <MAT>  
 A/Cross-references: UNIPARC:UPI0000177A9F  
 A/Note: sequence extracted from NCBI backbone (NCBIP:131440)  
 C/Suprafamily: milk fat globule protein; discoidin I amino-terminal homology; BGF homolo

Query Match 28.4%; Score 19; DB 2; Length 20;  
 Best Local Similarity 37.5%; Pred. No. 5.5e+03;  
 Matches 3; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 4 NSPECTIG 11  
 DB 13 NGGTCLFG 20

RESULT 37  
 A60100  
 fimbrial antigen CS4 - Escherichia coli (strain B8775) (fragment)  
 C/Species: Escherichia coli  
 C/Date: 10-Nov-1992 #sequence\_revision 10-Nov-1992 #text\_change 09-Jul-2004  
 C/Accession: A60100  
 R/Wolf, M.K.; Andrews, G.P.; Tall, B.D.; McConnell, M.M.; Levine, M.M.; Boedeker, E.C.  
 Infect. Immun. 57, 164-173, 1989  
 A/Title: Characterization of CS4 and CS6 antigenic components of PCF8775, a putative col  
 A/Reference number: A60100; PMID:89079281; PMID:2491834  
 A/Accession: A60100  
 A/Molecule type: protein  
 A/Residues: 1-20 <WOL>  
 A/Cross-references: UNIPROT:Q7M077; UNIPARC:UPI00001781C6  
 C/Suprafamily: CPA1 fimbrial protein  
 C/Keywords: fimbria

Query Match 28.4%; Score 19; DB 2; Length 20;  
 Best Local Similarity 57.1%; Pred. No. 5.5e+03;  
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 EKNSPEC 8  
 DB 2 EKNTVC 8

RESULT 38  
 S50743  
 proteinase inhibitor (Bowman-Birk) C-II-related protein - potato (fragment)  
 N/Alternate names: IOK protein  
 C/Species: Solanum tuberosum (potato)  
 C/Date: 14-Jul-1995 #sequence\_revision 12-Apr-1996 #text\_change 09-Jul-2004  
 C/Accession: S50743  
 R/Mitumori, C.; Yamagishi, K.; Fujino, K.; Kikuta, Y.  
 Plant Mol. Biol. 26, 961-969, 1994  
 A/Title: Detection of immunologically related Kunitz and Bowman-Birk proteinase inhibi  
 A/Reference number: S50743; PMID:95093035; PMID:8000008  
 A/Accession: S50743  
 A/Molecule type: protein

A/Residues: 1-20 <MT>  
A/Cross-references: UNIPROT:Q9S8K0, UNIPARC:UPI000009P9CF

Query Match 28.4%; Score 19; DB 2; Length 20;  
Best Local Similarity 37.5%; Pred. No. 5.5e+03;  
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 DEKNSPEC 8  
DB 1 DSSSKPC 8

## RESULT 39

S71593  
serine protease inhibitor, 33K - human (fragment)

C/Species: Homo sapiens (man)  
C/Date: 19-Mar-1998 #sequence\_revision 17-Apr-1998 #text\_change 09-Jul-2004  
C/Accession: S71593  
R/Rao, C.N.; Liu, Y.Y.; Peavey, C.L.; Woodley, D.T.

A/Title: Novel extracellular matrix-associated serine protease inhibitors from human  
A/Reference number: S71592; PMID:9517768; PMID:7872799  
C/Accession: S71593  
A/Molecule type: protein

A/Residues: 1-20 <RAO>  
A/Cross-references: UNIPROT:Q9UC86, UNIPARC:UPI00000727A3  
C/Function: involved in turnover of connective tissues  
C/Keywords: serine protease inhibitor

Query Match 28.4%; Score 19; DB 2; Length 20;  
Best Local Similarity 55.6%; Pred. No. 5.5e+03;  
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 NSPECTIGP 12  
DB 9 NNAXITLP 17

## RESULT 40

S08605

hypothetical protein 1 estrogen receptor 5'-region - chicken

C/Species: Gallus gallus (chicken)  
C/Date: 02-Dec-1993 #sequence\_revision 10-Nov-1995 #text\_change 16-Aug-2004  
C/Accession: S08605

R/Rtue, A.; Green, S.; Argos, P.; Kumar, V.; Walter, P.; Bornert, J.M.; Chambon, P.  
EMBO J. 5, 891-897, 1986

A/Title: The chicken oestrogen receptor sequence: homology with v-erbA and the human oes  
A/Reference number: S07192; PMID:8624758; PMID:3755102  
A/Accession: S08605

A/Status: translation not shown  
A/Molecule type: mRNA  
A/Residues: 1-20 <KRU>

A/Cross-references: UNIPARC:UPI000011DP1D; EMBL:X03805; NID:G63378; PIDN:CAA27431.1; PUI  
A/Note: the authors translated the codon TTT for residue 5 as Gly and TTC for residue 16

Query Match 28.4%; Score 19; DB 2; Length 20;  
Best Local Similarity 37.5%; Pred. No. 5.5e+03;  
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 DEKNSPEC 8  
DB 11 BQNRFWC 18

## RESULT 41

PH1180

T-cell receptor alpha chain V region (Cw3/SB8) - human (fragment)

C/Species: Homo sapiens (man)  
C/Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 16-Jul-1999  
C/Accession: PH1180

R/Casanova, J.L.; Cerottini, J.C.; Matthes, M.; Necker, A.; Gournier, H.; Barra, C.; Wi  
J. Exp. Med. 176, 439-447, 1992

A/Title: H-2-restricted cytolytic T lymphocytes specific for HLA display T cell recepto  
A/Reference number: S26512; PMID:92364546; PMID:1380061  
A/Accession: PH1180  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-12 <CAS>  
A/Cross-references: UNIPARC:UPI000017C39A

Query Match 26.9%; Score 18; DB 2; Length 12;  
Best Local Similarity 75.0%; Pred. No. 5e+03;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 CILG 11  
DB 1 CALG 4

## RESULT 42

PH1179

T-cell receptor alpha chain V region (Cw3/HLA1C8) - human (fragment)

C/Species: Homo sapiens (man)  
C/Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 16-Jul-1999  
C/Accession: PH1179

R/Casanova, J.L.; Cerottini, J.C.; Matthes, M.; Necker, A.; Gournier, H.; Barra, C.; Wi  
J. Exp. Med. 176, 439-447, 1992  
A/Title: H-2-restricted cytolytic T lymphocytes specific for HLA display T cell recepto  
A/Reference number: S26512; PMID:92364546; PMID:1380061  
A/Accession: PH1179

A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-12 <CAS>  
A/Cross-references: UNIPARC:UPI000017C3A1

Query Match 26.9%; Score 18; DB 2; Length 12;  
Best Local Similarity 75.0%; Pred. No. 5e+03;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 CILG 11  
DB 1 CALG 4

## RESULT 43

PH1181

T-cell receptor alpha chain V region (Cw3/HLA1G6) - human (fragment)

C/Species: Homo sapiens (man)  
C/Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 16-Jul-1999  
C/Accession: PH1181

R/Casanova, J.L.; Cerottini, J.C.; Matthes, M.; Necker, A.; Gournier, H.; Barra, C.; Wi  
J. Exp. Med. 176, 439-447, 1992  
A/Title: H-2-restricted cytolytic T lymphocytes specific for HLA display T cell recepto  
A/Reference number: S26512; PMID:92364546; PMID:1380061  
A/Accession: PH1181

A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-12 <CAS>  
A/Cross-references: UNIPARC:UPI000017C3A2

Query Match 26.9%; Score 18; DB 2; Length 12;  
Best Local Similarity 75.0%; Pred. No. 5e+03;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 CILG 11  
DB 1 CALG 4

## RESULT 44

NTKNA5

alpha-conotoxin S1A - cone shell (Conus striatus)

C/Species: Conus striatus (striated cone)  
C/Date: 30-Sep-1992 #sequence\_revision 30-Sep-1992 #text\_change 09-Jul-2004  
C/Accession: A40312

R.Myers, R.A.; Zafaralla, G.C.; Gray, W.R.; Abbott, J.; Cruz, L.J.; Olivera, B.M.  
 Biochemistry 30, 9370-9377, 1991  
 A>Title: alpha-Conotoxins, small peptide probes of nicotinic acetylcholine receptors.  
 A/Reference number: A40312; PMID:91369955; PMID:1692838  
 A/Accession: A40312  
 A/Molecule type: protein  
 A/Residues: 1-13 <MYE>  
 A/Cross-references: UNIPROT:P28878; UNIPARC:UPI0000035428  
 C/Comment: This paralytic toxin from a fish-hunting cone snail inhibits the acetylcholin  
 C/Superfamily: alpha-conotoxin  
 C/Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; postsynaptic neuro  
 P/2-7,3-13/Disulfide bonds: #status experimental  
 P/13/Modified site: amidated carboxyl end (Cys) #status experimental

Query Match 26.9%; Score 18; DB 1; Length 13;  
 Best Local Similarity 50.0%; Pred. No. 5.4e+03;  
 Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 SPFC 8  
 :|||  
 Db 10 NPFC 13

RESULT 45  
 149637  
 deoxynucleotidyltransferase - mouse (fragment)  
 C/Species: Mus musculus (house mouse)  
 C/Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 09-Jul-2004  
 C/Accession: I49637  
 R/Kotwal, O.; Kaneda, T.; Morishita, R.  
 Biochem. Biophys. Res. Commun. 144, 185-190, 1987  
 A>Title: Analysis of human terminal deoxynucleotidyl transferase cDNA expressible in man  
 A/Reference number: I45884; PMID:87213162; PMID:3579990  
 A/Accession: I49637  
 A/Status: preliminary; translated from GB/EMBL/DBDB  
 A/Molecule type: mRNA  
 A/Residues: 1-13 <RES>  
 A/Cross-references: UNIPROT:Q60517; UNIPARC:UPI0000055AC0; GB:M26145; NID:g951208; PIDD:  
 A/Genes: DNTT

Query Match 26.9%; Score 18; DB 2; Length 13;  
 Best Local Similarity 25.0%; Pred. No. 5.4e+03;  
 Matches 2; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 KNSPCL 10  
 :|||  
 Db 3 QTRDCL 10

RESULT 46  
 PH0795  
 T-cell receptor alpha chain (KI V-alpha-4.3) - mouse (fragment)  
 C/Species: Mus musculus (house mouse)  
 C/Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
 C/Accession: PH0795  
 R/Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.  
 J. Exp. Med. 174, 1371-1383, 1991  
 A>Title: T cell receptor genes in a series of class I major histocompatibility complex-  
 allelic exclusion and antigen-specific repertoire.  
 A/Reference number: PH0746; PMID:92078846; PMID:1836010  
 A/Accession: PH0795  
 A/Molecule type: mRNA  
 A/Residues: 1-14 <CAS>  
 A/Cross-references: UNIPARC:UPI000017C779; EMBL:X60900  
 A/Experimental source: T lymphocyte  
 C/Keywords: T-cell receptor

Query Match 26.9%; Score 18; DB 2; Length 14;  
 Best Local Similarity 75.0%; Pred. No. 5.8e+03;  
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 CILG 11

Db 1 CALG 4

RESULT 47  
 PH0804  
 T-cell receptor alpha chain (L4) - mouse (fragment)  
 C/Species: Mus musculus (house mouse)  
 C/Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
 C/Accession: PH0804  
 R/Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.  
 J. Exp. Med. 174, 1371-1383, 1991  
 A>Title: T cell receptor genes in a series of class I major histocompatibility complex-  
 allelic exclusion and antigen-specific repertoire.  
 A/Reference number: PH0746; PMID:92078846; PMID:1836010  
 A/Accession: PH0804  
 A/Molecule type: mRNA  
 A/Residues: 1-14 <CAS>  
 A/Cross-references: UNIPARC:UPI000017C77A; EMBL:X60913  
 A/Experimental source: T lymphocyte  
 C/Keywords: T-cell receptor

Query Match 26.9%; Score 18; DB 2; Length 14;  
 Best Local Similarity 75.0%; Pred. No. 5.8e+03;  
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 CILG 11  
 :|||  
 Db 1 CALG 4

RESULT 48  
 PH0776  
 T-cell receptor alpha chain (M1 V-alpha-8.F3.3) - mouse (fragment)  
 C/Species: Mus musculus (house mouse)  
 C/Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
 C/Accession: PH0776  
 R/Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.  
 J. Exp. Med. 174, 1371-1383, 1991  
 A>Title: T cell receptor genes in a series of class I major histocompatibility complex-  
 allelic exclusion and antigen-specific repertoire.  
 A/Reference number: PH0746; PMID:92078846; PMID:1836010  
 A/Accession: PH0776  
 A/Molecule type: mRNA  
 A/Residues: 1-14 <CAS>  
 A/Cross-references: UNIPARC:UPI000017C77C; EMBL:X60873  
 A/Experimental source: T lymphocyte  
 C/Keywords: T-cell receptor

Query Match 26.9%; Score 18; DB 2; Length 14;  
 Best Local Similarity 75.0%; Pred. No. 5.8e+03;  
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 CILG 11  
 :|||  
 Db 1 CALG 4

RESULT 49  
 S21747  
 glutamate dehydrogenase [NAD(P)] (EC 1.4.1.3) - Pyrococcus furiosus  
 C/Species: Pyrococcus furiosus  
 C/Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 09-Jul-2004  
 C/Accession: S21747  
 R/Robb, F.T.; Park, J.B.; Adams, M.W.W.  
 Biochem. Biophys. Acta 1120, 267-272, 1992  
 A>Title: Characterization of an extremely thermostable glutamate dehydrogenase: a key e  
 A/Reference number: S21747; PMID:92247806; PMID:1576153  
 A/Accession: S21747  
 A/Status: preliminary  
 A/Molecule type: protein  
 A/Residues: 1-14 <ROB>  
 A/Cross-references: UNIPROT:Q9UWM2; UNIPARC:UPI0000062915

C:Keywords: oxidoreductase

Query Match 26.9%; Score 18; DB 2; Length 14;  
Best Local Similarity 22.2%; Pred. No. 5.8e+03;  
Matches 2; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 2 EKNSPFCIL 10  
|:|:|:|:  
DB 3 EQDPYEIVY 11

#### RESULT 50

S26524

T-cell receptor alpha chain V region (clone Cw3/5B8) - mouse (fragment)

C:Species: Mus musculus (house mouse)

A/Variety: clone Cw3/5B8

C/Date: 11-Mar-1998 #sequence\_revision 17-Apr-1998 #text\_change 17-Mar-1999

C/Accession: S26524

R/Casanova, J.L.; Cerottini, J.C.; Matthes, M.; Necker, A.; Gournier, H.; Barra, C.; Wild

J. Exp. Med. 176, 439-447, 1992

A/Title: H-2-restricted cytolytic T lymphocytes specific for HLA display T cell receptor

A/Reference number: S26512; MUID:92364546; PMID:1380061

A/Accession: S26524

A/Molecule type: mRNA

A/Residues: 1-15 <CAS>

A/Cross-references: UNIPARC:UPI00001769B9; EMBL:X67975

A/Experimental source: cytolytic T-lymphocyte, clone Cw3/5B8

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: T-cell receptor

Query Match 26.9%; Score 18; DB 2; Length 15;  
Best Local Similarity 75.0%; Pred. No. 6.2e+03;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 CILG 11  
|:|:|:|:  
DB 1 CALG 4

#### RESULT 51

S26523

T-cell receptor alpha chain V region (clone Cw3/HLA1C8) - mouse (fragment)

C/Species: Mus musculus (house mouse)

A/Variety: clone Cw3/HLA1C8

C/Date: 11-Mar-1998 #sequence\_revision 17-Apr-1998 #text\_change 17-Mar-1999

C/Accession: S26523

R/Casanova, J.L.; Cerottini, J.C.; Matthes, M.; Necker, A.; Gournier, H.; Barra, C.; Wild

J. Exp. Med. 176, 439-447, 1992

A/Title: H-2-restricted cytolytic T lymphocytes specific for HLA display T cell receptor

A/Reference number: S26512; MUID:92364546; PMID:1380061

A/Accession: S26523

A/Molecule type: mRNA

A/Residues: 1-15 <CAS>

A/Cross-references: UNIPARC:UPI00001769B8; EMBL:X67974

A/Experimental source: cytolytic T-lymphocyte, clone Cw3/HLA1C8

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: T-cell receptor

Query Match 26.9%; Score 18; DB 2; Length 15;  
Best Local Similarity 75.0%; Pred. No. 6.2e+03;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 CILG 11  
|:|:|:|:  
DB 1 CALG 4

#### RESULT 52

S26525

T-cell receptor alpha chain V region (clone Cw3/HLA1G6) - mouse (fragment)

C/Species: Mus musculus (house mouse)

A/Variety: clone Cw3/HLA1G6

C/Date: 11-Mar-1998 #sequence\_revision 17-Apr-1998 #text\_change 17-Mar-1999

C/Accession: S26525

R/Casanova, J.L.; Cerottini, J.C.; Matthes, M.; Necker, A.; Gournier, H.; Barra, C.; Wild

J. Exp. Med. 176, 439-447, 1992

A/Title: H-2-restricted cytolytic T lymphocytes specific for HLA display T cell receptor

A/Reference number: S26512; MUID:92364546; PMID:1380061

A/Accession: S26525

A/Molecule type: mRNA

A/Residues: 1-15 <CAS>

A/Cross-references: UNIPARC:UPI00001769B8; EMBL:X67976

A/Experimental source: cytolytic T-lymphocyte, clone Cw3/HLA1G6

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: T-cell receptor

Query Match 26.9%; Score 18; DB 2; Length 15;  
Best Local Similarity 75.0%; Pred. No. 6.2e+03;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 CILG 11  
|:|:|:|:  
DB 1 CALG 4

#### RESULT 53

PA0020

Protein QA100028 - Arabidopsis thaliana (fragment)

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 30-Jun-1992 #sequence\_revision 06-Jan-1995 #text\_change 06-Jun-1997

C/Accession: PA0020

R/Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.

submitted to JIPID, July 1994

A/Description: Separation and characterization of Arabidopsis proteins by two-dimension

A/Reference number: PA0001

A/Accession: PA0020

A/Molecule type: protein

A/Residues: 1-15 <KAM>

A/Cross-references: UNIPARC:UPI000017AFB7

A/Experimental source: callus

Query Match 26.9%; Score 18; DB 2; Length 15;  
Best Local Similarity 50.0%; Pred. No. 6.2e+03;  
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 EKNSFPE 7  
|:|:|:|:  
DB 9 BBSGFB 14

#### RESULT 54

PH1762

T cell receptor alpha chain V region (clone IV alpha 23-1) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 16-Jul-1999

C/Accession: PH1762

R/Porcelli, S.; Yockey, C.R.; Brenner, M.B.; Balk, S.P.

J. Exp. Med. 178, 1-16, 1993

A/Title: Analysis of T cell antigen receptor (TCR) expression by human peripheral blood

A/Reference number: PH1754; MUID:93301585; PMID:8391057

A/Accession: PH1762

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-15 <POR>

A/Cross-references: UNIPARC:UPI000017C36D

Query Match 26.9%; Score 18; DB 2; Length 15;  
Best Local Similarity 37.5%; Pred. No. 6.2e+03;  
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 4 NSPFCILG 11  
|:|:|:|:  
DB 8 SSYKILFG 15

## RESULT 55

PH0782  
T-cell receptor alpha chain (H3 V-alpha-10. TA57) - mouse (fragment)  
C/Species: Mus musculus (house mouse)  
C/Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
C/Accession: PH0782  
R/Casanova, J.L.; Romero, P.; Widmann, C.; Kourilek, P.; Maryanski, J.L.  
J. Exp. Med. 174, 1371-1383, 1991  
A/Title: T cell receptor gene in a series of class I major histocompatibility complex-I allele exclusion and antigen-specific repertoire.  
A/Reference number: PH0746; MUID:92078846; PMID:1636010  
A/Accession: PH0782  
A/Molecule type: mRNA  
A/Residues: 1-15 <CAS>  
A/Cross-references: UNIPARC:UPI000017C771; EMBL:X60883  
A/Experimental source: T lymphocyte  
A/Note: the authors translated the codon TTC for residue 6 as Ieu  
C/Keywords: T-cell receptor

Query Match 26.9%; Score 18; DB 2; Length 15;  
Best Local Similarity 75.0%; Pred. No. 6.7e+03;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 8 CILG 11  
: : :  
Db 1 CALG 4

## RESULT 56

F44908  
Chitinase (EC 3.2.1.14), 23.4K - Streptomyces olivaceoviridis (fragment)  
C/Species: Streptomyces olivaceoviridis  
C/Date: 01-Apr-1993 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004  
C/Accession: F44908  
R/Romaguera, A.; Menge, U.; Breves, R.; Diekmann, H.  
J. Bacteriol. 174, 3450-3454, 1992  
A/Title: Chitinases of Streptomyces olivaceoviridis and significance of processing for  
A/Reference number: A44908; MUID:92276319; PMID:1592803  
A/Accession: F44908  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-16 <ROM>  
A/Cross-references: UNIPROT:Q9RSK7; UNIPARC:UPI0000088ADC  
A/Experimental source: ATCC 11238  
A/Note: sequence extracted from NCBI backbone (NCBIRP:104594)  
C/Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; p  
C/Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match 26.9%; Score 18; DB 2; Length 16;  
Best Local Similarity 75.0%; Pred. No. 6.7e+03;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 3 KNSP 6  
: : :  
Db 10 RNSP 13

## RESULT 57

PH1778  
T cell receptor alpha chain V region (clone 1PBL V alpha 24-5) - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 16-Jul-1999  
C/Accession: PH1778  
R/Portelli, S.; Yockey, C.E.; Brenner, M.B.; Balk, S.P.  
J. Exp. Med. 178, 1-16, 1993  
A/Title: Analysis of T cell antigen receptor (TCR) expression by human peripheral blood

A/Reference number: PH1754; MUID:93301585; PMID:8391057  
A/Accession: PH1778  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-16 <POR>  
A/Cross-references: UNIPARC:UPI000017C36C

Query Match 26.9%; Score 18; DB 2; Length 16;  
Best Local Similarity 40.0%; Pred. No. 6.7e+03;  
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 8 CILG 12  
: : :  
Db 3 CVRP 7

## RESULT 58

A60839  
neurokinin A homolog - marbled electric ray  
N/Alternate names: des-Ser(1), Pro(2) scyllorhinin II  
C/Species: Torpedo marmorata (marbled electric ray)  
C/Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 09-Jul-2004  
C/Accession: A60839  
R/Conlon, J.M.; Thim, L.  
Gen. Comp. Endocrinol. 71, 383-388, 1988  
A/Title: Isolation of the tachykinin, Des(Ser(1)Pro(2)) scyllorhinin II from the intestine  
A/Reference number: A60839; MUID:89053024; PMID:2847952  
A/Accession: A60839  
A/Molecule type: protein  
A/Residues: 1-16 <CON>  
A/Cross-references: UNIPROT:Q7LZ48; UNIPARC:UPI000017BF38  
C/Keywords: amidated carboxyl end; neuropeptide; tachykinin  
P/16/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 26.9%; Score 18; DB 2; Length 16;  
Best Local Similarity 40.0%; Pred. No. 6.7e+03;  
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 7 ECLG 11  
: : :  
Db 10 DCRV 14

## RESULT 59

B49404  
T-cell receptor beta chain VDJ region - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 07-Apr-1994 #sequence\_revision 18-Nov-1994 #text\_change 23-Jul-1999  
C/Accession: B49404  
R/Brooks, B.G.; Balk, S.P.; Aupetit, K.; Colonna, M.; Strominger, J.L.; Groh-Spies, V.  
Proc. Natl. Acad. Sci. U.S.A. 90, 11787-11791, 1993  
A/Title: Human T-cell receptor (TCR) alpha/beta + CD4-CD8- T cells express oligoclonal  
A/Reference number: A49404; MUID:94089717; PMID:7505446  
A/Accession: B49404  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-17 <BRO>  
A/Cross-references: UNIPARC:UPI0000176842; GB:SG7400; NID:9455868; PIND:AMB29275.1; PID  
A/Experimental source: alpha/beta + CD4-CD8- T cells  
A/Note: sequence extracted from NCBI backbone (NCBIN:141024, NCBIRP:141025)  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: T-cell receptor

Query Match 26.9%; Score 18; DB 2; Length 17;  
Best Local Similarity 30.0%; Pred. No. 7.1e+03;  
Matches 3; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

OY 3 KNSP 12  
: : :  
Db 7 QGGYEQYFG 16

## RESULT 60

B44873  
caldesmon - rabbit (fragment)  
C/Species: Oryctolagus cuniculus (domestic rabbit)  
C/Date: 31-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004  
C/Accession: B44873  
R/Rebe, M.; Hornick, T.



Arch. Biochem. Biophys. 288, 538-542, 1991  
 A/Title: Determination of the phosphorylation sites of smooth muscle caldesmon by proteolysis  
 A/Reference number: A44873; MUID:91378498; PMID:1898046  
 A/Accession: B44873  
 A/Status: preliminary  
 A/Molecule type: protein  
 A/Residues: 1-17 <IKB>  
 A/Cross-references: UNIPROT:O9TRW1; UNIPARC:UPI0000086A69  
 A/Experimental source: skeletal myosin  
 A/Note: sequence extracted from NCBI Backbone (NCBIP:63202)  
 C/Superfamily: caldesmon

Query Match 26.9%; Score 18; DB 2; Length 17;  
 Best Local Similarity 66.7%; Pred. No. 7.1e+03;  
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 EKNSP 7  
 DB 4 EKQSV 9

RESULT 61  
 I49593  
 cystic fibrosis transmembrane conductance regulator - mouse (fragment)  
 C/Species: Mus musculus (house mouse)  
 C/Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 20-Aug-1999  
 C/Accession: I49593  
 R/Denamur, B.; Chehab, P.F.  
 Hum. Mol. Genet. 3, 1089-1094, 1994  
 A/Title: Analysis of the mouse and rat CFTR promoter regions.  
 A/Reference number: I49593; MUID:95072572; PMID:7526924  
 A/Accession: I49593  
 A/Status: preliminary; translated from GB/EMBL/DBJ  
 A/Molecule type: DNA  
 A/Residues: 1-17 <RES>  
 A/Cross-references: UNIPARC:UPI000016CC99; GB:L04873; NID:G414726; FIDN:AAA73562.1; PID:  
 C/Genetic:  
 A/Genes: CFTR  
 C/Superfamily: cystic fibrosis transmembrane conductance regulator; ATP-binding cassette

Query Match 26.9%; Score 18; DB 2; Length 17;  
 Best Local Similarity 80.0%; Pred. No. 7.1e+03;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 EKNSP 6  
 DB 7 EKASF 11

RESULT 62  
 I84733  
 gene CFTR protein - rat (fragment)  
 C/Species: Rattus norvegicus (Norway rat)  
 C/Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 09-Jul-2004  
 C/Accession: I84733  
 R/Denamur, B.; Chehab, P.F.  
 Hum. Mol. Genet. 3, 1089-1094, 1994  
 A/Title: Analysis of the mouse and rat CFTR promoter regions.  
 A/Reference number: I49593; MUID:95072572; PMID:7526924  
 A/Accession: I84733  
 A/Status: preliminary; translated from GB/EMBL/DBJ  
 A/Molecule type: DNA  
 A/Residues: 1-17 <RES>  
 A/Cross-references: UNIPROT:P34158; UNIPARC:UPI000016CC99; GB:L26098; NID:G425185; FIDN:  
 C/Genetic:  
 A/Genes: CFTR  
 C/Superfamily: cystic fibrosis transmembrane conductance regulator; ATP-binding cassette

Query Match 26.9%; Score 18; DB 2; Length 17;  
 Best Local Similarity 80.0%; Pred. No. 7.1e+03;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 EKNSP 6

DB 7 EKASF 11

RESULT 63  
 P70234  
 Ig heavy chain CDR3 region (clone 1-130) - human (fragment)  
 C/Species: Homo sapiens (man)  
 C/Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996  
 C/Accession: P70234  
 R/Yamada, M.; Wasserman, R.; Richard, B.A.; Shane, S.; Caton, A.J.; Rivera, G.  
 J. Exp. Med. 173, 395-407, 1991  
 A/Title: Preferential utilization of specific immunoglobulin heavy chain diversity and  
 A/Reference number: P70222; MUID:91108337; PMID:1899102  
 A/Accession: P70234  
 A/Molecule type: DNA  
 A/Residues: 1-17 <YAM>  
 A/Cross-references: UNIPARC:UPI000017C1B0  
 A/Experimental source: B lymphocyte  
 C/Keywords: heterotrimer; immunoglobulin

Query Match 26.9%; Score 18; DB 2; Length 17;  
 Best Local Similarity 50.0%; Pred. No. 7.1e+03;  
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 6 PECTIG 11  
 DB 10 FDMWLG 15

RESULT 64  
 P0809  
 T-cell receptor alpha chain (RF3.10.3) - mouse (fragment)  
 C/Species: Mus musculus (house mouse)  
 C/Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
 C/Accession: P0809  
 R/Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.  
 J. Exp. Med. 174, 1371-1383, 1991  
 A/Title: T cell receptor genes in a series of class I major histocompatibility complex-  
 allelic exclusion and antigen-specific repertoire.  
 A/Reference number: P0746; MUID:92078846; PMID:1896010  
 A/Accession: P0809  
 A/Molecule type: mRNA  
 A/Residues: 1-17 <CAS>  
 A/Cross-references: UNIPARC:UPI000017C785; EMBL:X60920  
 A/Experimental source: T lymphocyte  
 C/Keywords: T-cell receptor

Query Match 26.9%; Score 18; DB 2; Length 17;  
 Best Local Similarity 75.0%; Pred. No. 7.1e+03;  
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 CILG 11  
 DB 1 CALG 4

RESULT 65  
 PH1794  
 T cell receptor alpha chain V region (clone 3DN V alpha 24-4) - human (fragment)  
 C/Species: Homo sapiens (man)  
 C/Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 16-Jul-1999  
 C/Accession: PH1794  
 R/Porcelll, S.; Yockey, C.B.; Brenner, M.B.; Balk, S.P.  
 J. Exp. Med. 178, 1-16, 1993  
 A/Title: Analysis of T cell antigen receptor (TCR) expression by human peripheral blood  
 A/Reference number: PH1754; MUID:93301585; PMID:8391057  
 A/Accession: PH1794  
 A/Status: preliminary  
 A/Molecule type: mRNA  
 A/Residues: 1-18 <POR>  
 A/Cross-references: UNIPARC:UPI000017C382

Query Match 26.9%; Score 18; DB 2; Length 18;  
 Best Local Similarity 40.0%; Pred. No. 7.5e+03;  
 Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 8 CILGP 12  
 |||  
 Db 3 CVVTP 7

## RESULT 66

S36121

lectin - spurge (Euphorbia characias)

C/Species: Euphorbia characias

C/Date: 09-Dec-1993 #sequence\_revision 27-Feb-1997 #text\_change 09-Jul-2004

C/Accession: S36121

R/Title: Purification and partial characterization of a mitogenic lectin from the latex

A/Reference number: S36120; PMID:9357266; PMID:8353129

A/Accession: S36121

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-18 <SN1>

A/Cross-references: UNIPROT:P33888; UNIPARC:UPI00001256C0

Query Match 26.9%; Score 18; DB 2; Length 18;  
 Best Local Similarity 50.0%; Pred. No. 7.5e+03;  
 Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 5 SPECILGP 12  
 |||  
 Db 3 SYTPISGP 10

## RESULT 67

B24867

scyllorhin II - smaller spotted catshark

C/Species: Scyllorhinus canicula (smaller spotted dogfish)

C/Date: 02-Jun-1988 #sequence\_revision 02-Jun-1988 #text\_change 09-Jul-2004

C/Accession: B24867

R/Conlon, J.M.; Deacon, C.F.; O'Toole, L.; Thim, L.

FEBS Lett. 200, 111-116, 1986

A/Title: Scyllorhin II and II: two novel tachykinins from dogfish gut.

A/Reference number: A91359; PMID:8612829; PMID:2422058

A/Accession: B24867

A/Molecule type: protein

A/Residues: 1-18 <CON>

A/Cross-references: UNIPROT:P08609; UNIPARC:UPI0000035237

F/Keywords: amidated carboxyl end; neuropeptide

Query Match 26.9%; Score 18; DB 2; Length 18;  
 Best Local Similarity 40.0%; Pred. No. 7.5e+03;  
 Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 7 ECLIG 11  
 |||  
 Db 12 DCFVG 16

## RESULT 68

A21182

4K prothoracicotropic hormone I - silkworm (fragment)

C/Species: Bombyx mori (silkworm)

C/Date: 03-Aug-1990 #sequence\_revision 03-Aug-1990 #text\_change 09-Jul-2004

C/Accession: A21182

R/Nagasawa, H.; Kataoka, H.; Iseogi, A.; Tamura, S.; Suzuki, A.; Ishizaki, H.; Mizoguchi

Science 226, 1344-1345, 1994

A/Title: Amino-terminal amino acid sequence of the silkworm prothoracicotropic hormone:

A/Reference number: A21182

A/Accession: A21182

A/Status: preliminary

A/Molecule type: protein  
 A/Residues: 1-19 <NAG>  
 A/Cross-references: UNIPROT:P26733; UNIPARC:UPI0000176660  
 C/Superfamily: Insulin

Query Match 26.9%; Score 18; DB 2; Length 19;  
 Best Local Similarity 50.0%; Pred. No. 7.9e+03;  
 Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 7 ECLIGP 12  
 |||  
 Db 5 ECCFRP 10

## RESULT 69

H61491

seed protein ws-24 - winged bean (fragment)

C/Species: Psophocarpus tetragonolobus (winged bean)

C/Date: 07-Oct-1994 #sequence\_revision 07-Oct-1994 #text\_change 07-Oct-1994

C/Accession: H61491

R/Hirano, H.

J. Protein Chem. 8, 115-130, 1989

A/Title: Microsequence analysis of winged bean seed proteins electrophoretically separated from two di-

A/Reference number: A61491; PMID:89351606; PMID:2765119

A/Accession: H61491

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-19 <HR>

A/Cross-references: UNIPARC:UPI000017B071

C/Keywords: glycoprotein; seed

Query Match 26.9%; Score 18; DB 2; Length 19;  
 Best Local Similarity 66.7%; Pred. No. 7.9e+03;  
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 EKNSFE 7  
 |||  
 Db 12 EKNSNE 17

## RESULT 70

S50175

kallikrein (PK-120) - human

C/Species: Homo sapiens (man)

C/Date: 14-Jul-1995 #sequence\_revision 21-Jul-1995 #text\_change 21-Jul-1995

C/Accession: S50175

R/Fu, X.P.; Iwamoto, A.; Nishimura, H.; Nagasawa, S.

Biochim. Biophys. Acta 1208, 338-343, 1994

A/Title: Purification and characterization of a novel substrate for plasma kallikrein (

A/Reference number: S50175; PMID:95035036; PMID:7947966

A/Accession: S50175

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-20 <PDX>

A/Cross-references: UNIPARC:UPI000017C287

Query Match 26.9%; Score 18; DB 2; Length 20;  
 Best Local Similarity 50.0%; Pred. No. 8.3e+03;  
 Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 EKNSFE 7  
 |||  
 Db 1 EKNGID 6

## RESULT 71

PH1783

T cell receptor alpha chain V region (clone 2D9 V alpha 24-4) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 16-Jul-1999

C/Accession: PH1783

R/Porelli, S.; Yockey, C.E.; Brenner, M.B.; Balk, S.P.

J. Exp. Med. 176, 1-16, 1993

A/Title: Analysis of T cell antigen receptor (TCR) expression by human peripheral blood

A/Reference number: PH1754; MUID:93301585; PMID:8391057

A/Accession: PH1783

A/Structure: preliminary

A/Molecule type: mRNA

A/Residues: 1-20 <FOR>

A/Cross-references: UNIPARC:UPI000017C376

#### Query Match

Best Local Similarity 26.9%; Score 18; DB 2; Length 20;

Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 8 ILGP 12

DB 3 CVRP 7

#### RESULT 72

A31516

lectin, galactose/N-acetylglucosamine-specific - rat (fragment)

C/Species: Rattus norvegicus (Norway rat)

C/Date: 28-Feb-1990 #sequence\_revision 28-Feb-1990 #text\_change 18-Jun-1993

C/Accession: A31516

R/II, M.; Kawasaki, T.; Yamashina, I.

Biochem. Biophys. Res. Commun. 155, 720-725, 1988

A/Title: Structural similarity between the macrophage lectin specific for galactose/N-ac

A/Reference number: A31516; MUID:8833956; PMID:3421964

A/Accession: A31516

A/Molecule type: protein

A/Residues: 1-20 <IX>

A/Cross-references: UNIPARC:UPI000017C946

#### Query Match

Best Local Similarity 26.9%; Score 18; DB 2; Length 20;

Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEKN 4

DB 6 EKN 9

#### RESULT 73

S29636

Jacalin beta-1 chain - Artocarpus champeden (fragment)

C/Species: Artocarpus champeden

C/Date: 19-Mar-1997 #sequence\_revision 17-Jul-1998 #text\_change 09-Jul-2004

C/Accession: S29636

R/NGOC, L.D.; Brillard, M.; Hoebeke, J.

Biochim. Biophys. Acta 1156, 219-222, 1993

A/Title: The alpha- and beta-subunits of the jacalins are cleavage products from a 17-kD

A/Reference number: S29635; MUID:93152601; PMID:8427879

A/Accession: S29636

A/Molecule type: protein

A/Residues: 1-20 <NGO>

A/Cross-references: UNIPROT:Q9S8T0; UNIPARC:UPI00000A4123

A/Experimental source: seed

C/Function: heterotetramer; two alpha and two beta chains

A/Description: seed storage protein

A/Note: lectin for D-galactoseyl-beta-1->3-N-acetylgalactosamine, a tumor-associated T-ce

C/Keywords: heterotetramer, lectin, seed, storage protein

Query Match 26.9%; Score 18; DB 2; Length 20;

Best Local Similarity 75.0%; Pred. No. 8.3e+03;

Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 9 ILGP 12

DB 11 IVGP 14

RESULT 74

S03987

agglutinin beta-2 chain - Oage orange

C/Species: Machura pomifera (Oage orange)

C/Date: 28-Feb-1990 #sequence\_revision 28-Feb-1990 #text\_change 09-Jul-2004

C/Accession: S03987

R/Young, N.M.; Johnston, R.A.Z.; Szabo, A.G.; Watson, D.C.

Arch. Biochem. Biophys. 270, 596-603, 1989

A/Title: Homology of the D-galactose-specific lectins from Artocarpus integrifolia and

A/Reference number: S03983; MUID:89206218; PMID:2705782

A/Accession: S03987

A/Molecule type: protein

A/Residues: 1-20 <YOU>

A/Cross-references: UNIPROT:P18676; UNIPARC:UPI0000111F85

#### Query Match

Best Local Similarity 26.9%; Score 18; DB 2; Length 20;

Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 9 ILGP 12

DB 10 IVGP 13

#### RESULT 75

B61497

seed protein w8-20 - winged bean (fragment)

C/Species: Psophocarpus tetragonolobus (winged bean)

C/Date: 07-Oct-1994 #sequence\_revision 07-Oct-1994 #text\_change 09-Jul-2004

C/Accession: B61497

R/Hirano, H.

J. Protein Chem. 8, 115-130, 1989

A/Title: Microsequence analysis of winged bean seed proteins electrophoretically from two di

A/Reference number: A61491; MUID:89351606; PMID:2765119

A/Accession: B61497

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-20 <HIR>

A/Cross-references: UNIPROT:Q9S8J4; UNIPARC:UPI000017B06E

C/Keywords: glycoprotein; seed

Query Match 26.9%; Score 18; DB 2; Length 20;

Best Local Similarity 66.7%; Pred. No. 8.3e+03;

Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 EKNSFE 7

DB 12 EKNSE 17

#### RESULT 76

AB0120

Insertion element protein (partial) [imported] - Yersinia pestis (strain CO92)

C/Species: Yersinia pestis

C/Date: 02-Nov-2001 #sequence\_revision 02-Nov-2001 #text\_change 09-Jul-2004

C/Accession: AB0120

R/Parikh, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B

deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;

11, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,

Nature 413, 523-527, 2001

A/Title: Genome sequence of Yersinia pestis, the causative agent of plague.

A/Reference number: AB0001; MUID:21470413; PMID:11586360

A/Accession: AB0120

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-20 <KIR>

A/Cross-references: UNIPROT:Q8ZHC1; UNIPARC:UPI00000CD77D; GB:AL590842; PIDN:CA089824.1

C/Genetics: 1nsb

A/Gene: 1nsb

Query Match 26.9%; Score 18; DB 2; Length 20;

Best Local Similarity 66.7%; Pred. No. 8.3e+03;

Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DEKNSF 6  
||:|  
Db 8 DEQMSF 13

# RESULT 77

A33098  
244K exoantigen - malaria parasite (Plasmodium falciparum) (fragments)  
C/Species: Plasmodium falciparum  
C/Date: 24-Aug-1990 #sequence\_revision 24-Aug-1990 #text\_change 09-Jun-2000  
C/Accession: A33098  
R/Nichols, J.H.; Hager, L.P.  
submitted to the Protein Sequence Database, May 1990  
A/Reference number: A33098  
A/Accession: A33098  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-7 <NIC>  
A/Cross-references: UNIPARC:UPI000017B5B9

Query Match 25.4%; Score 17; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 LGP 12  
|||  
Db 2 LGP 4

# RESULT 78

I54017  
granulocyte-colony stimulating factor precursor - synthetic (fragment)  
C/Species: synthetic  
A/Note: human gene engineered and expressed in Escherichia coli  
C/Date: 28-Jan-2000 #sequence\_revision 28-Jan-2000 #text\_change 28-Jan-2000  
C/Accession: I54017  
R/Devlin, P.E.; Drummond, R.J.; Toy, P.; Mark, D.F.; Watt, K.W.; Devlin, J.J.  
Gene 65, 13-22, 1988  
A/Title: Alteration of amino-terminal codons of human granulocyte-colony-stimulating fac  
1.  
A/Reference number: I54017; MUID:88284374; PMID:2456256  
A/Accession: I54017  
A/Status: translated from GB/EMBL/DBJ  
A/Molecule type: mRNA  
A/Residues: 1-8 <DEV>  
A/Cross-references: UNIPARC:UPI0000000448; GB:M20922; NID:g806638; PIND:AAA6353.1; PID:

Query Match 25.4%; Score 17; DB 4; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 LGP 12  
|||  
Db 4 LGP 6

# RESULT 79

S65728  
hemoglobin, extracellular, chain d1 - earthworm (Lumbricus terrestris) (fragment)  
C/Species: Lumbricus terrestris (common earthworm)  
C/Date: 06-Dec-1996 #sequence\_revision 13-Mar-1997 #text\_change 31-Dec-2004  
C/Accession: S65728  
R/Puhtiant, K.; Higashiyama, K.; Asao, M.; Hosokawa, K.  
Biochim. Biophys. Acta 1292, 273-280, 1996  
A/Title: Characterization of the constituent polypeptides of the extracellular hemoglobin  
A/Reference number: S65721; MUID:9617685; PMID:8597573  
A/Accession: S65728  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-10 <FUS>  
A/Cross-references: UNIPROT:O61233; UNIPARC:UPI000017BD82  
C/Superfamily: extracellular hemoglobin

Query Match 25.4%; Score 17; DB 2; Length 10;  
Best Local Similarity 50.0%; Pred. No. 6.3e+03;  
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 7 ECIL 10  
||:|  
Db 1 ECLV 4

# RESULT 80

PH1583  
Ig H chain V-D-J region (wild-type clone 6) - mouse (fragment)  
C/Species: Mus musculus (house mouse)  
C/Date: 02-Jun-1994 #sequence\_revision 02-Jun-1994 #text\_change 17-Mar-1999  
C/Accession: PH1583  
R/Levinson, D.A.; Campos-Torres, J.; Leder, P.  
J. Exp. Med. 178, 317-329, 1993  
A/Title: Molecular characterization of transgene-induced immunodeficiency in B-less mcr  
A/Reference number: PH1580; MUID:93301609; PMID:8315387  
A/Accession: PH1583  
A/Molecule type: DNA  
A/Residues: 1-11 <LEV>  
A/Cross-references: UNIPARC:UPI000017C6C9  
A/Experimental source: bone marrow pre-B lymphocyte  
C/Keywords: immunoglobulin

Query Match 25.4%; Score 17; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 6.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 LGP 12  
|||  
Db 5 LGP 7

# RESULT 81

I41978  
calliphoramide 9 - blowfly (Calliphora vomitoria)  
C/Species: Calliphora vomitoria  
C/Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 09-Jul-2004  
C/Accession: I41978  
R/Duve, H.; Johnsen, A.H.; Sewell, J.C.; Scott, A.G.; Orchard, I.; Rehfeld, J.F.; Thorp  
Proc. Natl. Acad. Sci. U.S.A. 89, 2326-2330, 1992  
A/Title: Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH-2 neuropeptides (des  
A/Reference number: A41978; MUID:92196111; PMID:1549595  
A/Accession: I41978  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-11 <DUV>  
A/Cross-references: UNIPROT:P41664; UNIPARC:UPI000012A52B  
C/Keywords: amidated carboxyl end; neuropeptide  
P/11/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 25.4%; Score 17; DB 2; Length 11;  
Best Local Similarity 75.0%; Pred. No. 6.9e+03;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 KNSF 6  
|||  
Db 5 KNSF 8

# RESULT 82

C37196  
bradykinin-potentiating peptide 3 - island jararaca  
C/Species: Bothrops inulalis (island jararaca)  
C/Date: 14-Feb-1992 #sequence\_revision 01-Dec-1992 #text\_change 09-Jul-2004  
C/Accession: C37196  
R/Cintrra, A.C.O.; Vieira, C.A.; Giglio, J.R.  
J. Protein Chem. 9, 221-227, 1990  
A/Title: Primary structure and biological activity of bradykinin potentiating peptides  
A/Reference number: A37196; MUID:90351557; PMID:2386615  
A/Accession: C37196

A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-11 <CIN>  
A/Cross-references: UNIPROT:P30423, UNIPARC:UPI0000126A91  
F/I/Modified site: pyroglutamic acid  
F/I/Modified site: pyroglutamic acid (Gln) #status experimental

Query Match 25.4%; Score 17; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 6.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 LGP 12  
|||  
Db 2 LGP 4

## RESULT 83

C20907  
Ig kappa-1 chain J3 region - rabbit  
C/Species: Oryctolagus cuniculus (domestic rabbit)  
C/Date: 10-Aug-1990 #sequence\_revision 10-Aug-1990 #text\_change 16-Aug-1996  
C/Accession: C20907  
R/Author: L. J. Max, E. E.  
Nucleic Acids Res. 11, 8877-8890, 1983

A/Title: Structural analysis of a rabbit immunoglobulin kappa2 J-C locus reveals multiple  
A/Reference number: A20907; MUID:84169523; PMID:6324107  
A/Accession: C20907  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-12 <EMO>  
A/Cross-references: UNIPARC:UPI000017C5CF  
C/Keywords: heterotetramer; immunoglobulin

Query Match 25.4%; Score 17; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 7.6e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 LGP 12  
|||  
Db 3 LGP 5

## RESULT 84

A49637

MHC class II histocompatibility antigen DRB6 - chimpanzee (fragment)  
C/Species: Pan troglodytes (chimpanzee)  
C/Date: 16-Feb-1996 #sequence\_revision 16-Feb-1996 #text\_change 09-Jul-2004  
C/Accession: A49637  
R/Mayer, W.E.; O'Huigin, C.; Klein, J.  
Proc. Natl. Acad. Sci. U.S.A. 90, 10720-10724, 1993

A/Title: Resolution of the HLA-DRB6 puzzle: a case of grafting a de novo-generated exon  
A/Reference number: A49637; MUID:94068473; PMID:8248165  
A/Accession: A49637  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-12 <RBS>  
A/Cross-references: UNIPROT:Q07884; UNIPARC:UPI000008A9D0; GB:L19439; NID:9304431; PIDN:  
C/Genetics:  
A/Gene: MHC-DRB6

Query Match 25.4%; Score 17; DB 2; Length 12;  
Best Local Similarity 57.1%; Pred. No. 7.6e+03;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 4 NSPECIL 10  
|||  
Db 4 NSLCLRL 10

## RESULT 85

PT0305  
Ig heavy chain CRD3 region (clone 5-121) - human (fragment)  
C/Species: Homo sapiens (man)

C/Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996  
C/Accession: PT0305  
R/Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.  
J. Exp. Med. 173, 395-407, 1991  
A/Title: Preferential utilization of specific immunoglobulin heavy chain diversity and  
A/Reference number: PT0222; MUID:91108337; PMID:1899102  
A/Accession: PT0305

A/Molecule type: DNA  
A/Residues: 1-13 <YAM>  
A/Cross-references: UNIPARC:UPI000017C20D  
A/Experimental source: B lymphocyte  
C/Keywords: heterotetramer; immunoglobulin

Query Match 25.4%; Score 17; DB 2; Length 13;  
Best Local Similarity 66.7%; Pred. No. 8.2e+03;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 6 FFC 8  
|||  
Db 2 FDC 4

## RESULT 86

PH0787

T-cell receptor alpha chain (F8) - mouse (fragment)  
C/Species: Mus musculus (house mouse)  
C/Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
C/Accession: PH0787  
R/Caenova, J.L.; Romero, P.; Midmann, C.; Kourilsky, P.; Maryanski, J.L.  
J. Exp. Med. 174, 1371-1383, 1991

A/Title: T cell receptor genes in a series of class I major histocompatibility complex-  
allelic exclusion and antigen-specific repertoire.  
A/Reference number: PH0746; MUID:92078846; PMID:1836010  
A/Accession: PH0787  
A/Molecule type: mRNA  
A/Residues: 1-13 <CAS>  
A/Cross-references: UNIPARC:UPI000017C76D; EMBL:X60891  
A/Experimental source: T lymphocyte  
C/Keywords: T-cell receptor

Query Match 25.4%; Score 17; DB 2; Length 13;  
Best Local Similarity 100.0%; Pred. No. 8.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 CIL 10  
|||  
Db 1 CIL 3

## RESULT 87

B42762

proteasome endopeptidase complex (EC 3.4.25.1) subunit 13 - bovine (fragment)  
C/Species: Bos primigenius taurus (cattle)  
C/Date: 04-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change 17-Feb-2003  
C/Accession: B42762  
R/Dick, L.R.; Moomaw, C.R.; Pramank, B.C.; Demartino, G.N.; Slaughter, C.A.  
Biochemistry 31, 7347-7355, 1992

A/Title: Identification and localization of a cysteine1 residue critical for the trypsin  
A/Reference number: A42762; MUID:92378961; PMID:11510924  
A/Accession: B42762  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-13 <DIC>  
A/Cross-references: UNIPARC:UPI000017CE37  
A/Note: sequence extracted from NCBI backbone (NCBIF:112180)  
C/Keywords: hydrolase

Query Match 25.4%; Score 17; DB 2; Length 13;  
Best Local Similarity 44.4%; Pred. No. 8.2e+03;  
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 1 DEKNSPECI 9  
|||

Db 2 DPEXLPETI 10

# RESULT 88

PH1615

ig H chain V-D-J region (clone B-less 22) - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 02-Jun-1994 #sequence\_revision 02-Jun-1994 #text\_change 17-Mar-1999

C/Accession: PH1615

R/Levinson, D.A.; Campos-Torres, J.; Leder, P.

J. Exp. Med. 178, 317-329, 1993

A/Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice

A/Reference number: PH1580; PMID:93301609; PMID:8315387

A/Accession: PH1615

A/Molecule type: DNA

A/Residues: 1-14 <LEV>

A/Cross-references: UNIPARC:UPI000017C69E

A/Experimental source: bone marrow pre-B lymphocyte

C/Keywords: immunoglobulin

Query Match 25.4%; Score 17; DB 2; Length 14;

Best Local Similarity 75.0%; Pred. No. 8.8e+03;

Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DEKN 4

Db 3 DESN 6

# RESULT 89

PT0210

T-cell receptor alpha chain V-J region (4-1-K.1) - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 31-Dec-1991 #sequence\_revision 31-Dec-1991 #text\_change 30-May-1997

C/Accession: PT0210

R/Nakano, N.; Kikutani, H.; Nishimoto, H.; Kishimoto, T.

J. Exp. Med. 173, 1091-1097, 1991

A/Title: T cell receptor V gene usage of islet beta cell-reactive T cells is not restricted

A/Reference number: PT0209; PMID:91217621; PMID:1902501

A/Accession: PT0210

A/Molecule type: mRNA

A/Residues: 1-14 <NAK>

A/Cross-references: UNIPARC:UPI000017C78E

C/Keywords: T-cell receptor

Query Match 25.4%; Score 17; DB 2; Length 14;

Best Local Similarity 100.0%; Pred. No. 8.8e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CIL 10

Db 1 CIL 3

# RESULT 90

A41589

25K elastin-binding protein - Staphylococcus aureus (fragment)

C/Species: Staphylococcus aureus

C/Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 09-Jul-2004

C/Accession: A41589

R/Park, P.W.; Roberts, D.D.; Grosso, L.E.; Parke, W.C.; Rosenblom, J.; Abrams, W.R.; Mc

J. Biol. Chem. 266, 23399-23406, 1991

A/Title: Binding of elastin to Staphylococcus aureus.

A/Reference number: A41589; PMID:92078218; PMID:1744133

A/Accession: A41589

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-14 <PAR>

A/Cross-references: UNIPROT:Q9RSR5; UNIPARC:UPI00000BC64C

Query Match

Best Local Similarity 25.4%; Score 17; DB 2; Length 14;

Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 KNSFE 7

Db 5 KODFE 9

# RESULT 91

S33802

chaperone, TCP1-related - cat

C/Species: Avena sativa (cat)

C/Date: 02-Dec-1993 #sequence\_revision 27-Feb-1997 #text\_change 09-Jul-2004

C/Accession: S33802

R/Mumme, R.; Grimm, R.; Specht, V.; Eckerskorn, C.; Schiltz, B.; Gatenby, A.A.; Schaefer

Nature 363, 644-648, 1993

A/Title: A TCP1-related molecular chaperone from plants refolds phytochrome to its phot

A/Reference number: S33800; PMID:93288140; PMID:8099715

A/Accession: S33802

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-14 <MDM>

A/Cross-references: UNIPROT:Q7MIG6; UNIPARC:UPI000017B0D7

Query Match 25.4%; Score 17; DB 2; Length 14;

Best Local Similarity 100.0%; Pred. No. 8.8e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 LCP 12

Db 7 LCP 9

# RESULT 92

S68095

calcium-binding protein, 23k - Orchestia cavimana (fragment)

C/Species: Orchestia cavimana

C/Date: 21-Apr-1997 #sequence\_revision 21-Apr-1997 #text\_change 09-Jul-2004

C/Accession: S68095

R/Linnet, G.; Testeniere, O.; Graf, F.

Biochim. Biophys. Acta 1293, 272-276, 1996

A/Title: Characterization and N-terminal sequencing of a calcium binding protein from ci

A/Reference number: S68095; PMID:96202045; PMID:8620040

A/Accession: S68095

A/Molecule type: protein

A/Residues: 1-14 <LUQ>

A/Cross-references: UNIPROT:Q7M3J6; UNIPARC:UPI000017CA5F

C/Keywords: calcium binding

Query Match 25.4%; Score 17; DB 2; Length 14;

Best Local Similarity 60.0%; Pred. No. 8.8e+03;

Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DEKNS 5

Db 9 DEKRS 13

# RESULT 93

B83836

hypothetical protein BH1490 [imported] - Bacillus halodurans (strain C-125)

C/Species: Bacillus halodurans

C/Date: 01-Dec-2000 #sequence\_revision 01-Dec-2000 #text\_change 09-Jul-2004

C/Accession: B83836

R/Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hir

Nucleic Acids Res. 28, 4317-4331, 2000

A/Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and

A/Reference number: A83650; PMID:20512582; PMID:11058132

A/Accession: B83836

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-14 <STO>

A/Cross-references: UNIPROT:Q9KCS9; UNIPARC:UPI00000C3BC; GB:AF001512; GB:BA000004; NI

A/Experimental source: strain C-125

C/Genetics:

A:Gene: BH1490

Query Match 25.4%; Score 17; DB 2; Length 14;  
Best Local Similarity 50.0%; Pred. No. 8.8e+03;  
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 DEKNSF 6  
| : ||  
Db 9 EASFSF 14

RESULT 94

S27140

hypothetical protein 1 estrogen receptor 5'-region - human

C/Species: Homo sapiens (man)

C/Date: 05-Mar-1994 #sequence\_revision 12-May-1995 #text\_change 16-Aug-2004

C/Accession: S27140

R/Keaveney, M.; Klug, J.; Gannon, F.

DNA Seq. 2, 347-358, 1992

A/Title: Sequence analysis of the 5' flanking region of the human estrogen receptor gene

A/Reference number: S27140; MUID:93075998; PMID:1476547

A/Accession: S27140

A/Status: translation not shown

A/Molecule type: DNA

A/Residues: 1-14 &lt;KEA&gt;

A/Cross-references: UNIPARC:UPI000011DPF5; EMBL:X62462; NID:931201; PIDD:CAA44319.1; PII

Query Match 25.4%; Score 17; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 8.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 LGP 12  
| : ||  
Db 12 LGP 14

RESULT 95

PM0004

chlorophyll a/b-binding protein 24.5K - green alga (Dunaliella tertiolecta) (fragment)

N/Alternate names: photosystem II light-harvesting chlorophyll 24.5K protein

C/Species: Dunaliella tertiolecta

C/Date: 04-Sep-1998 #sequence\_revision 24-Nov-1999 #text\_change 24-Nov-1999

C/Accession: PM0004

R/Laroche, J.; Bennett, J.; Falkowski, P.G.

Gene 95, 165-171, 1990

A/Title: Characterization of a cDNA encoding for the 28.5-kDa LHClI apoprotein from the

A/Reference number: JMW040; MUID:91065528; PMID:2249775

A/Accession: PM0004

A/Molecule type: protein

A/Residues: 1-15 &lt;LAR&gt;

A/Cross-references: UNIPARC:UPI0000178174

A/Supfamily: chlorophyll a/b-binding protein

C/Keywords: chloroplast; grana; light-harvesting complex; membrane adhesion; membrane pr

Query Match 25.4%; Score 17; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 9.5e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 LGP 12  
| : ||  
Db 12 LGP 14

RESULT 96

PH1342

Ig heavy chain DJ region (clone C507-95) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999

C/Accession: PH1342

R/Wasserman, R.; Gallili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.

J. Exp. Med. 176, 1577-1581, 1992

A/Title: Predominance of fetal type DJH joining in young children with B precursor lymph

A/Accession: PH1342  
A/Molecule type: DNA  
A/Residues: 1-15 <MAS>  
A/Cross-references: UNIPARC:UPI000017C240  
C/Keywords: heterotetramer; immunoglobulin

Query Match 25.4%; Score 17; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 9.5e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 LGP 12  
| : ||  
Db 10 LGP 12

RESULT 97

PT0097

glutathione peroxidase, non-selenium containing - mouse (fragment)

N/Alternate names: antioxidant protein 2

C/Species: Mus musculus (house mouse)

C/Date: 21-Aug-1998 #sequence\_revision 21-Aug-1998 #text\_change 24-Nov-1999

C/Accession: PT0097

R/Kawakami, T.; Uchida, T.; Sakai, T.; Kamo, M.; Morimasa, T.; Tsugita, A.

submitted to JIPD, July 1998

A/Description: Proteome analysis of mouse brain.

A/Reference number: PT0091

A/Accession: PT0097

A/Molecule type: protein

A/Residues: 1-15 &lt;KAW&gt;

A/Cross-references: UNIPARC:UPI000017C66B

A/Experimental source: Brain, striatum

Query Match 25.4%; Score 17; DB 2; Length 15;  
Best Local Similarity 66.7%; Pred. No. 9.5e+03;  
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 EKNSPF 7  
| : ||  
Db 9 EAPSPF 14

RESULT 98

PH1455

T-cell receptor alpha chain (clone A24/PBF4) - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 10-Mar-1994 #sequence\_revision 10-Mar-1994 #text\_change 15-Mar-2004

C/Accession: PH1455

R/Casanova, J.L.; Martinon, F.; Gournier, H.; Barra, C.; Pannetier, C.; Regnault, A.; K

J. Exp. Med. 177, 811-820, 1993

A/Title: T cell receptor selection by and recognition of two class I major histocompati

A/Reference number: PH1430; MUID:93171821; PMID:8436911

A/Accession: PH1455

A/Molecule type: mRNA

A/Residues: 1-15 &lt;CAS&gt;

A/Cross-references: UNIPARC:UPI000017C762

A/Experimental source: cytolytic T-lymphocyte

C/Keywords: receptor; T-cell

Query Match 25.4%; Score 17; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 9.5e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CTL 10  
| : ||  
Db 1 CTL 3

RESULT 99  
PA0008  
lectin B2 - Peophocarpus scandens (fragment)  
C/Species: Peophocarpus scandens  
C/Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 09-Jul-2004  
C/Accession: PA0008

R:Kort, A.A.  
 Phytochemistry 27, 2847-2855, 1988  
 A>Title: Isolation and characterization of the lectins from the seeds of Psophocarpus sc  
 A/Reference number: PA0005  
 A/Accession: PA0008  
 A/Molecule type: protein  
 A/Residues: 1-15 <KOR>  
 A/Cross-references: UNIPROT:P22585; UNIPARC:UPI000012E3B8  
 A/Experimental source: seed  
 C/Comment: The seeds of Psophocarpus contain two distinct groups of lectins which can be  
 C/Keywords: lectin

Query Match 25.4%; Score 17; DB 2; Length 15;  
 Best Local Similarity 75.0%; Pred. No. 9.5e+03;  
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 NSPE 7  
 | | |  
 | | |  
 Db 9 NKPE 12

## RESULT 100

A61612  
 allatostatin - tobacco hornworm  
 C/Species: Manduca sexta (tobacco hornworm)  
 C/Date: 21-Jul-1995 #sequence\_revision 21-Jul-1995 #text\_change 09-Jul-2004  
 C/Accession: A61612  
 R/Kramer, S.V.; Toschl, A.; Miller, C.A.; Kataoka, H.; Quistad, G.B.; Li, J.P.; Carney,  
 Proc. Natl. Acad. Sci. U.S.A. 88, 9458-9462, 1991  
 A/Title: Identification of an allatostatin from the tobacco hornworm Manduca sexta.  
 A/Reference number: A61612; MUID:92052112; PMID:1946359  
 A/Accession: A61612  
 A/Status: preliminary  
 A/Molecule type: protein  
 A/Residues: 1-15 <KRA>  
 A/Cross-references: UNIPROT:P42559; UNIPARC:UPI00001258A8  
 C/Keywords: neuropeptide; pyroglutamic acid  
 F/1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 25.4%; Score 17; DB 2; Length 15;  
 Best Local Similarity 75.0%; Pred. No. 9.5e+03;  
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 ECTIGP 12  
 : | |  
 : | |  
 Db 6 QCYFNP 11

Search completed: January 20, 2006, 19:12:12  
 Job time : 6.80769 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 20, 2006, 18:54:54 : Search time 39.9231 Seconds  
(without alignments)  
212.066 Million cell updates/sec

Title: US-09-662-293-5  
Perfect score: 67  
Sequence: 1 DEKNSFECILGP 12

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 14590

Minimum DB seq length: 0  
Maximum DB seq length: 20

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : Uniprot 05.80:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	27	40.3	14	2	016332_HUMAN
2	27	40.3	17	2	092633_CHLTR
3	27	40.3	19	2	071236_CAIER
4	26	38.8	18	2	09ERQ0_MOUSE
5	26	38.8	20	2	09DR23_CHICK
6	25	37.3	13	2	08WEKO_CYCCT
7	25	37.3	17	2	08HKG8_PACAR
8	25	37.3	20	2	09S835_PSORB
9	24	35.8	12	2	06DK20_HUMAN
10	24	35.8	13	2	05DA49_9RH12
11	24	35.8	13	2	091874_HPV16
12	24	35.8	13	2	091876_HPV16
13	24	35.8	16	2	091871_HPV16
14	24	35.8	16	2	091879_HPV16
15	24	35.8	16	2	091802_HPV16
16	24	35.8	16	2	091804_HPV16
17	24	35.8	16	2	091806_HPV16
18	24	35.8	16	2	091808_HPV16
19	24	35.8	17	1	091808_HPV16
20	24	35.8	19	2	071239_CAIER
21	24	35.8	12	2	04YR89_PLABR
22	24	35.8	12	2	09YR91_9CORO
23	23	34.3	13	2	05F3D0_CHICK
24	23	34.3	16	2	09N0P9_CANFA
25	23	34.3	17	2	08HKR2_PACAR
26	23	34.3	17	2	08HKR6_PACAR
27	23	34.3	17	2	08HKR2_PACAR
28	23	34.3	18	2	04XX11_PLACH
29	23	34.3	20	2	072579_HUMAN
30	23	34.3	20	2	04XN21_PLACH
31	23	34.3	20	2	095M29_PANTR

32	23	34.3	20	2	095MK0_PONPY
33	23	34.3	20	2	095MK1_COLAN
34	23	34.3	20	2	095MK2_PAPCY
35	22	32.8	10	1	RCA_PINS
36	22	32.8	10	2	07RQJ0_PLAVO
37	22	32.8	11	2	08UDP1_XENLA
38	22	32.8	13	2	06LDS1_BPT3
39	22	32.8	14	2	081027_MOUSE
40	22	32.8	14	2	093202_PICRC
41	22	32.8	14	2	077NR3_PICRC
42	22	32.8	14	2	077RC0_PICRC
43	22	32.8	14	2	077RM6_PICRC
44	22	32.8	14	2	077S02_PICRC
45	22	32.8	14	2	077S09_PICRC
46	22	32.8	14	2	077S13_PICRC
47	22	32.8	15	1	FIBA_ANAPL
48	22	32.8	15	2	05RLM1_HUMAN
49	22	32.8	17	2	09TWC6_DIRIM
50	22	32.8	17	2	06OLM0_GINFA
51	22	32.8	17	2	06OLM1_GINFA
52	22	32.8	17	2	09DFB5_BRABE
53	22	32.8	19	2	06SE40_DROSI
54	22	32.8	19	2	09TWH8_PARCW
55	22	32.8	19	2	06OLM2_GINFA
56	22	32.8	20	2	04X7B9_PLACH
57	21	31.3	10	2	09R791_BORAP
58	21	31.3	11	2	09R790_BORAP
59	21	31.3	14	2	06LEW9_ARATH
60	21	31.3	14	2	056127_PICRC
61	21	31.3	15	2	06LC27_HUMAN
62	21	31.3	15	2	09RAU8_ACTCA
63	21	31.3	16	1	PA2_NAUSP
64	21	31.3	17	2	Q14316_HUMAN
65	21	31.3	17	2	06OL17_GINFA
66	21	31.3	18	2	06OL19_GINFA
67	21	31.3	18	2	04X7V0_PLACH
68	21	31.3	19	2	04Y1S4_PLACH
69	21	31.3	19	2	08URH2_CHICK
70	21	31.3	19	2	08UVE0_CHICK
71	21	31.3	19	2	05PU92_BRABE
72	21	31.3	20	1	MHT_BOMMX
73	21	31.3	20	1	MHT_BOMMX
74	21	31.3	20	2	04YTB5_PLABR
75	21	31.3	20	2	049448_MYCSE
76	21	31.3	20	2	04G2P1_MYCTU
77	21	31.3	20	2	06TH87_MOUSE
78	21	31.3	20	2	07LZ97_RANCA
79	20	29.9	12	2	012036_CAVY
80	20	29.9	14	2	06LCK3_HUMAN
81	20	29.9	15	2	09Y4Z9_HUMAN
82	20	29.9	16	2	07M2P4_PIG
83	20	29.9	17	2	05B1H5_EMEHI
84	20	29.9	17	2	04XMI0_PLACH
85	20	29.9	17	2	0704V9_BOVIN
86	20	29.9	17	2	0712K0_CAPIH
87	20	29.9	18	1	HSTB_ECOLI
88	20	29.9	18	2	07M532_HALMA
89	20	29.9	18	2	07S364_NEURC
90	20	29.9	18	2	07MGU3_CITPR
91	20	29.9	18	2	07M076_RAT
92	20	29.9	19	1	DURA_STRGV
93	20	29.9	19	1	DURA_STRGV
94	20	29.9	19	1	LANC_STRS6
95	20	29.9	19	2	09TWK8_9TRYP
96	20	29.9	19	2	04X4E2_PLACH
97	20	29.9	19	2	04Y9U4_PLABR
98	20	29.9	19	2	09G197_9PHAS
99	20	29.9	19	2	0570L9_ARATH
100	20	29.9	20	2	Q16129_HUMAN

## ALIGNMENTS

095mk0	pongo pygma
095mk1	colobus ang
095mk2	papio cynos
P81084	pinus pinas
Q7CJ10	plasmodium
08UUP1	xenopus lae
06LDS1	bacterioph
081027	mus musculu
093202	porcine cir
077NR3	porcine cir
077RC0	porcine cir
077RM6	porcine cir
077S02	porcine cir
077S09	porcine cir
077S13	porcine cir
Q77813	bovine cirtc
Q5RLM1	anae platyr
09TWH8	homo sapien
06OLM0	influenza a
06OLM1	influenza a
09DFB5	brachydanio
06SE40	drosophila
09TWH8	paralithode
06OLM2	influenza a
04X7B9	plasmodium
09R791	borrelia af
09R790	borrelia ga
06LEW9	arabidopsis
056127	porcine cir
06LC27	homo sapien
09RAU8	actinobact
Q10756	naja sputat
Q14316	homo sapien
06OL17	influenza a
06OL19	influenza a
04X7V0	plasmodium
04Y1S4	plasmodium
08URH2	gallus gall
08UVE0	gallus gall
05PU92	brachydanio
P83086	bombina max
P83087	bombina max
04YUS5	plasmodium
Q49448	mycoplasma
Q4G2P1	mycobacteri
06TH87	mus musculu
07LZ97	rana catesb
012036	caprine art
06LCK3	homo sapien
09Y4Z9	homo sapien
07M2P4	sus scrofa
05B1H5	aspergillus
04XMI0	plasmodium
0704V9	bos taurus
0712K0	capra hircu
Q712K0	capra hircu
P01560	escherichia
Q7S364	halocaula
07S364	neurospora
07MGU3	citrobacter
07M076	rattus norv
P36504	streptococ
P36502	streptococ
P38655	trypanosoma
09TWK8	trypanosoma
04X4E2	plasmodium
04Y9U4	plasmodium
09G197	sargassum p
0570L9	arabidopsis
Q16129	homo sapien

```

RESULT 1
Q16332_HUMAN
ID Q16332_HUMAN PRELIMINARY; PRT; 14 AA.
AC Q16332;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE FLT (Fragment).
GN Name=flt;
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=95222657; PubMed=7707437;
RA Boocock C.A., Charnock-Jones D.S., Sharkey A.M., McLaren J.,
RA Barker P.J., Wright K.A., Twentymen P.R., Smith S.K.;
RT "Expression of vascular endothelial growth factor and its receptors
RT flt and KDR in ovarian carcinoma."
RL J. Natl. Cancer Inst. 87:506-516 (1995).
DR EMBL; S77812; AAB34001.1; -; mRNA.
DR PIR; I56493; I56493.
FT NON_TER 14
SQ SEQUENCE 14 AA; 1636 MW; 9141470E2648F62E CRC64;

Query Match 40.3%; Score 27; DB 2; Length 14;
Best Local Similarity 50.0%; Pred. No. 9.1e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 EKXSFECI 9
DB 1 ELSNFECI 8

RESULT 2
Q9ZG33_CHLTR
ID Q9ZG33_CHLTR PRELIMINARY; PRT; 17 AA.
AC Q9ZG33;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
DE Subtilisin/chymotrypsin inhibitor (Fragment).
OS Chlamydia trachomatis.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=813;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=L2 434B;
RA Wang L., Steenburg S.D., Zheng Y., Larsen S.H.;
RA Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF087336; AAD04110.1; -; Genomic_DNA.
FT NON_TER 17
SQ SEQUENCE 17 AA; 2043 MW; 4FEE704EBB041E120 CRC64;

Query Match 40.3%; Score 27; DB 2; Length 17;
Best Local Similarity 83.3%; Pred. No. 1.1e+03;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DEKNSF 6
DB 10 DRKNSF 15

RESULT 3
Q7LZ96_CAICR
ID Q7LZ96_CAICR PRELIMINARY; PRT; 19 AA.
AC Q7LZ96;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)

```

```

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Gamma crystallin II (Fragment).
OS Catman crocodilus (Speckled catman) (Catman sclerops).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Crocodylidae; Alligatorinae; Catman.
OX NCBI_TaxID=8499;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=89351593; PubMed=3255376;
RA Chion S.H.;
RT "The protein sequence homology of gamma-crystallins among major
RT vertebrate classes and their DNA sequence homology to heat-shock
RT protein genes."
RL J. Protein Chem. 7:527-534 (1988).
DR PIR; A60894; A60894.
DR HSSP; P07320; 1HA4.
DR InterPro; IPR001064; Crystallin.
DR Pfam; PF00030; Crystallin_1.
DR PROSITE; PS50915; CRYSTALLIN_BETAGAMMA; 1.
FT NON_TER 19
SQ SEQUENCE 19 AA; 2236 MW; A95AFC3551E3885A CRC64;

Query Match 40.3%; Score 27; DB 2; Length 19;
Best Local Similarity 50.0%; Pred. No. 1.2e+03;
Matches 6; Conservative 2; Mismatches 0; Indels 4; Gaps 1;

QY 1 DEKN---SFEC 8
DB 7 ESKNFQGRSYEC 18

RESULT 4
Q9ER00_MOUSE
ID Q9ER00_MOUSE PRELIMINARY; PRT; 18 AA.
AC Q9ER00;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Amelogenin (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathu;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20515040; PubMed=11063035;
RA Snead M.L., Paine M.L., Wen L., Zhu D.-H., Yoshida B., Lei Y.,
RA Chen L., Paine C.T., Burestein J.M., Jitpukdeeбудинтра S., White S.N.,
RA Bringas P. Jr.;
RT "Transgene animal model for protein expression and accumulation into
RT forming enamel."
RT Connect. Tissue Res. 38:279-286 (1998).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RL Snead M.L., Zhu D., Lei Y., Paine M.L.;
RA Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF294397; AAG10078.1; -; Genomic_DNA.
DR GO; GO:0005578; C:extracellular matrix (sensu Metazoa); IEA.
DR GO; GO:0007275; P:development; IEA.
DR InterPro; IPR004116; Amelogenin.
DR PANTHER; PTHR10039; Amelogenin; 1.
FT NON_TER 18
SQ SEQUENCE 18 AA; 1913 MW; 302AA3BA4FBB6FC CRC64;

Query Match 38.8%; Score 26; DB 2; Length 18;
Best Local Similarity 66.7%; Pred. No. 1.8e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 FECTIG 11
DB 7 FACIIG 12

```

## RESULT 5

Q9DE23\_CHICK PRELIMINARY; PRT; 20 AA.  
 ID Q9DE23;  
 AC Q9DE23;  
 DT 01-MAR-2001 (TREMBlrel. 16, Created)  
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)  
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)  
 DE UORF2.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianine;  
 CC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=20528616; PubMed=11073974;  
 RX DOI=10.1128/MCB.20.23.8731-8739.2000;  
 RA Kobayashi M., Yu R.T., Yasuda K., Umesono K.;  
 RT "Cell-type-specific regulation of the retinoid acid receptor mediated  
 by the orphan nuclear receptor RXR."  
 RL Mol. Cell. Biol. 20:8731-8739(2000).  
 DR EMBL; AF220160; AAC35363.1; -; Genomic DNA.  
 SQ SEQUENCE 20 AA; 2261 MW; AA7738B0B3C482 CRC64;

Query Match 38.8%; Score 26; DB 2; Length 20;  
 Best Local Similarity 30.0%; Pred. No. 2e+03;

Matches 3; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 DEKNSPECIL 10

DB 7 DQDAFSCV 16

## RESULT 6

Q8WKO\_CYCCI PRELIMINARY; PRT; 13 AA.  
 ID Q8WKO;  
 AC Q8WKO;  
 DT 01-MAR-2002 (TREMBlrel. 20, Created)  
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)  
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)  
 DE NADH dehydrogenase (Fragment).  
 GN Nemeiad.  
 OS Cycaea citrinalis (Queen bsgo).  
 OC Mitochondrion.  
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 CC Spermatophyta; Cycadophyta; Cycadales; Cycadaceae; Cycaea.  
 OX NCBI\_TaxID=3397;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=2155473; PubMed=11697913; DOI=10.1006/mpev.2001.1004;  
 RA Gugerli F., Sperisen C., Buchler U., Brunner I., Brodbeck S.,  
 RA Palmer J.D., Qiu Y.L.;  
 RT "The evolutionary split of Pinaceae from other conifers: evidence from  
 an insertion loss and a multigene phylogeny."  
 RL Mol. Phylogenet. Evol. 21:167-175(2001).  
 DR EMBL; AF227465; AAL38909.1; -; Genomic DNA.  
 DR GO; GO:0005739; C:mitochondrion; IEA.  
 KM Mitochondrion.  
 FT NON\_TER  
 SQ SEQUENCE 13 AA; 1339 MW; C00F6BDA894945BD CRC64;

Query Match 37.3%; Score 25; DB 2; Length 13;  
 Best Local Similarity 50.0%; Pred. No. 2e+03;

Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 SPECILGP 12

DB 3 SYEASIGP 10

## RESULT 7

Q8HKG8\_9ACAR PRELIMINARY; PRT; 17 AA.  
 ID Q8HKG8;  
 AC Q8HKG8;  
 DT 01-MAR-2003 (TREMBlrel. 23, Created)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)  
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)  
 DE NADH dehydrogenase subunit 1 (Fragment).  
 GN Name=ND1;  
 OS Boophilus geiogyi.  
 OC Mitochondrion.  
 CC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;  
 CC Parasitiformes; Ixodida; Ixodidae; Ixodidae; Boophilus.  
 OX NCBI\_TaxID=136141;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=2260786; PubMed=12775521; DOI=10.1086/10635150309325;  
 RA Murrell A., Campbell N.J.H., Barker S.C.;  
 RT "The value of idiosyncratic markers and changes to conserved tRNA  
 sequences from the mitochondrial genome of hard ticks (Acari: Ixodida:  
 Ixodidae) for phylogenetic inference."  
 RL Syst. Biol. 52:296-310(2003).  
 DR EMBL; AY059200; AAL79403.1; -; Genomic DNA.  
 DR GO; GO:0005739; C:mitochondrion; IEA.  
 KM Mitochondrion.  
 FT NON\_TER  
 SQ SEQUENCE 17 AA; 2035 MW; 2E2FE0BFD529C379 CRC64;

Query Match 37.3%; Score 25; DB 2; Length 17;  
 Best Local Similarity 57.1%; Pred. No. 2.6e+03;

Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 NSPECIL 10

DB 8 NNFICIL 14

## RESULT 8

Q9S8J5\_PSOTE PRELIMINARY; PRT; 20 AA.  
 ID Q9S8J5;  
 AC Q9S8J5;  
 DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)  
 DE Lectin 1 (Fragment).  
 GN Psophocarpus tetragonolobus (Gua bean) (Asparagus bean).  
 OS Psophocarpus tetragonolobus (Gua bean) (Asparagus bean).  
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 CC eustoids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;  
 CC Psophocarpus.  
 OX NCBI\_TaxID=3891;  
 RN [1]  
 RP PROTEIN SEQUENCE.  
 RX MEDLINE=95120265; PubMed=7820375;  
 RA Yagi F., Sawada R., Tanada T., Toyonaga S., Tadera K., Ishinata K.;  
 RT "Two isolectins from leaves of winged bean, Psophocarpus  
 tetragonolobus (L.) DC.";  
 RL Plant Cell Physiol. 35:1087-1095(1994).  
 SQ SEQUENCE 20 AA; 2363 MW; 1BF1B347020D3DCE CRC64;

Query Match 37.3%; Score 25; DB 2; Length 20;  
 Best Local Similarity 66.7%; Pred. No. 3.1e+03;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 EKNSPECIL 10

DB 12 EKNSNEIL 20

## RESULT 9

Q6DKZ0\_HUMAN PRELIMINARY; PRT; 12 AA.  
 ID Q6DKZ0;  
 AC Q6DKZ0;

DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
DE DnaU-like heat shock protein (Fragment).  
GN Name=DnaJB4;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae;  
OC Homo.  
NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Liver;  
RX PubMed=15782117;  
RA Wang C.C., Tsai M.P., Hong T.M., Chang G.C., Chen C.Y., Yang W.M.,  
RA Chen J.C., Yang P.C.;  
RT "The transcriptional factor YY1 upregulates the novel invasion  
RT suppressor HLI1 expression and inhibits cancer cell invasion.";  
RL Oncogene 24:4081-4093(2005).  
[2]  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Liver;  
RA Wang C.C., Chen J.C., Yang P.C.;  
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY669319; AAT70409.1; -, Genomic DNA.  
DR GO; GO:0006457; P:protein folding; IEA.  
KW GO; GO:0006986; P:response to unfolded protein; IEA.  
KW Heat shock.  
KW NON\_TER  
FT SEQUENCE 12 AA; 1405 MW; 121CA8B3195EAB4B CRC64;  
SQ

Query Match 35.8%; Score 24; DB 2; Length 12;  
Best Local Similarity 66.7%; Pred. No. 2.8e+03;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 FECLIG 11  
:|:|:|  
Db 5 YCCILG 10

RESULT 10  
QSD409.9RHIZ  
ID QSD409.9RHIZ PRELIMINARY; PRT; 13 AA.  
AC QSD409;  
DT 10-MAY-2005 (TrEMBLrel. 30, Created)  
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)  
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)  
DE TmRNA-encoded proteolysis-inducing peptide tag (Fragment).  
GN Name=SPR1;  
OS Agrobacterium tumefaciens.  
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
OC Rhizobiales; Rhizobium/Agrobacterium group; Agrobacterium.  
NCBI\_TaxID=358;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=NT4;  
RA Williams K.P.;  
RT "Phylogenetic analysis of tmRNA.";  
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY911526; AAX12897.1; -, Genomic DNA.  
FT NON\_TER  
SQ SEQUENCE 13 AA; 1304 MW; C47752578B8133D CRC64;  
FT

Query Match 35.8%; Score 24; DB 2; Length 13;  
Best Local Similarity 40.0%; Pred. No. 3.1e+03;  
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 DEKNSPECIL 10  
:|:|:|  
Db 2 NDNNAKCAL 11

RESULT 11

Q918T4.HPV16  
ID Q918T4.HPV16 PRELIMINARY; PRT; 13 AA.  
AC Q918T4;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DE E1 protein (Fragment).  
OS Human papillomavirus type 16.  
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
OC Alphapapillomavirus.  
NCBI\_TaxID=333760;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=21846229; PubMed=11857370;  
RA Watts K.J., Thompson C.H., Cossart Y.B., Rose B.R.;  
RT "Sequence variation and physical state of human papillomavirus type 16  
RT cervical cancer isolates from Australia and New Caledonia.";  
RL Int. J. Cancer 97:868-874(2002).  
DR EMBL; AF407220; AAL01406.1; -, Genomic DNA.  
FT NON\_TER  
SQ SEQUENCE 13 AA; 1413 MW; 8ABD73A03A52D865 CRC64;  
FT

Query Match 35.8%; Score 24; DB 2; Length 13;  
Best Local Similarity 42.9%; Pred. No. 3.1e+03;  
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 5 SFECLIG 11  
:|:|:|  
Db 1 TFKCVSG 7

RESULT 12  
Q918T6.HPV16  
ID Q918T6.HPV16 PRELIMINARY; PRT; 13 AA.  
AC Q918T6;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE E1 protein (Fragment).  
OS Human papillomavirus type 16.  
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
OC Alphapapillomavirus.  
NCBI\_TaxID=333760;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=21846229; PubMed=11857370;  
RA Watts K.J., Thompson C.H., Cossart Y.B., Rose B.R.;  
RT "Sequence variation and physical state of human papillomavirus type 16  
RT cervical cancer isolates from Australia and New Caledonia.";  
RL Int. J. Cancer 97:868-874(2002).  
DR EMBL; AF407219; AAL01403.1; -, Genomic DNA.  
FT NON\_TER  
SQ SEQUENCE 13 AA; 1413 MW; 8ABD73A03A52D865 CRC64;  
FT

Query Match 35.8%; Score 24; DB 2; Length 13;  
Best Local Similarity 42.9%; Pred. No. 3.1e+03;  
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 5 SFECLIG 11  
:|:|:|  
Db 1 TFKCVSG 7

RESULT 13  
Q918T1.HPV16  
ID Q918T1.HPV16 PRELIMINARY; PRT; 16 AA.  
AC Q918T1;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE E1 protein (Fragment).  
OS Human papillomavirus type 16.  
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
OC

OC Alphapapillomavirus.  
OX NCBI\_TaxID=333760;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=21846229; PubMed=11857370;  
RA Watts K.J., Thompson C.H., Cozzart Y.E., Rose B.R.;  
RT "Sequence variation and physical state of human papillomavirus type 16  
cervical cancer isolates from Australia and New Caledonia."  
RL Int. J. Cancer 97:868-874(2002).  
DR EMBL, AF407221; AL01409.1; -; Genomic\_DNA.  
FT NON TER 1  
SQ SEQUENCE 16 AA; 1710 MW; 2C7D73A03A17965F CRC64;  
  
Query Match 35.8%; Score 24; DB 2; Length 16;  
Best Local Similarity 42.9%; Pred. No. 3.8e+03;  
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
  
QY 5 SPECIIG 11  
Db 4 TPKCVSG 10  
  
RESULT 14  
Q91879 HPV16  
ID Q91879 HPV16 PRELIMINARY; PRT; 16 AA.  
AC Q91879;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE E1 protein (Fragment).  
OS Human papillomavirus type 16.  
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
OX Alphapapillomavirus.  
OX NCBI\_TaxID=333760;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=21846229; PubMed=11857370;  
RA Watts K.J., Thompson C.H., Cozzart Y.E., Rose B.R.;  
RT "Sequence variation and physical state of human papillomavirus type 16  
cervical cancer isolates from Australia and New Caledonia."  
RL Int. J. Cancer 97:868-874(2002).  
DR EMBL, AF407218; AL01400.1; -; Genomic\_DNA.  
FT NON TER 1  
SQ SEQUENCE 16 AA; 1710 MW; 2C7D73A03A17965F CRC64;  
  
Query Match 35.8%; Score 24; DB 2; Length 16;  
Best Local Similarity 42.9%; Pred. No. 3.8e+03;  
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
  
QY 5 SPECIIG 11  
Db 4 TPKCVSG 10  
  
RESULT 15  
Q918U2 HPV16  
ID Q918U2 HPV16 PRELIMINARY; PRT; 16 AA.  
AC Q918U2;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE E1 protein (Fragment).  
OS Human papillomavirus type 16.  
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
OX Alphapapillomavirus.  
OX NCBI\_TaxID=333760;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=21846229; PubMed=11857370;  
RA Watts K.J., Thompson C.H., Cozzart Y.E., Rose B.R.;  
RT "Sequence variation and physical state of human papillomavirus type 16  
cervical cancer isolates from Australia and New Caledonia."  
RL Int. J. Cancer 97:868-874(2002).  
DR EMBL, AF407218; AL01400.1; -; Genomic\_DNA.  
FT NON TER 1  
SQ SEQUENCE 16 AA; 1710 MW; 2C7D73A03A17965F CRC64;  
  
Query Match 35.8%; Score 24; DB 2; Length 16;  
Best Local Similarity 42.9%; Pred. No. 3.8e+03;  
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
  
QY 5 SPECIIG 11  
Db 4 TPKCVSG 10  
  
RESULT 16  
Q918U4 HPV16  
ID Q918U4 HPV16 PRELIMINARY; PRT; 16 AA.  
AC Q918U4;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE E1 protein (Fragment).  
OS Human papillomavirus type 16.  
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
OX Alphapapillomavirus.  
OX NCBI\_TaxID=333760;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=21846229; PubMed=11857370;  
RA Watts K.J., Thompson C.H., Cozzart Y.E., Rose B.R.;  
RT "Sequence variation and physical state of human papillomavirus type 16  
cervical cancer isolates from Australia and New Caledonia."  
RL Int. J. Cancer 97:868-874(2002).  
DR EMBL, AF407216; AL01394.1; -; Genomic\_DNA.  
FT NON TER 1  
SQ SEQUENCE 16 AA; 1710 MW; 2C7D73A03A17965F CRC64;  
  
Query Match 35.8%; Score 24; DB 2; Length 16;  
Best Local Similarity 42.9%; Pred. No. 3.8e+03;  
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
  
QY 5 SPECIIG 11  
Db 4 TPKCVSG 10  
  
RESULT 17  
Q918U6 HPV16  
ID Q918U6 HPV16 PRELIMINARY; PRT; 16 AA.  
AC Q918U6;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE E1 protein (Fragment).  
OS Human papillomavirus type 16.  
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
OX Alphapapillomavirus.  
OX NCBI\_TaxID=333760;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=21846229; PubMed=11857370;  
RA Watts K.J., Thompson C.H., Cozzart Y.E., Rose B.R.;  
RT "Sequence variation and physical state of human papillomavirus type 16  
cervical cancer isolates from Australia and New Caledonia."  
RL Int. J. Cancer 97:868-874(2002).  
DR EMBL, AF407215; AL01391.1; -; Genomic\_DNA.  
FT NON TER 1  
SQ SEQUENCE 16 AA; 1710 MW; 2C7D73A03A17965F CRC64;  
  
Query Match 35.8%; Score 24; DB 2; Length 16;  
Best Local Similarity 42.9%; Pred. No. 3.8e+03;  
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
  
QY 5 SPECIIG 11

DR EMBL, AF407217; AL01397.1; -; Genomic\_DNA.  
FT NON TER 1  
SQ SEQUENCE 16 AA; 1710 MW; 2C7D73A03A17965F CRC64;  
  
Query Match 35.8%; Score 24; DB 2; Length 16;  
Best Local Similarity 42.9%; Pred. No. 3.8e+03;  
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
  
QY 5 SPECIIG 11  
Db 4 TPKCVSG 10  
  
RESULT 16  
Q918U4 HPV16  
ID Q918U4 HPV16 PRELIMINARY; PRT; 16 AA.  
AC Q918U4;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE E1 protein (Fragment).  
OS Human papillomavirus type 16.  
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
OX Alphapapillomavirus.  
OX NCBI\_TaxID=333760;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=21846229; PubMed=11857370;  
RA Watts K.J., Thompson C.H., Cozzart Y.E., Rose B.R.;  
RT "Sequence variation and physical state of human papillomavirus type 16  
cervical cancer isolates from Australia and New Caledonia."  
RL Int. J. Cancer 97:868-874(2002).  
DR EMBL, AF407216; AL01394.1; -; Genomic\_DNA.  
FT NON TER 1  
SQ SEQUENCE 16 AA; 1710 MW; 2C7D73A03A17965F CRC64;  
  
Query Match 35.8%; Score 24; DB 2; Length 16;  
Best Local Similarity 42.9%; Pred. No. 3.8e+03;  
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
  
QY 5 SPECIIG 11  
Db 4 TPKCVSG 10  
  
RESULT 17  
Q918U6 HPV16  
ID Q918U6 HPV16 PRELIMINARY; PRT; 16 AA.  
AC Q918U6;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE E1 protein (Fragment).  
OS Human papillomavirus type 16.  
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
OX Alphapapillomavirus.  
OX NCBI\_TaxID=333760;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=21846229; PubMed=11857370;  
RA Watts K.J., Thompson C.H., Cozzart Y.E., Rose B.R.;  
RT "Sequence variation and physical state of human papillomavirus type 16  
cervical cancer isolates from Australia and New Caledonia."  
RL Int. J. Cancer 97:868-874(2002).  
DR EMBL, AF407215; AL01391.1; -; Genomic\_DNA.  
FT NON TER 1  
SQ SEQUENCE 16 AA; 1710 MW; 2C7D73A03A17965F CRC64;  
  
Query Match 35.8%; Score 24; DB 2; Length 16;  
Best Local Similarity 42.9%; Pred. No. 3.8e+03;  
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
  
QY 5 SPECIIG 11

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Db          4 TFKCVSG 10

RESULT 18
Q918U8_HPV16
ID Q918U8_HPV16 PRELIMINARY; PRT; 16 AA.
AC Q918U8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE B1 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
NCBI_TaxID=333760;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21846229; PubMed=11857370;
RA Matte K.J., Thompson C.H., Cosart Y.E., Rose B.R.;
RT "Sequence variation and physical strate of human papillomavirus type 16
cervical cancer isolates from Australia and New Caledonia."
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF407214; AAL01388.1; -; Genomic_DNA.
FT NON_TER 1
SQ SEQUENCE 16 AA; 1710 MW; 2C7D73A03A17965F CRC64;

Query Match 35.8%; Score 24; DB 2; Length 16;
Best Local Similarity 42.9%; Pred. No. 3.4e+03;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 5 SPECIFIC 11
DB 4 TFKCVSG 10

RESULT 19
CXM4A CONPE
ID CXM4A CONPE STANDARD; PRT; 17 AA.
AC P58926;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Mu-conotoxin Pn1VA.
OS Conus pennaceus (Feathered cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OC NCBI_TaxID=37335;
RN [1]
RP PROTEIN SEQUENCE, AND MASS SPECTROMETRY.
RX MEDLINE=95337083; PubMed=7612605;
RA Fainzilber M., Nakamura T., Gaathon A., Lodder J.C., Kitz K.S.,
RA Burlingame A.L., Zlotkin E.;
RT "A new cysteine framework in sodium channel blockings conotoxins."
RL Biochemistry 34:8649-8656(1995).
CC -1- FUNCTION: Mu-conotoxins bind and block voltage-sensitive sodium
channel. Blocks reversibly sodium channels in molluscan neurons,
but has no effect on sodium currents in bovine chromaffin cells or
in rat brain synaptosomes. Induces paralysis in bivalve mollusks
(Mytilus). No effect are observed on fish (Gambusia) and fly
larvae (Sarcophaga). Pn1VA is approximately 6 times more potent
than Pn1VA in blockade of the sodium current in Lymnaea neurons.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -1- MASS SPECTROMETRY: MW=1789.5; METHOD=ESI; RANGE=1-17; NOTE=Ref.1.
CC -1- SIMILARITY: Belongs to the conotoxin M superfamily. Mu-type
family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not

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CC removed.
CC -----
CC Direct protein sequencing; Ionic channel inhibitor; Neurotoxin;
KW Sodium channel inhibitor; Toxin.
FT SITE 4
FT DISULFID 12
FT DISULFID 2
FT DISULFID 15
FT DISULFID 8
SQ SEQUENCE 17 AA; 1797 MW; P9B721E0E96B9D82 CRC64;

Query Match 35.8%; Score 24; DB 1; Length 17;
Best Local Similarity 44.4%; Pred. No. 4e+03;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 KNSPECIFIC 11
DB 3 KTGWTCCLG 11

RESULT 20
Q7L299 CAICR
ID Q7L299_CAICR PRELIMINARY; PRT; 19 AA.
AC Q7L299;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Gamma crystallin IV (Fragment).
OS Catman crocodilus (Speciated catman) (Catman sclerops).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Crocodylidae; Alligatorinae; Catman.
OC NCBI_TaxID=8499;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=89351593; PubMed=3255376;
RA Chlou S.H.;
RT "The protein sequence homology of gamma-crystallins among major
vertebrate classes and their DNA sequence homology to heat-shock
protein genes."
RL J. Protein Chem. 7:527-534(1988).
DR PIR; B60894; B60894.
DR InterPro; IPR001064; Crystallin.
DR Pfam; PF00030; Crystallin.
DR PROSITE; PS50915; CRYSTALLIN_BETAGAMMA; 1.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 19 AA; 2325 MW; 26DAE30ADBFB23FF CRC64;

Query Match 35.8%; Score 24; DB 2; Length 19;
Best Local Similarity 57.1%; Pred. No. 4.5e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 EKNSPEC 8
DB 12 EGRSYEC 18

RESULT 21
Q4YR89_PLABR
ID Q4YR89_PLABR PRELIMINARY; PRT; 20 AA.
AC Q4YR89;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein (Fragment).
GN ORFNames=PB107323.00.0;
OS Plasmodium berghei.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OC NCBI_TaxID=5821;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=95337083; PubMed=7612605;
RA Hall N., Karas M., Raine J.D., Carlton J.M., Kool T.W.A.,
RA Bertrman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.,

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RA Quail M.A., Ormond D., Doggett J., Trueman H.B., Mendoza J.,  
 RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,  
 RA Janse C.J., Barrall B., Turner C.M.R., Waters A.P., Stiden R.S.,  
 RT "A comprehensive survey of the Plasmodium life cycle by genomic,  
 RL transcriptomic, and proteomic analyses.";  
 CC science 307:82-86 (2005).  
 CC -1 CAUTION: The sequence shown here is derived from an  
 CC EMBL/Genbank/DBJ whole genome shotgun (WGS) entry which is  
 CC preliminary data.  
 DR EMBL, CAAT01002802; CAH99438.1; -; Genomic\_DNA.  
 KM Hypothetical protein.  
 FT NON\_TER 1  
 SQ SEQUENCE 20 AA; 2708 MW; DF40072FE751448D CRC64;  
 QY Query Match 35.8%; Score 24; DB 2; Length 20;  
 DB Best Local Similarity 71.4%; Pred. No. 4.8e+03;  
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 4 NSPECIL 10  
 DB 2 NFPICIL 8  
 RESULT 22  
 ID Q9YPU1\_9CORO PRELIMINARY; PRT; 12 AA.  
 AC Q9YPU1\_9CORO  
 DT 01-MAY-1999 (TREMBLrel. 10, Created)  
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)  
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)  
 DE Matrix glycoprotein (Fragment).  
 OS Avian infectious bronchitis virus.  
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;  
 OC Coronaviridae; Coronavirinae.  
 OC NCBI\_TaxID=11120;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=UK12;  
 RX MEDLINE=88171451; PubMed=2832526;  
 RA Cavanagh D., Davis P.J.;  
 RT "Evolution of Avian Coronavirus IBV: sequence of the matrix  
 RL J. Gen. Virol. 69:621-629 (1988).  
 DR EMBL, D00415; BAA20959.1; -; Genomic\_RNA.  
 FT NON\_TER 12  
 SQ SEQUENCE 12 AA; 1224 MW; 02D6B87F8D51B1A4 CRC64;  
 QY Query Match 34.3%; Score 23; DB 2; Length 12;  
 DB Best Local Similarity 50.0%; Pred. No. 4.4e+03;  
 Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
 QY 4 NSPECIL 11  
 DB 5 NTINCTIL 12  
 RESULT 23  
 ID Q5F3D0\_CHICK PRELIMINARY; PRT; 13 AA.  
 AC Q5F3D0\_CHICK  
 DT 10-MAY-2005 (TREMBLrel. 30, Created)  
 DT 10-MAY-2005 (TREMBLrel. 30, Last sequence update)  
 DT 10-MAY-2005 (TREMBLrel. 30, Last annotation update)  
 DE Hypothetical protein.  
 GN ORFNames=RCJMB04\_21c11;  
 OS Gallus gallus (Chicken).  
 OC Buckyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinoptera; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OC NCBI\_TaxID=9031;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=CB; TISSUE=Bursa;

RA Caldwell R.B., Klerzek A.M., Arakawa H., Bezubov Y., Zaim J.,  
 RA Pichler P., Kutter S., Blagoderetki A., Kostovska D., Kotter M.,  
 RA Pichler J., Carninci P., Hayashizaki Y., Buerstedde U.M.,  
 RT "Full-length cDNAs from chicken bursa lymphocytes to facilitate  
 RT gene function analysis.";  
 RL Genome Biol. 6:R6-R6 (2005).  
 DR EMBL, AJ851720; CAH65354.1; -; mRNA.  
 KM Hypothetical protein.  
 FT NON\_TER 13  
 SQ SEQUENCE 13 AA; 1550 MW; 6ADCB330C4D4B1B CRC64;  
 QY Query Match 34.3%; Score 23; DB 2; Length 13;  
 DB Best Local Similarity 66.7%; Pred. No. 4.7e+03;  
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 2 EKNSFE 7  
 DB 6 EENGFPE 11  
 RESULT 24  
 ID Q9NOP9\_CANFA PRELIMINARY; PRT; 16 AA.  
 AC Q9NOP9\_CANFA  
 DT 01-OCT-2000 (TREMBLrel. 15, Created)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
 DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)  
 DE Class II beta-tubulin (Fragment).  
 OS Canis familiaris (Dog).  
 OC Buckyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;  
 OC Canis.  
 OC NCBI\_TaxID=9615;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Aral K.;  
 RL Submitted (JAN-1999) to the EMBL/Genbank/DBJ databases.  
 DR EMBL, AB022055; BAA96410.2; -; mRNA.  
 FT NON\_TER 1  
 SQ SEQUENCE 16 AA; 1813 MW; 7BEC91EDC77B5E1F CRC64;  
 QY Query Match 34.3%; Score 23; DB 2; Length 16;  
 DB Best Local Similarity 57.1%; Pred. No. 5.8e+03;  
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 DEKNSFE 7  
 DB 2 DEGEFPE 8  
 RESULT 25  
 ID Q8HKE2\_9ACAR PRELIMINARY; PRT; 17 AA.  
 AC Q8HKE2\_9ACAR  
 DT 01-MAR-2003 (TREMBLrel. 23, Created)  
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)  
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)  
 DE NADH dehydrogenase subunit 1 (Fragment).  
 GN Name=ND1;  
 OS Rhipilephalus punctatus.  
 OC Mitochondrion.  
 OC Buckyota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;  
 OC Parasitiformes; Ixodida; Ixodidae; Ixodidae; Rhipilephalus.  
 OC NCBI\_TaxID=72860;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=22660766; PubMed=12775521; DOI=10.1080/10635150309325;  
 RA Murrell A., Campbell N.J.H., Barker S.C.;  
 RT "The value of idiosyncratic markers and changes to conserved tRNA  
 RT sequences from the mitochondrial genome of hard ticks (Acari: Ixodidae;  
 RT Ixodidae) for phylogenetic inference.";  
 RL Syst. Biol. 52:296-310 (2003).  
 DR EMBL, AY059231; AAL79429.1; -; Genomic\_DNA.

DR GO; GO:0005739; C:mitochondrion; IEA.  
 KM Mitochondrion.  
 FT NON\_TER 1  
 SQ SEQUENCE 17 AA; 2069 MW; 15AFEP9B3743422 CRC64;

Query Match 34.3%; Score 23; DB 2; Length 17;  
 Best Local Similarity 66.7%; Pred. No. 6.2e+03;  
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 NSPECT 9  
 DB 8 NMFICI 13

## RESULT 25

Q8HKF6\_9ACAR  
 ID Q8HKF6\_9ACAR PRELIMINARY; PRT; 17 AA.  
 AC Q8HKF6;  
 DT 01-MAR-2003 (TREMBLrel. 23, Created)  
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)  
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)  
 DE NADH dehydrogenase subunit 1 (Fragment).  
 GN Name=ND1;  
 OS Rhizopneustis evertsi.  
 OC Mitochondrion.  
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;  
 OC Parasitiformes; Ixodidae; Ixodidae; Ixodidae; Rhizopneustis.  
 OC NCBI\_TaxID=60190;  
 RN NCBIOTIDE SEQUENCE.  
 RA MEDLINE=22660786; PubMed=12775521; DOI=10.1080/10635150309325;  
 RA Murrell A., Campbell N.J.H., Barker S.C.;

RT "The value of idiosyncratic markers and changes to conserved tRNA  
 sequences from the mitochondrial genome of hard ticks (Acari: Ixodidae:  
 Ixodidae) for phylogenetic inference."  
 RL Syst. Biol. 52:296-310(2003).  
 DR EMBL; AY059219; AL79415.1; -; Genomic\_DNA.  
 DR GO; GO:0005739; C:mitochondrion; IEA.  
 KM Mitochondrion.  
 FT NON\_TER 1  
 SQ SEQUENCE 17 AA; 2071 MW; 15AFED0CC1743422 CRC64;

Query Match 34.3%; Score 23; DB 2; Length 17;  
 Best Local Similarity 66.7%; Pred. No. 6.2e+03;  
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 NSPECT 9  
 DB 8 NMFICI 13

## RESULT 27

Q8HKH2\_9ACAR  
 ID Q8HKH2\_9ACAR PRELIMINARY; PRT; 17 AA.  
 AC Q8HKH2;  
 DT 01-MAR-2003 (TREMBLrel. 23, Created)  
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)  
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)  
 DE NADH dehydrogenase subunit 1 (Fragment).  
 GN Name=ND1;  
 OS Boophilus decoloratus.  
 OC Mitochondrion.  
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;  
 OC Parasitiformes; Ixodidae; Ixodidae; Ixodidae; Boophilus.  
 OC NCBI\_TaxID=60189;  
 RN NCBIOTIDE SEQUENCE.  
 RA MEDLINE=22660786; PubMed=12775521; DOI=10.1080/10635150309325;  
 RA Murrell A., Campbell N.J.H., Barker S.C.;

RT "The value of idiosyncratic markers and changes to conserved tRNA  
 sequences from the mitochondrial genome of hard ticks (Acari: Ixodidae:  
 Ixodidae) for phylogenetic inference."  
 RL Syst. Biol. 52:296-310(2003).

DR EMBL; AY059197; AL79399.1; -; Genomic\_DNA.  
 DR GO; GO:0005739; C:mitochondrion; IEA.  
 KM Mitochondrion.  
 FT NON\_TER 1  
 SQ SEQUENCE 17 AA; 2130 MW; 8B7FE0A737438DD CRC64;

Query Match 34.3%; Score 23; DB 2; Length 17;  
 Best Local Similarity 66.7%; Pred. No. 6.2e+03;  
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 NSPECT 9  
 DB 8 NMFICI 13

## RESULT 28

Q4XXL1\_PLACH  
 ID Q4XXL1\_PLACH PRELIMINARY; PRT; 18 AA.  
 AC Q4XXL1;  
 DT 13-SEP-2005 (TREMBLrel. 31, Created)  
 DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)  
 DT 13-SEP-2005 (TREMBLrel. 31, Last annotation update)  
 DE Hypothetical protein (Fragment).  
 GN ORFNames=PC10478.00.0;  
 OS Plasmodium chabaudi.  
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporidia; Plasmodium.  
 OC NCBI\_TaxID=5825;  
 RN NCBIOTIDE SEQUENCE.  
 RA Hall N., Karrae M., Raine J.D., Carlton J.M., Kool J.T.W.A.,  
 RA Bertram M., Plorens L., Janssen C.S., Pain A., Christophides G.K.,  
 RA James K., Rutherford K., Harris B., Harris D., Churcher C.,  
 RA Chail M.A., Ormond D., Doggett J., Trueman H.B., Mendoza J.,  
 RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,  
 RA Jansse C.J., Barrett B., Turner C.M.R., Waters A.P., Sinden R.S.,  
 RT "A comprehensive survey of the Plasmodium life cycle by genomic,  
 RT transcriptomic, and proteomic analyses."  
 RL Science 307:82-86(2005).  
 CC -!- CAUTION: The sequence shown here is derived from an  
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
 CC preliminary data.  
 DR EMBL; CAJ01002428; CH78350.1; -; Genomic\_DNA.  
 KM Hypothetical protein.  
 FT NON\_TER 1  
 SQ SEQUENCE 18 AA; 2124 MW; 754D7D9B16643A74 CRC64;

Query Match 34.3%; Score 23; DB 2; Length 18;  
 Best Local Similarity 57.1%; Pred. No. 6.6e+03;  
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 6 FBCTIGP 12  
 DB 2 FVCTVRP 8

## RESULT 29

Q7Z579\_HUMAN  
 ID Q7Z579\_HUMAN PRELIMINARY; PRT; 20 AA.  
 AC Q7Z579;  
 DT 01-OCT-2003 (TREMBLrel. 25, Created)  
 DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)  
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
 DE 5-hydroxytryptamine receptor 2C variant b (Fragment).  
 GN Name=HTR2C;  
 OS Homo sapiens (human).  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Homo.  
 OC NCBI\_TaxID=9606;  
 RN NCBIOTIDE SEQUENCE.  
 RA MEDLINE=22651194; PubMed=12767050; DOI=10.1002/jcp.10287;  
 RA Slowinski A., Plearchik A., Zbytek B., Tobin D.J., Kauser S.,

RT "The value of idiosyncratic markers and changes to conserved tRNA  
 sequences from the mitochondrial genome of hard ticks (Acari: Ixodidae:  
 Ixodidae) for phylogenetic inference."  
 RL Syst. Biol. 52:296-310(2003).



RA Wortman J.,  
 RT "Functional activity of serotonergic and melatonergic systems  
 expressed in the skin."  
 RL J. Cell. Physiol. 196:144-153(2003).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Piarachik A.V., Slominski A.,  
 RL Submitted (May-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY114104; AAM78371.1; -; mRNA.  
 DR GO: 0004872; F:receptor activity; IEA.  
 KW Receptor.  
 FT NON\_TER  
 KW RECEPTOR  
 SQ SEQUENCE 20 AA; 2232 MW; EA74DCAFD4BCBB9 CRC64;  
 Query Match 34.3%; Score 23; DB 2; Length 20;  
 Best Local Similarity 62.5%; Pred. No. 7.3e+03;  
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 QY 4 EKNSPECI 11  
 DB 8 NSFOIGS 15

RESULT 30  
 ID 04XN21 PLACH PRELIMINARY; PRT; 20 AA.  
 AC 04XN21  
 DT 13-SEP-2005 (TREMBlrel. 31, Created)  
 DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)  
 DE Hypothetical protein.  
 GN ORFNames=PC108623.00.0;  
 OS Plasmodium chabaudi.  
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
 OK NCBI\_TaxID=5825;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Hall N., Karyas M., Raine J.D., Carlton J.M., Kooij T.W.A.,  
 RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,  
 RA James K., Rutherford K., Harris B., Harris D., Churcher C.,  
 RA Quail M.A., Ormond D., Duggett J., Trueman H.B., Mendoza J.,  
 RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,  
 RA Jense C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.,  
 RT "A comprehensive survey of the Plasmodium life cycle by genomic,  
 RT transcriptomic, and proteomic analyses."  
 RL Science 307:82-86(2005).  
 CC -1- CAUTION: The sequence shown here is derived from an  
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
 CC preliminary data.  
 DR EMBL; CAJ01004522; CAH81691.1; -; Genomic\_DNA.  
 KW Hypothetical protein.  
 SQ SEQUENCE 20 AA; 2470 MW; 4730C7869162447F CRC64;  
 Query Match 34.3%; Score 23; DB 2; Length 20;  
 Best Local Similarity 50.0%; Pred. No. 7.3e+03;  
 Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
 QY 2 EKNSPECI 9  
 DB 12 KSNFLBCT 19

RESULT 31  
 ID 095M09\_PANTR PRELIMINARY; PRT; 20 AA.  
 AC 095M09  
 DT 01-DEC-2001 (TREMBlrel. 19, Created)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)  
 DE Growth hormone receptor (Fragment).  
 OS Pan troglodytes (Hominidae).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae;

OC Pan.  
 OK NCBI\_TaxID=9598;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=21265430; PubMed=11371582;  
 RA Liu J.-C., Makova K.D., Adkins R.M., Gibson S., Li W.-H.,  
 RT "Episodic evolution of growth hormone in primates and emergence of the  
 RT species specificity of human growth hormone receptor."  
 RL Mol. Biol. Evol. 18:945-953(2001).  
 DR EMBL; AF339077; AAK62304.1; -; Genomic\_DNA.  
 DR HSSP; P10912; 3HR.  
 DR GO: 0004872; F:receptor activity; IEA.  
 KW Receptor.  
 FT NON\_TER  
 KW RECEPTOR  
 SQ SEQUENCE 20 AA; 2412 MW; 3BD9P94636B5ABE7 CRC64;  
 Query Match 34.3%; Score 23; DB 2; Length 20;  
 Best Local Similarity 42.9%; Pred. No. 7.3e+03;  
 Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
 QY 2 EKNSPEC 8  
 DB 4 ERRTFSC 10

RESULT 32  
 ID 095M09\_PONPY PRELIMINARY; PRT; 20 AA.  
 AC 095M09  
 DT 01-DEC-2001 (TREMBlrel. 19, Created)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)  
 DE Growth hormone receptor (Fragment).  
 OS Pongo pygmaeus (Orangutan).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae;  
 OC Pongo.  
 OK NCBI\_TaxID=9600;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=21265430; PubMed=11371582;  
 RA Liu J.-C., Makova K.D., Adkins R.M., Gibson S., Li W.-H.,  
 RT "Episodic evolution of growth hormone in primates and emergence of the  
 RT species specificity of human growth hormone receptor."  
 RL Mol. Biol. Evol. 18:945-953(2001).  
 DR EMBL; AF339076; AAK62303.1; -; Genomic\_DNA.  
 DR HSSP; P10912; 1AXI.  
 DR GO: 0004872; F:receptor activity; IEA.  
 KW Receptor.  
 FT NON\_TER  
 KW RECEPTOR  
 SQ SEQUENCE 20 AA; 2366 MW; 3FC9F95C86B38BE7 CRC64;  
 Query Match 34.3%; Score 23; DB 2; Length 20;  
 Best Local Similarity 42.9%; Pred. No. 7.3e+03;  
 Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
 QY 2 EKNSPEC 8  
 DB 4 ERRTFSC 10

RESULT 33  
 ID 095M09\_COLAN PRELIMINARY; PRT; 20 AA.  
 AC 095M09  
 DT 01-DEC-2001 (TREMBlrel. 19, Created)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)  
 DE Growth hormone receptor (Fragment).  
 OS Colobus angolensis (Angolan colobus).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

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OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Cercopitheciidae; Colobinae; Colobus.
OX NCBI_TaxID=54131;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21265430; PubMed=11371582;
RA Liu J.-C., Makova K.D., Adkins R.M., Gibson S., Li W.-H.;
RT "Epilodic evolution of growth hormone in primates and emergence of the
RT species specificity of human growth hormone receptor.";
RL Mol. Biol. Evol. 18:945-953(2001).
DR EMBL; AF339075; AAK62302.1; -; Genomic_DNA.
DR HSSP; P10912; IAXI.
DR GO; GO:0004872; F:receptor activity; IEA.
KM Receptor.
FT NON_TER 1
FT TER 20
SQ SEQUENCE 20 AA; 2359 MW; 3FC9ECA636B38BE7 CRC64;

Query Match 34.3%; Score 23; DB 2; Length 20;
Best Local Similarity 42.9%; Pred. No. 7.3e+03;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 EKNSPEC 8
Db 4 ERRTFSC 10

RESULT 34
QY 095MK2_PAPCY PRELIMINARY; PRT; 20 AA.
ID 095MK2_PAPCY
AC 095MK2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Growth hormone receptor (Fragment).
OS Papio cynocephalus (Yellow baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Cercopitheciidae; Cercopithecinae; Papio.
OX NCBI_TaxID=9556;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21265430; PubMed=11371582;
RA Liu J.-C., Makova K.D., Adkins R.M., Gibson S., Li W.-H.;
RT "Epilodic evolution of growth hormone in primates and emergence of the
RT species specificity of human growth hormone receptor.";
RL Mol. Biol. Evol. 18:945-953(2001).
DR EMBL; AF339074; AAK62301.1; -; Genomic_DNA.
DR HSSP; P10912; IAXI.
DR GO; GO:0004872; F:receptor activity; IEA.
KM Receptor.
FT NON_TER 1
FT TER 20
SQ SEQUENCE 20 AA; 2339 MW; 3FC9F94636B38BE7 CRC64;

Query Match 34.3%; Score 23; DB 2; Length 20;
Best Local Similarity 42.9%; Pred. No. 7.3e+03;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 EKNSPEC 8
Db 4 ERRTFSC 10

RESULT 35
RCA_PINPS STANDARD; PRT; 10 AA.
ID RCA_PINPS
AC P81084;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Ribulose biphosphate carboxylase/oxygenase activase, chloroplast
DE (Rubisco activase) (RA) (Water stress responsive protein 4)

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DE (Fragment).
DE Pinus pinaster (Maritime pine).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.
OX NCBI_TaxID=71647;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=98418576; PubMed=9747804; DOI=10.1006/A.1006006132120;
RA Costa P., Bahman N., Frigerio J.-M., Kremer A., Plomion C.;
RT "Water-deficit-responsive proteins in maritime pine.";
RL Plant Mol. Biol. 38:587-596(1998).
RN [2]
RP PROTEIN SEQUENCE.
RX MEDLINE=99274088; PubMed=10344291;
RX DOI=10.1002/(SICI)1522-2683(19990101)20:4<51098::AID-ELPS1098>3.3.CO;2-Q;
RA Costa P., Plomion C., Bauw G., Dubos C., Bahman N., Kremer A.,
RA Frigerio J.-M., Plomion C.;
RT "Separation and characterization of needle and xylem maritime pine
RT proteins.";
RL Electrophoresis 20:1098-1108(1999).
CC -I- FUNCTION: Activation of Rubisco (ribulose-1,5-bisphosphate
CC carboxylase/oxygenase; EC 4.1.1.39) involves the ATP-dependent
CC carboxylation of the epsilon-amino group of lysine leading to a
CC carbamate structure (By similarity).
CC -I- SUBCELLULAR LOCATION: Chloroplast stroma (By similarity).
CC -I- INDUCTION: By water stress.
CC -I- SIMILARITY: Belongs to the Rubisco activase family.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
KM ATP-binding; Chloroplast; Direct protein sequencing;
KM Nucleotide-binding.
FT NON_TER 1
FT TER 10
SQ SEQUENCE 10 AA; 1171 MW; C0A506D2C72B1E86 CRC64;

Query Match 32.8%; Score 22; DB 1; Length 10;
Best Local Similarity 66.7%; Pred. No. 5.6e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 SFFCIL 10
Db 1 SFFCEL 6

RESULT 36
Q7ROUO_PLAYO PRELIMINARY; PRT; 10 AA.
ID Q7ROUO_PLAYO
AC Q7ROUO;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein (Fragment).
GN Name=EY01107;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporidia; Plasmodium.
OX NCBI_TaxID=73239;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=17XNL;
RX MEDLINE=22255706; PubMed=12368865; DOI=10.1038/nature01099;
RA Carlton J.M., Angluot S.V., Suh B.B., Kool J.T.W., Perera M.,
RA Silva J.C., Ernolava M.D., Allen J.E., Selengut J.P., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA Shallow S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,
RA Cho J.K., Quackenbush J., Sedegah M., Shoabli A., Cummings L.M.,
RA Florens L., Yates J.R. III, Raine J.D., Sinden R.E., Harris M.A.,

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RA Cunningham D.A., Pfeleer P.R., Bergman L.W., Valdiva A.B.,  
 RA van Lin L.H., Jense C.J., Waters A.P., Smith H.O., White O.R.,  
 RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.T.,  
 RA Carucci D.J.,  
 RT "Genome sequence and comparative analysis of the model rodent malaria  
 parasite *Plasmodium yoelii yoelii*." ,  
 RL Nature 419:512-519(2002).  
 CC -!- CAUTION: The sequence shown here is derived from an  
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
 CC preliminary data.  
 DR EMBL, AAB0100292; EAA03037.1; -; Genomic\_DNA.  
 KW Hypothetical protein.  
 FT NON TER  
 SQ SEQUENCE 10 AA; 1225 MW; 1F0267BB10572724 CRC64;

Query Match 32.8%; Score 22; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 5.6e+03;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 ECIL 10  
 Db 7 ECIL 10

RESULT 37  
 080UP1\_XENLA PRELIMINARY; PRT; 11 AA.  
 AC 080UP1;  
 DT 01-MAR-2002 (TREMBlrel. 20, Created)  
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)  
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)  
 DE Beta-TrCP protein (Fragment).  
 GN Name=beta-TrCP;  
 OS *Xenopus laevis* (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;  
 OC Xenopodinae; Xenopus; Xenopus.  
 OX NCBI\_Taxid=8355;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Ballarino M.;  
 RT "Analisi strutturale e funzionale del gene beta-TrCP in *Xenopus laevis*." ,  
 RL Thesis (2001), Department of Genetica e Biologia Molecolare,  
 RL University of Rome La Sapienza, Rome, Italy.  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Carnevali P.;  
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL, AJ428930; CAD21927.1; -; Genomic\_DNA.  
 FT NON TER  
 SQ SEQUENCE 11 AA; 1195 MW; CEB938BE35BEA5B9 CRC64;

Query Match 32.8%; Score 22; DB 2; Length 11;  
 Best Local Similarity 57.1%; Pred. No. 6.1e+03;  
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 6 FSCSLGP 12  
 Db 4 FSCSLGP 10

RESULT 38  
 06LDS1\_BPT3  
 ID 06LDS1\_BPT3 PRELIMINARY; PRT; 13 AA.  
 AC 06LDS1;  
 DT 05-JUN-2004 (TREMBlrel. 27, Created)  
 DT 05-JUN-2004 (TREMBlrel. 27, Last sequence update)  
 DT 05-JUN-2004 (TREMBlrel. 27, Last annotation update)  
 DE RNA polymerase III (Fragment).  
 OS Bacteriophage T3.  
 OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Podoviridae;  
 OC T7-like viruses.

OX NCBI\_Taxid=10759;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=86221699; PubMed=3011596; DOI=10.1016/0378-1119(86)90098-3;  
 RA Morris C.E., Klement J.F., McAllister W.T.;  
 RT "Cloning and expression of the bacteriophage T3 RNA polymerase gene." ,  
 RL Gene 41:193-200(1986).  
 DR EMBL, M22609; AAA63781.1; -; Genomic\_DNA.  
 FT NON TER  
 SQ SEQUENCE 13 AA; 1567 MW; 16F2BD5EA021054 CRC64;

Query Match 32.8%; Score 22; DB 2; Length 13;  
 Best Local Similarity 80.0%; Pred. No. 7.3e+03;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 EKNSF 6  
 Db 8 EKNSF 12

RESULT 39  
 0810Z7\_MOUSE PRELIMINARY; PRT; 14 AA.  
 AC 0810Z7;  
 DT 01-JUN-2003 (TREMBlrel. 24, Created)  
 DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)  
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)  
 DE Kinesin KIFCI (Fragment).  
 GN Name=KIFCI;  
 OS *Mus musculus* (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Murinae; Mus.  
 OX NCBI\_Taxid=10090;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=129/Sv;  
 RA Negaraja R., Brathwaite M.E., Abe K.;  
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL, AF528162; AAO27574.1; -; Genomic\_DNA.  
 FT NON TER  
 SQ SEQUENCE 14 AA; 1474 MW; 225CE886C694FA8 CRC64;

Query Match 32.8%; Score 22; DB 2; Length 14;  
 Best Local Similarity 40.0%; Pred. No. 7.8e+03;  
 Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 7 ECILG 11  
 Db 3 QCVIG 7

RESULT 40  
 093202\_9CIRC PRELIMINARY; PRT; 14 AA.  
 AC 093202; Q9YJ34;  
 DT 01-NOV-1998 (TREMBlrel. 08, Created)  
 DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)  
 DT 01-FEB-2005 (TREMBlrel. 29, Last annotation update)  
 DE ORF11.  
 OS Porcine circovirus.  
 OC Viruses; ssDNA viruses; Circoviridae; Circovirus.  
 OX NCBI\_Taxid=46221;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=Porcine circovirus Type II;  
 RX MEDLINE=86418498; PubMed=9747726;  
 RA Meenan B.M., McNeill F.M., Todd D., Kennedy S., Jewhurst V.,  
 RA Ellis J.A., Haasard L.E., Clark E.G., Haines D.M., Allan G.M.;  
 RT "Characterisation of novel circovirus DNAs associated with wasting  
 RT syndromes in pigs." ,  
 RL J. Gen. Virol. 79:2171-2199(1998).  
 DR EMBL, AF055394; AAC35336.1; -; Genomic\_DNA.

DR EMBL: AF055392; AAC35316.1; -; Genomic DNA.  
 DR EMBL: AF055393; AAC35326.1; -; Genomic DNA.  
 DR EMBL: AF055391; AAC35305.1; -; Genomic DNA.  
 SQ SEQUENCE 14 AA; 1747 MW; 00F50DC89AEBF20B CRC64;

Query Match 32.8%; Score 22; DB 2; Length 14;  
 Best Local Similarity 44.4%; Pred. No. 7.8e+03;  
 Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 DEKNSPECT 9  
 : ||: ||  
 Db 2 NNKNHYEVI 10

RESULT 41  
 Q77NR3\_9CIRC  
 ID Q77NR3\_9CIRC PRELIMINARY; PRT; 14 AA.  
 AC Q77NR3;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE ORF-11.  
 GN Name=ORF11;  
 OS Porcine circovirus 2.  
 OC Viruses; ssDNA viruses; Circoviridae; Circovirus.  
 OX NCBI\_TaxID=85708;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA STRAIN=24657 NL;  
 RA Wellenberg G.J., Pesch S., Berntsen F.W., Steverink P.J.G.M.,  
 RA Hunneman W., Van der Vorst T.J.K., Peperkamp N.H.M.T., Ohlinger V.F.,  
 RA Schippers R., Van Oirschot J.T., de Jong M.F.;  
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF201897; AAC41230.1; -; Genomic DNA.  
 SQ SEQUENCE 14 AA; 1747 MW; 00F50DC89AEBF20B CRC64;

Query Match 32.8%; Score 22; DB 2; Length 14;  
 Best Local Similarity 44.4%; Pred. No. 7.8e+03;  
 Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 DEKNSPECT 9  
 : ||: ||  
 Db 2 NNKNHYEVI 10

RESULT 42  
 Q77RC0\_9CIRC  
 ID Q77RC0\_9CIRC PRELIMINARY; PRT; 14 AA.  
 AC Q77RC0;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE ORF-11.  
 OS Porcine circovirus type 2-D.  
 OC Viruses; ssDNA viruses; Circoviridae; Circovirus.  
 OX NCBI\_TaxID=86385;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA MEDLINE=20142849; PubMed=10680656;  
 RA Hamel A.L., Lin L.L., Sachvie C., Grudecki E., Nayar G.P.S.;  
 RT "PCR detection and characterization of type-2 porcine circovirus.";  
 RL Can. J. Vet. Res. 64:44-52(2000).  
 DR EMBL: AF117753; AAD12313.1; -; Genomic DNA.  
 SQ SEQUENCE 14 AA; 1747 MW; 00F50DC89AEBF20B CRC64;

Query Match 32.8%; Score 22; DB 2; Length 14;  
 Best Local Similarity 44.4%; Pred. No. 7.8e+03;  
 Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 DEKNSPECT 9  
 : ||: ||  
 Db 2 NNKNHYEVI 10

RESULT 43  
 Q77RM6\_9CIRC  
 ID Q77RM6\_9CIRC PRELIMINARY; PRT; 14 AA.  
 AC Q77RM6;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE ORF-11.

OS Porcine circovirus type 2-B.  
 OC Viruses; ssDNA viruses; Circoviridae; Circovirus.  
 OX NCBI\_TaxID=85709;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.

RA MEDLINE=20142849; PubMed=10680656;  
 RA Hamel A.L., Lin L.L., Sachvie C., Grudecki E., Nayar G.P.S.;  
 RT "PCR detection and characterization of type-2 porcine circovirus.";  
 RL Can. J. Vet. Res. 64:44-52(2000).  
 DR EMBL: AF112862; AAD03090.1; -; Genomic DNA.  
 SQ SEQUENCE 14 AA; 1747 MW; 00F50DC89AEBF20B CRC64;

Query Match 32.8%; Score 22; DB 2; Length 14;  
 Best Local Similarity 44.4%; Pred. No. 7.8e+03;  
 Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 DEKNSPECT 9  
 : ||: ||  
 Db 2 NNKNHYEVI 10

RESULT 44  
 Q77S02\_9CIRC  
 ID Q77S02\_9CIRC PRELIMINARY; PRT; 14 AA.  
 AC Q77S02;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE ORF-11.  
 OS Porcine circovirus type 2-E.  
 OC Viruses; ssDNA viruses; Circoviridae; Circovirus.  
 OX NCBI\_TaxID=85544;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA MEDLINE=20142849; PubMed=10680656;  
 RA Hamel A.L., Lin L.L., Sachvie C., Grudecki E., Nayar G.P.S.;  
 RT "PCR detection and characterization of type-2 porcine circovirus.";  
 RL Can. J. Vet. Res. 64:44-52(2000).  
 DR EMBL: AF109399; AAD03080.1; -; Genomic DNA.  
 SQ SEQUENCE 14 AA; 1747 MW; 00F50DC89AEBF20B CRC64;

Query Match 32.8%; Score 22; DB 2; Length 14;  
 Best Local Similarity 44.4%; Pred. No. 7.8e+03;  
 Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 DEKNSPECT 9  
 : ||: ||  
 Db 2 NNKNHYEVI 10

RESULT 45  
 Q77S09\_9CIRC  
 ID Q77S09\_9CIRC PRELIMINARY; PRT; 14 AA.  
 AC Q77S09;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE ORF-11.  
 OS Porcine circovirus type 2-C.  
 OC Viruses; ssDNA viruses; Circoviridae; Circovirus.  
 OX NCBI\_TaxID=85543;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA MEDLINE=20142849; PubMed=10680656;

RA Hamel A.L., Lin L.L., Sachvie C., Grudecki E., Nayyar G.P.S.;  
 RT "CCR detection and characterization of type-2 porcine circovirus";  
 RL Can. J. Vet. Res. 64:44-52(2000)  
 DR EMBL, AF109398; AAD03069.1; -; Genomic DNA.  
 SO SEQUENCE 14 AA, 1747 MW, 00F50DC89AEBF20B CRC64;

Query Match 32.8%; Score 22; DB 2; Length 14;  
 Best Local Similarity 44.4%; Pred. No. 7.8e+03;  
 Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 DEKNSPECI 9  
 DB 2 NNNKHYEVI 10

RESULT 46  
 Q77S13\_9CIRC  
 ID Q77S13\_9CIRC PRELIMINARY; PRT; 14 AA.  
 AC Q77S13;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE ORF-11.  
 OS Bovine circovirus.  
 OC Viruses; ssDNA viruses; Circoviridae; Circovirus.  
 OX NCBI\_TaxID=85542;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Hamel A.L., Nayyar G.P.S.;  
 RL Submitted (FEBS-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL, AF109397; AAD11937.1; -; Genomic DNA.  
 SO SEQUENCE 14 AA, 1747 MW, 00F50DC89AEBF20B CRC64;

Query Match 32.8%; Score 22; DB 2; Length 14;  
 Best Local Similarity 44.4%; Pred. No. 7.8e+03;  
 Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 DEKNSPECI 9  
 DB 2 NNNKHYEVI 10

RESULT 47  
 FIBA\_ANAPL  
 ID FIBA\_ANAPL STANDARD; PRT; 15 AA.  
 AC P12801;  
 DT 01-OCT-1989 (Rel. 12, Created)  
 DT 01-OCT-1989 (Rel. 12, Last sequence update)  
 DT 01-FEB-2005 (Rel. 46, Last annotation update)  
 DE Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).  
 GN Name=Fga;  
 OS Anas platyrhynchos (Domestic duck).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anas.  
 OX NCBI\_TaxID=8839;  
 RN [1]  
 RP PROTEIN SEQUENCE.  
 RX MEDLINE=85168193; PubMed=3983613;  
 RA Min Y., Ping Z., Yaoehi Z.;  
 RT "Purification and primary structures of duck fibrinopeptides A and B";  
 RL Sci. Sin., Ser. B, Chem. Biol. Agric. Med. Earth Sci. 28:31-35(1985).  
 CC -1- FUNCTION: Fibrinogen has a double function: yielding monomers that polymerize into fibrin and acting as a cofactor in platelet aggregation.  
 CC -1- SUBUNIT: Heterohexamer; disulfide linked. Contains 2 sets of 3 nonidentical chains (alpha, beta and gamma). The 2 heterochains are in head to head conformation with the N-termini in a small central domain (by similarity).  
 CC -1- DOMAIN: A long coiled coil structure formed by 3 polypeptide chains connects the central node to the C-terminal domains (distal nodules). The long C-terminal ends of the alpha chains fold back, contributing a fourth strand to the coiled coil

CC structure.  
 CC -1- PPM: Conversion of fibrinogen to fibrin is triggered by thrombin, which cleaves fibrinopeptides A and B from alpha and beta chains, and thus exposes the N-terminal polymerization sites responsible for the formation of the soft clot.

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DR PIR; JP0101; JP0101.  
 KW Blood coagulation; Coiled coil; Direct protein sequencing; Plasma;  
 KW Pyroldone carboxylic acid.  
 FT PEPTIDE 1 15 Fibrinopeptide A.  
 FT MOD RES 1 1 Pyroldone carboxylic acid.  
 FT NON TER 15 15  
 SO SEQUENCE 15 AA, 1580 MW, D78A51FF88B40373 CRC64;

Query Match 32.8%; Score 22; DB 1; Length 15;  
 Best Local Similarity 57.1%; Pred. No. 8.4e+03;  
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 DEKNSPE 7  
 DB 2 DGKSFQ 8

RESULT 48  
 Q5RLM1\_HUMAN  
 ID Q5RLM1\_HUMAN PRELIMINARY; PRT; 15 AA.  
 AC Q5RLM1;  
 DT 01-FEB-2005 (TrEMBLrel. 29, Created)  
 DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)  
 DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)  
 DE Neuronal acetylcholine receptor alpha-4 subunit (Fragment).  
 GN Name=CHRNA4;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Butheria; Eumarchontoglires; Primates; Catarrhini; Homidae;  
 OC Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Qi Y.F., Shan K.R., Ren X.L., Xu Y., Zhang T., Li Y.;  
 RT "Research of association between genetic polymorphisms of CHRNA4 and Alzheimer's Disease";  
 RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.

DR EMBL, AY816234; AAV66461.1; -; Genomic DNA.  
 DR GO; GO:0004872; F:receptor activity; IEA.  
 DR InterPro; IPR006202; Neur\_chan\_LBD.  
 DR Pfam; PF02931; Neur\_chan\_LBD; 1.  
 KW Receptor.  
 FT NON TER 1 1  
 FT NON TER 15 15  
 SO SEQUENCE 15 AA, 1852 MW, 9DB55FDACC3614E5 CRC64;

Query Match 32.8%; Score 22; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 8.4e+03;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEKN 4  
 DB 1 DEKN 4

RESULT 49  
 Q9TWC6\_DIRIM  
 ID Q9TWC6\_DIRIM PRELIMINARY; PRT; 17 AA.  
 AC Q9TWC6;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-JUN-2002 (TrEMBLrel. 21, last annotation update)  
 DB 22L kDa excretory-secretory protein (Fragment).  
 OC Dirofilaria immitis (Canine heartworm).  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidae;  
 OC Onchocercidae; Dirofilaria.  
 OK NCBI\_TaxID=6287;  
 RN (1)  
 RP PROTEIN SEQUENCE.  
 RX MEDLINE=96258562; PubMed=8992320; DOI=10.1016/0166-6851(95)02533-2;  
 RA Frank G.R., Griewe R.B.,  
 RT "Purification and characterization of three larval excretory-secretory  
 RL proteins of Dirofilaria immitis.";  
 RL Mol. Biochem. Parasitol. 75:221-229(1996).  
 FT NON\_TER 1 1  
 FT NON\_TER 17 17  
 SQ SEQUENCE 17 AA; 2048 MW; 478557C5392BAE7 CRC64;  
 Query Match 32.8%; Score 22; DB 2; Length 17;  
 Best Local Similarity 80.0%; Pred. No. 9.5e+03;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 8 CILGP 12  
 DB 6 CILKP 10

RESULT 50  
 ID O6QLM0\_91NFA PRELIMINARY; PRT; 17 AA.  
 AC O6QLM0;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, last annotation update)  
 DE Neuraminidase (Fragment).  
 OS Influenza A virus (A/chicken/Thailand/W3Nf/2004(H5N1)).  
 OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;  
 OC Influenzavirus A.  
 OK NCBI\_TaxID=264511;  
 RN (1)  
 RP NUCLEOTIDE SEQUENCE.  
 RA Oraveerakul K., Keawcharoen J., Wattanodorn S., Khanda S.,  
 RA Paphavast T., Theamboonlers A., Poovorawan Y.,  
 RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY535026; AA557879.1; -; Genomic RNA.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0004308; F:exo-alpha-sialidase activity; IEA.  
 DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.  
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.  
 DR InterPro; IPR001860; Glyco\_hydro\_34.  
 DR Pfam; PF00064; Neur; 1.  
 DR ProDom; PD000431; Glyco\_hydro\_34; 1.  
 KW Glycosidase; Hydrolase; Transmembrane.  
 FT NON\_TER 1 1  
 FT NON\_TER 17 17  
 SQ SEQUENCE 17 AA; 1954 MW; F35F7F3FPD8AF26F CRC64;  
 Query Match 32.8%; Score 22; DB 2; Length 17;  
 Best Local Similarity 33.3%; Pred. No. 9.5e+03;  
 Matches 4; Conservative 3; Mismatches 5; Indels 0; Gaps 0;  
 QY 1 DEKNSPECTLGP 12  
 DB 1 NSRSGFEMTMDP 12

RESULT 51  
 ID O6QLM1\_91NFA PRELIMINARY; PRT; 17 AA.  
 AC O6QLM1;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, last annotation update)

DE Neuraminidase (Fragment).  
 OS Influenza A virus (A/chicken/Thailand/LV1NF/2004(H5N1)).  
 OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;  
 OC Influenzavirus A.  
 OK NCBI\_TaxID=264510;  
 RN (1)  
 RP NUCLEOTIDE SEQUENCE.  
 RA Oraveerakul K., Keawcharoen J., Wattanodorn S., Khanda S.,  
 RA Paphavast T., Thongmee C., Theamboonlers A., Poovorawan Y.,  
 RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY535025; AA557878.1; -; Genomic RNA.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0004308; F:exo-alpha-sialidase activity; IEA.  
 DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.  
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.  
 DR InterPro; IPR001860; Glyco\_hydro\_34.  
 DR Pfam; PF00064; Neur; 1.  
 DR ProDom; PD000431; Glyco\_hydro\_34; 1.  
 KW Glycosidase; Hydrolase; Transmembrane.  
 FT NON\_TER 1 1  
 FT NON\_TER 17 17  
 SQ SEQUENCE 17 AA; 1954 MW; F35F7F3FPD8AF26F CRC64;  
 Query Match 32.8%; Score 22; DB 2; Length 17;  
 Best Local Similarity 33.3%; Pred. No. 9.5e+03;  
 Matches 4; Conservative 3; Mismatches 5; Indels 0; Gaps 0;  
 QY 1 DEKNSPECTLGP 12  
 DB 1 NSRSGFEMTMDP 12

RESULT 52  
 ID O9DPB5\_BRARE PRELIMINARY; PRT; 17 AA.  
 AC O9DPB5;  
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 16, last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, last annotation update)  
 DE Ftz-F1 alpha isoform 1 (Fragment).  
 GN Name=nr5a2; Synonym=fta;  
 OS Brachydanio rerio (Zebrafish) (Danio rerio).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
 OC Cyprinidae; Danio.  
 OK NCBI\_TaxID=7955;  
 RN (1)  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=20277948; PubMed=10816440; DOI=10.1042/0264-6021:3480439;  
 RA Lin W., Wang H.W., Sun C., Liu D., Hew C.L., Chung B.,  
 RA "Zebrafish ftz-f1 gene has two promoters, is alternatively spliced,  
 RT and is expressed in digestive organs.";  
 RT Biochem. J. 348:439-446(2000).  
 DR EMBL; AF286364; AAG28162.1; -; Genomic DNA.  
 DR ZFIN; ZDB-GENE-990415-79; nr5a2.  
 FT NON\_TER 1 1  
 FT NON\_TER 17 17  
 SQ SEQUENCE 17 AA; 1932 MW; FA22C4B4FD2C8F41 CRC64;  
 Query Match 32.8%; Score 22; DB 2; Length 17;  
 Best Local Similarity 62.5%; Pred. No. 9.5e+03;  
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 QY 4 NSPECTLIG 11  
 DB 3 SSFSESLG 10

RESULT 53  
 ID O6SR40\_DROST PRELIMINARY; PRT; 19 AA.  
 AC O6SR40;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)

DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Descr (Fragment).  
 OS Drosophila simulans (Fruit fly).  
 CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 CC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 CC Ephyridiidae; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7240;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX PubMed14762063; DOI=10.1101/gr.1329204;  
 RA Halligan D.L., Byrne-Walker A., Andolfatto P., Keightley P.D.;  
 RT "Patterns of evolutionary constraints in intronic and intergenic DNA  
 of Drosophila."  
 RL Genome Res. 14:273-279(2004).  
 DR EMBL: AY459578; AAC3029.1; -; Genomic\_DNA.  
 FT NON\_TER 19  
 SQ SEQUENCE 19 AA; 2068 MW; D13CFB2A110C762C CRC64;  
 Query Match 32.8%; Score 22; DB 2; Length 19;  
 Best Local Similarity 40.0%; Pred. No. 1.1e+04;  
 Matches 4; Conservative 1; Mismatches 5; Indels 0; Gaps 0;  
 QY 3 KNSPFCILGP 12  
 DB 3 KKKLNLVLP 12

RESULT 54  
 Q9TWH8\_PACM  
 ID Q9TWH8\_PACM PRELIMINARY; PRT; 19 AA.  
 AC Q9TWH8;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)  
 DE Carboxypeptidase PC (Fragment).  
 OS Paratithodes cantabatica (Kamchatka crab) (Red king crab).  
 CC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 CC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Anomura; Paguroidea;  
 CC Lithodidae; Paratithodes.  
 OX NCBI\_TaxID=6741;  
 RN [1]  
 RP PROTEIN SEQUENCE.  
 RX MEDLINE=95305881; PubMed=7786315;  
 RA Rudenskaya G.N., Kopenko O.G., Isaev V.A., Stepanov V.M.,  
 RA Dunaevskii I.A.B.;  
 RT "[Isolation and properties of carboxypeptidase from the Kamchatka crab  
 Paratithodes cantabatica]."  
 RL Bioorg. Khim. 21:249-255(1995).  
 SQ SEQUENCE 19 AA; 2213 MW; 2D7B894F238D5670 CRC64;  
 Query Match 32.8%; Score 22; DB 2; Length 19;  
 Best Local Similarity 80.0%; Pred. No. 1.1e+04;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DEKNS 5  
 DB 11 DEKNS 15

RESULT 55  
 O6QLM2\_GINPA  
 ID O6QLM2\_GINPA PRELIMINARY; PRT; 19 AA.  
 AC O6QLM2;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Neuraminidase (Fragment).  
 OS Influenza A virus (A/chicken/Thailand/KF1NF/2004(H5N1)).  
 CC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;  
 CC Influenzavirus A.  
 OX NCBI\_TaxID=264509;  
 RN [1]

RP NUCLEOTIDE SEQUENCE.  
 RA Oraveerakul K., Keavcharoen J., Wattanadorn S., Khanda S.,  
 RA Paphavast T., Theamboonlers A., Poonvorawan Y.;  
 RL Submitted (JAN-2004) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: AY535024; AAC57877.1; -; Genomic RNA.  
 DR GO: GO:0016021; C: integral to membrane; IEA.  
 DR GO: GO:0016020; C: membrane; IEA.  
 DR GO: GO:0004308; F: exo-alpha-sialidase activity; IEA.  
 DR GO: GO:0016798; F: hydrolase activity, acting on glycosyl bonds; IEA.  
 DR GO: GO:0005975; P: carbohydrate metabolism; IEA.  
 DR InterPro: IPR001860; Glyco\_hydro\_34.  
 DR Pfam: PF00064; Neur. 1.  
 DR Prodom: PD000431; Glyco\_hydro\_34; 1.  
 KM Glycosidase; Hydrolase; Transmembrane.  
 FT NON\_TER 19  
 SQ SEQUENCE 19 AA; 2142 MW; F33310F96DBAF26F CRC64;  
 Query Match 32.8%; Score 22; DB 2; Length 19;  
 Best Local Similarity 33.3%; Pred. No. 1.1e+04;  
 Matches 4; Conservative 3; Mismatches 5; Indels 0; Gaps 0;  
 QY 1 DEKNSFCILGP 12  
 DB 3 NSRSGFEMIDP 14

RESULT 56  
 O4X7B9\_PLACH  
 ID O4X7B9\_PLACH PRELIMINARY; PRT; 20 AA.  
 AC O4X7B9;  
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
 DE Hypothetical protein (Fragment).  
 GN ORFNames=PC405454.00.0;  
 OS Plasmodium chabaudi.  
 CC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
 OX NCBI\_TaxID=5825;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Hall N., Karrae M., Ratne J.D., Carlton J.M., Kool J.T.W.A.,  
 RA Bettman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,  
 RA James K., Rutherford K., Harris B., Harris D., Churcher C.,  
 RA Qiall M.A., Ormond D., Doggett J., Trueman H.B., Mendoza J.,  
 RA Bidwell S.L., Rajendram M.A., Carucci D.J., Yates J.R., Kafatos F.C.,  
 RA Jansz C.J., Barrett B., Turner C.M.R., Waters A.P., Sinden R.S.;  
 RT "A comprehensive survey of the Plasmodium life cycle by genomic,  
 transcriptomic, and proteomic analyses."  
 RL Science 307:82-86(2005).  
 CC -1- CAUTION: The sequence shown here is derived from an  
 EMBL/Genbank/DBJ whole genome shotgun (WGS) entry which is  
 preliminary data.  
 DR EMBL: CAJ01009247; CAH87207.1; -; Genomic\_DNA.  
 KM Hypothetical protein.  
 FT NON\_TER 1  
 SQ SEQUENCE 20 AA; 2432 MW; C6C090AB73A055F9 CRC64;  
 Query Match 32.8%; Score 22; DB 2; Length 20;  
 Best Local Similarity 80.0%; Pred. No. 1.1e+04;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 KNSFE 7  
 DB 15 KNSFE 19

RESULT 57  
 Q9R791\_BORAF  
 ID Q9R791\_BORAF PRELIMINARY; PRT; 10 AA.  
 AC Q9R791;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Outer surface protein C (Fragment).  
 GN Name=ospC;  
 OS Borrelia afzelii.  
 OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia;  
 OC Borrelia burgdorferi group.  
 OX NCBI\_TaxID=29518;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=US461;  
 RX MEDLINE=97426044; PubMed=9282748;  
 RA Tilly K., Casjens S., Stevenson B., Bono J.L., Samuels D.S., Hogan D.,  
 Rosa P.;  
 RL "The Borrelia burgdorferi circular plasmid cp26: conservation of  
 plasmid structure and targeted inactivation of the ospC gene.";  
 RT Mol. Microbiol. 25:361-374(1997).  
 DR EMBL; U93699; AAC4552.1; -; Genomic DNA.  
 DR GO; GO:0009279; C:outer membrane (sensu Gram-negative Bacteria); IEA.  
 DR GO; GO:0006952; P:defense response; IEA.  
 DR InterPro; IPR001800; Lipoprotein\_6.  
 DR Pfam; PF01441; Lipoprotein\_6; 1.  
 RT NON\_TER  
 FT SEQUENCE 10 AA; 1118 MW; 480864C5B731A443 CRC64;  
 SQ

Query Match 31.3%; Score 21; DB 2; Length 10;  
 Best Local Similarity 44.4%; Pred. No. 8.5e+03;  
 Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 2 EKNSPECIL 10  
 Db 2 KKNLTSAIIL 10

RESULT 58  
 Q9R790\_BORGA  
 ID Q9R790\_BORGA PRELIMINARY; PRT; 11 AA.  
 AC Q9R790;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Outer surface protein C (Fragment).  
 GN Name=ospC;  
 OS Borrelia garinii.  
 OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia;  
 OC Borrelia burgdorferi group.  
 OX NCBI\_TaxID=29519;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=G25;  
 RX MEDLINE=97426044; PubMed=9282748;  
 RA Tilly K., Casjens S., Stevenson B., Bono J.L., Samuels D.S., Hogan D.,  
 Rosa P.;  
 RL "The Borrelia burgdorferi circular plasmid cp26: conservation of  
 plasmid structure and targeted inactivation of the ospC gene.";  
 RT Mol. Microbiol. 25:361-374(1997).  
 DR EMBL; U93700; AAC4553.1; -; Genomic DNA.  
 DR GO; GO:0009279; C:outer membrane (sensu Gram-negative Bacteria); IEA.  
 DR GO; GO:0006952; P:defense response; IEA.  
 DR InterPro; IPR001800; Lipoprotein\_6.  
 DR Pfam; PF01441; Lipoprotein\_6; 1.  
 RT NON\_TER  
 FT SEQUENCE 11 AA; 1250 MW; 0868D864C5B731A4 CRC64;  
 SQ

Query Match 31.3%; Score 21; DB 2; Length 11;  
 Best Local Similarity 44.4%; Pred. No. 9.4e+03;  
 Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 2 EKNSPECIL 10  
 Db 2 KKNLTSAIIL 10

RESULT 59

Q6LEW9\_ARATH  
 ID Q6LEW9\_ARATH PRELIMINARY; PRT; 14 AA.  
 AC Q6LEW9;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE RNA polymerase beta subunit (Fragment).  
 GN Name=rpob;  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eurosid II; Brassicales; Brassicaceae; Arabidopsie.  
 OX NCBI\_TaxID=3702;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC MEDLINE=97304680; PubMed=9161043;  
 RA Inada H., Seki M., Morikawa H., Nishimura M., Iba K.;  
 RT "Existence of three regulatory regions each containing a highly  
 conserved motif in the promoter plastid-encoded RNA polymerase gene  
 (rpob)";  
 RT Plant J. 11:883-890(1997).  
 DR EMBL; D84552; BAA21502.1; -; Genomic DNA.  
 DR GO; GO:0009507; C:chloroplast; IEA.  
 KW Chloroplast.  
 RT NON\_TER  
 FT SEQUENCE 14 AA; 1405 MW; 7195255E082917B CRC64;  
 SQ

Query Match 31.3%; Score 21; DB 2; Length 14;  
 Best Local Similarity 45.5%; Pred. No. 1.2e+04;  
 Matches 5; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 1 DEKNSPECILG 11  
 Db 4 DEKEGTSAIPG 14

RESULT 60  
 O56127\_9CIRC  
 ID O56127\_9CIRC PRELIMINARY; PRT; 14 AA.  
 AC O56127;  
 DT 01-JUN-1998 (TrEMBLrel. 06, Created)  
 DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE ORF1; predicted 1.8 kDa protein.  
 OS Porcine circovirus.  
 OC Viruses; ssDNA viruses; Circoviridae; Circovirus.  
 OX NCBI\_TaxID=46221;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=pms PCV;  
 RX MEDLINE=98241772; PubMed=9573301;  
 RA Hamel A.L., Lin L.L., Nayar G.P.;  
 RT "Nucleotide sequence of porcine circovirus associated with postweaning  
 multisystemic wasting syndrome in pigs."  
 RL J. Virol. 72:5262-5267(1998).  
 DR EMBL; AF027217; AAC59472.1; -; Genomic DNA.  
 DR InterPro; IPR001800; Lipoprotein\_6.  
 RT NON\_TER  
 FT SEQUENCE 14 AA; 1761 MW; 00F50DC89EBAF20B CRC64;  
 SQ

Query Match 31.3%; Score 21; DB 2; Length 14;  
 Best Local Similarity 57.1%; Pred. No. 1.2e+04;  
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 3 KNSPECT 9  
 Db 4 KKHYEVI 10

RESULT 61  
 Q6LCZ7\_HUMAN  
 ID Q6LCZ7\_HUMAN PRELIMINARY; PRT; 15 AA.  
 AC Q6LCZ7;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)



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DT 05-JUN-2004 (TRENBLREL. 27, Last sequence update)
DT 01-FEB-2005 (TRENBLREL. 29, Last annotation update)
DE Interleukin-8 receptor type B (Fragment).
GN Name=IL8RB;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=95014476; PubMed=7929358;
RA Ahuja S.K., Shetty A., Tiffany H.L., Murphy P.M.;
RT "Comparison of the genomic organization and promoter function for
human interleukin-8 receptors A and B."
RL J. Biol. Chem. 269:26381-26389(1994).
DR EMBL/ U11873; AAA64381.1; -; mRNA.
DR EMBL/ U11874; AAA64382.1; -; mRNA.
DR EMBL/ U11875; AAA64383.1; -; mRNA.
DR EMBL/ U11876; AAA64384.1; -; mRNA.
DR EMBL/ U11877; AAA64385.1; -; mRNA.
DR EMBL/ U11878; AAA64386.1; -; mRNA.
DR EMBL/ U11872; AAA64380.1; -; mRNA.
DR GO: 0004872; P:receptor activity; IEA.
KW Receptor.
FT NON_TER.
SQ SEQUENCE 15 AA; 1929 MW; 8937AF0B93D4F48C CRC64;

Query Match 31.3%; Score 21; DB 2; Length 15;
Best Local Similarity 66.7%; Pred. No. 1.3e+04;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 EKNSFE 7
DB 7 ESDSFE 12

RESULT 62
Q9R4U8 ACTCA PRELIMINARY; PRT; 15 AA.
AC Q9R4U8;
DT 01-MAY-2000 (TRENBLREL. 13, Created)
DT 01-MAY-2000 (TRENBLREL. 13, Last sequence update)
DT 01-JUN-2000 (TRENBLREL. 14, Last annotation update)
DE Malonate decarboxylase beta subunit (Fragment).
OS Acinetobacter calcoaceticus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Moraxellaceae; Acinetobacter.
OX NCBI_TaxID=471;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=95050812; PubMed=7961952;
RA Kim Y.S., Byun H.S.;
RT "Purification and properties of a novel type of malonate decarboxylase
from Acinetobacter calcoaceticus."
RL J. Biol. Chem. 269:29636-29641(1994).
SQ SEQUENCE 15 AA; 1790 MW; 03388040DB71DE8D CRC64;

Query Match 31.3%; Score 21; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KNSF 6
DB 7 KNSF 10

RESULT 63
PA2_NAJSF STANDARD; PRT; 16 AA.
ID PA2_NAJSF
AC Q10756;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)

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DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Phospholipase A2 (EC 3.1.1.4) (Phosphatidylcholine 2-acylhydrolase)
DE Muscarinic inhibitor (Fragment).
OS Naja sputatrix (Malayan spitting cobra).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidae;
OC Elapidae; Elapinae; Naja.
OX NCBI_TaxID=33626;
RN [1]
RP PROTEIN SEQUENCE.
RX TISSUE-Venom;
RX MEDLINE=96195757; PubMed=8638927; DOI=10.1006/abbi.1996.0137;
RA Miyoshi S.-I., Yu A.T.;
RT "Phospholipase A2 from Naja naja sputatrix venom is a muscarinic
acetylcholine receptor inhibitor."
RL Arch. Biochem. Biophys. 328:17-25(1996).
CC -1 FUNCTION: PA2 catalyzes the calcium-dependent hydrolysis of the 2-
acyl groups in 3-sn-phosphoglycerides. Blocks neuromuscular
transmission at the postsynaptic site. Binds to the muscarinic
acetylcholine receptor.
CC -1 CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-
acylglycerophosphocholine + a carboxylate.
CC -1 COFACTOR: Binds 1 calcium ion (By similarity).
CC -1 SUBUNIT: Monomer.
CC -1 SUBCELLULAR LOCATION: Secreted.
CC -1 SIMILARITY: Belongs to the phospholipase A2 family. Group I
subfamily.
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CC The Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC PIR; S65520; S65520.
DR HSSP; P00598; IPOA.
DR InterPro; IPR001211; PhospholipaseA2.
DR Pfam; PF00068; Phospholip_A2_1; 1.
DR PROSITE; PS00119; PA2_ASP; PARTIAL.
DR PROSITE; PS00118; PA2_HIS; PARTIAL.
KW Acetylcholine receptor inhibitor; Calcium; Direct protein sequencing;
KW Hydrolase; Lipid degradation; Neurotoxin; Postsynaptic neurotoxin;
KW Toxin.
FT NON_TER.
SQ SEQUENCE 16 AA; 1969 MW; 9AC1F9834B585F0 CRC64;

Query Match 31.3%; Score 21; DB 1; Length 16;
Best Local Similarity 50.0%; Pred. No. 1.4e+04;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 KNSFEC 8
DB 6 KNNIQC 11

RESULT 64
Q14316 HUMAN PRELIMINARY; PRT; 17 AA.
ID Q14316
AC Q14316;
DT 01-NOV-1996 (TRENBLREL. 01, Created)
DT 01-JUN-2004 (TRENBLREL. 24, Last sequence update)
DT 01-JUN-2004 (TRENBLREL. 26, Last annotation update)
DE Factor IX protein (Fragment).
GN Name=Factor IX;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=88327116; PubMed=3416069;
RA Reitsma P.A., Bertina R.M., Ploos van Amstel J.K., Riemens A.,

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RA Briel E.;  
 RT "The putative factor IX gene promoter in hemophilia B Leyden."  
 RL Blood 72:1074-1076(1988).  
 DR EMBL; X55008; CAB38245.2; -; Genomic\_DNA.  
 DR HSSP; P00734; IUMA.  
 FT NON\_TER 17  
 SQ SEQUENCE 17 AA; 1807 MW; 73887873A971A4F1 CRC64;  
 Query Match 31.3%; Score 21; DB 2; Length 17;  
 Best Local Similarity 75.0%; Pred. No. 1.5e+04;  
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 8 CILG 11  
 DB 11 CILG 14

RESULT 65  
 ID O6QL7\_9INPA PRELIMINARY; PRT; 17 AA.  
 AC O6QL7;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Neuraminidase (Fragment).  
 OS Influenza A virus (A/Thailand/EK42NF/2004(H5N1)).  
 OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;  
 OC Influenzavirus A.  
 OC NCBI\_TaxID=264514;  
 RN [1]  
 RP NCLECTIDE SEQUENCE.  
 RA Oraveerakul K., Keawcharoen J., Wattanodorn S., Patanarangsarn S.,  
 Paphavast T., Theamboonlers A., Poovorawan Y.;  
 RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY355029; AAS57882.1; -; Genomic\_RNA.  
 DR GO; GO:0016021; C:membrane; IEA.  
 DR GO; GO:0004308; F:exo-alpha-sialidase activity; IEA.  
 DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.  
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.  
 DR InterPro; IPR001860; Glyco\_hydro\_34.  
 DR Pfam; PF0064; Neur; 1.  
 DR ProDom; PD000431; Glyco\_hydro\_34; 1.  
 KM Glycosidase; Hydrolase; Transmembrane.  
 FT NON\_TER 1  
 FT NON\_TER 1  
 SQ SEQUENCE 17 AA; 2003 MW; EBB82F3FFD8AF26F CRC64;  
 Query Match 31.3%; Score 21; DB 2; Length 17;  
 Best Local Similarity 40.0%; Pred. No. 1.5e+04;  
 Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
 QY 3 KNSPECTIGP 12  
 DB 3 RSGFEMIWDP 12

RESULT 66  
 ID O6QL9\_9INPA PRELIMINARY; PRT; 17 AA.  
 AC O6QL9;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Neuraminidase (Fragment).  
 OS Influenza A virus (A/chicken/Thailand/LV3NF/2004(H5N1)).  
 OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;  
 OC Influenzavirus A.  
 OC NCBI\_TaxID=264512;  
 RN [1]  
 RP NCLECTIDE SEQUENCE.  
 RA Oraveerakul K., Keawcharoen J., Wattanodorn S., Khanda S.,  
 Paphavast T., Theamboonlers A., Poovorawan Y.;

RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY355027; AAS57880.1; -; Genomic\_RNA.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0004308; F:exo-alpha-sialidase activity; IEA.  
 DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.  
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.  
 DR InterPro; IPR001860; Glyco\_hydro\_34.  
 DR Pfam; PF0064; Neur; 1.  
 DR ProDom; PD000431; Glyco\_hydro\_34; 1.  
 KM Glycosidase; Hydrolase; Transmembrane.  
 FT NON\_TER 1  
 FT NON\_TER 1  
 SQ SEQUENCE 17 AA; 2003 MW; EBB82F3FFD8AF26F CRC64;  
 Query Match 31.3%; Score 21; DB 2; Length 17;  
 Best Local Similarity 40.0%; Pred. No. 1.5e+04;  
 Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
 QY 3 KNSPECTIGP 12  
 DB 3 RSGFEMIWDP 12

RESULT 67  
 ID Q4X7V0\_PLACH PRELIMINARY; PRT; 18 AA.  
 AC Q4X7V0;  
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
 DE Hypothetical protein (Fragment).  
 GN ORFNames=PC405248.00.0;  
 OS Plasmodium chabaudi.  
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
 OC NCBI\_TaxID=5825;  
 RN [1]  
 RP NCLECTIDE SEQUENCE.  
 RA Hall N., Kariya M., Raine J.D., Carlton J.M., Kooll T.W.A.,  
 Berrieman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,  
 James K., Rutherford K., Harris B., Harris H.B., Churcher C.,  
 Quail M.A., Ormond D., Doggett J., Trueman H.B., Mendoza J.,  
 Radebeli S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,  
 Jansz C.J., Barrett B., Turner C.M.R., Waters A.P., Sinden R.S.;  
 RA "A comprehensive survey of the Plasmodium life cycle by genomic,  
 transcriptomic, and proteomic analyses."  
 RT Science 307:82-86(2005).  
 RL Science 307:82-86(2005).  
 CC -!- CAUTION: The sequence shown here is derived from an  
 EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
 preliminary data.  
 DR EMBL; CAJ01009092; CAH87026.1; -; Genomic\_DNA.  
 KM Hypothetical protein.  
 FT NON\_TER 1  
 FT NON\_TER 1  
 SQ SEQUENCE 18 AA; 2225 MW; 2E5832A217F96845 CRC64;  
 Query Match 31.3%; Score 21; DB 2; Length 18;  
 Best Local Similarity 75.0%; Pred. No. 1.6e+04;  
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 6 FBCI 9  
 DB 15 FDCI 18

RESULT 68  
 ID Q4Y1S4\_PLACH PRELIMINARY; PRT; 19 AA.  
 AC Q4Y1S4;  
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
 DE Hypothetical protein (Fragment).  
 GN ORFNames=PC103036.00.0;

OS Plasmodium chabaudi.  
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
 OX NCBI\_TaxID=5825;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Hall N., Karras M., Raine J.D., Carlton J.M., Kool J.T.W.A.,  
 RA Bertram M., Florens L., Janssen C.S., Pain A., Christophides G.K.,  
 RA James K., Rutherford K., Harris B., Harris D., Churcher C.,  
 RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,  
 RA Bivell S.L., Rajandream K.A., Carucci D.J., Yates J.R., Kafatos F.C.,  
 RA James C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.;  
 RT "A comprehensive survey of the Plasmodium life cycle by genomic,  
 RT transcriptomic, and proteomic analyses."  
 RL Science 307:82-86 (2005).  
 CC -! CAUTION: The sequence shown here is derived from an  
 CC EMBL/Genbank/DBJ whole genome shotgun (WGS) entry which is  
 CC preliminary data.  
 DR EMBL; CAU01001723; CAH76886.1; -; Genomic\_DNA.  
 KW Hypothetical protein.  
 FT NON TER 1  
 SQ SEQUENCE 19 AA; 2211 MW; EP1P95ACE6A07PFP4 CRC64;  
 OY Query Match 31.3%; Score 21; DB 2; Length 19;  
 Best Local Similarity 42.9%; Pred. No. 1.6e+04;  
 Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
 OY 3 KNSPECI 9  
 DB 11 KNAILCV 17  
 RESULT 69  
 O8UHQ2\_CHICK PRELIMINARY; PRT; 19 AA.  
 AC O8UHQ2;  
 DT 01-MAR-2002 (TREMBlrel. 20, Created)  
 DT 01-FEB-2005 (TREMBlrel. 29, Last sequence update)  
 DE TGF-beta4 (Fragment).  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Blood;  
 RA Li H., Deeb N., Zhou H., Ashwell C.M., Lamont S.J.;  
 RL Submitted (DEC-2001) to the EMBL/Genbank/DBJ databases.  
 DR EMBL; AF459837; AAL67517.1; -; Genomic\_DNA.  
 FT NON TER 1  
 FT NON TER 1  
 SQ SEQUENCE 19 AA; 2046 MW; 1250C1CBFE03C2F7 CRC64;  
 OY Query Match 31.3%; Score 21; DB 2; Length 19;  
 Best Local Similarity 60.0%; Pred. No. 1.6e+04;  
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 OY 8 CILGP 12  
 DB 3 CEMGP 7  
 RESULT 70  
 O8UVE0\_CHICK PRELIMINARY; PRT; 19 AA.  
 AC O8UVE0;  
 DT 01-MAR-2002 (TREMBlrel. 20, Created)  
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)  
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)  
 DE TGF-beta4 (Fragment).  
 OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Blood;  
 RA Li H., Deeb N., Zhou H., Ashwell C.M., Lamont S.J.;  
 RL Submitted (DEC-2001) to the EMBL/Genbank/DBJ databases.  
 DR EMBL; AF459839; AAL67519.1; -; Genomic\_DNA.  
 FT NON TER 1  
 FT NON TER 1  
 SQ SEQUENCE 19 AA; 2032 MW; 1315C1CBFE03C2F7 CRC64;  
 OY Query Match 31.3%; Score 21; DB 2; Length 19;  
 Best Local Similarity 60.0%; Pred. No. 1.6e+04;  
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 OY 8 CILGP 12  
 DB 3 CEMGP 7  
 RESULT 71  
 O5PU92\_BRARE PRELIMINARY; PRT; 19 AA.  
 AC O5PU92;  
 DT 01-FEB-2005 (TREMBlrel. 29, Created)  
 DT 01-FEB-2005 (TREMBlrel. 29, Last sequence update)  
 DT 01-FEB-2005 (TREMBlrel. 29, Last annotation update)  
 DE T-cell factor 7 isoform D (Fragment).  
 GN Name=tcf7;  
 OS Brachydanio rerio (Zebrafish) (Danio rerio).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Cypriniformes;  
 OC Cyprinidae; Danio.  
 OX NCBI\_TaxID=7955;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=AB;  
 RX PubMed=15765502; DOI=10.1002/dvdy.20330;  
 RA Velen B.S., Grierson M.J., Sand R.S., Dorisky R.I.;  
 RT "Expression pattern of zebrafish tcf7 suggests unexplored domains of  
 RT Wnt/beta-catenin activity."  
 RL Dev. Dyn. 233:233-239 (2005).  
 DR EMBL; AY825027; AAV84017.1; -; mRNA.  
 DE ZFIN; ZDB-GENE-050222-4; tcf7.  
 FT NON TER 1  
 SQ SEQUENCE 19 AA; 2239 MW; 30C5948AC4B9B9A2 CRC64;  
 OY Query Match 31.3%; Score 21; DB 2; Length 19;  
 Best Local Similarity 60.0%; Pred. No. 1.6e+04;  
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 OY 4 NSFEC 8  
 DB 14 NSLDC 18  
 RESULT 72  
 MHT\_BOMMX STANDARD; PRT; 20 AA.  
 ID MHT\_BOMMX  
 AC P83086;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 13-SEP-2005 (Rel. 48, Last annotation update)  
 DE Maxin-hc (Maxin-hc-7).  
 OS Bombina maxima (Giant fire-bellied toad) (Chinese red belly toad).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Archaeobatrachia; Bombinatoridae; Bombina.  
 OX NCBI\_TaxID=161274;  
 RN [1]  
 RP PROTEIN SEQUENCE, FUNCTION, SUBCELLULAR LOCATION, AND TISSUE

RP SPECIFICITY.  
RC TISSUE=Skin secretion;  
RA Chen T.B., McClean S., Orr D.F., Bjourson A.J., Rao P.F., Shaw C.;  
RT "Isolation and structural characterisation of antimicrobial peptides  
from the venom of the Chinese large-webbed bell toad (Bombina  
maxima).";  
RL Submitted (JUL-2001) to Swiss-Prot.  
CC -1- FUNCTION: Has antimicrobial activity.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- TISSUE SPECIFICITY: Expressed by the skin glands.  
CC -1- SIMILARITY: Belongs to the bombinin family.  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use as long as its content is in no way modified and this statement is not  
CC removed.  
CC Amphibian defense peptide; Antibiotic; Antimicrobial;  
KW Direct protein sequencing.  
SQ SEQUENCE 20 AA; 1977 MW; EC7541AD6B2F949 CRC64;  
Query Match 31.3%; Score 21; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.7e+04;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 9 ILGP 12  
DB 1 ILGP 4  
RESULT 73  
MHU\_BOMMX STANDARD; PRT; 20 AA.  
ID MHU\_BOMMX  
AC P83087;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 13-SEP-2005 (Rel. 48, Last annotation update)  
DE Maximin-Hu (Maximin-8), last annotation update)  
OS Bombina maxima (Giant fire-bellied toad) (Chinese red belly toad).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Archaeobatrachia; Bombinatoridae; Bombina.  
OX NCBI\_Taxid=161274;  
RN [1]  
RP PROTEIN SEQUENCE, FUNCTION, SUBCELLULAR LOCATION, AND TISSUE  
RP SPECIFICITY.  
RC TISSUE=Skin secretion;  
RA Chen T.B., McClean S., Orr D.F., Bjourson A.J., Rao P.F., Shaw C.;  
RT "Isolation and structural characterisation of antimicrobial peptides  
from the venom of the Chinese large-webbed bell toad (Bombina  
maxima).";  
RL Submitted (JUN-2001) to Swiss-Prot.  
CC -1- FUNCTION: Has antimicrobial activity.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- TISSUE SPECIFICITY: Expressed by the skin glands.  
CC -1- SIMILARITY: Belongs to the bombinin family.  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use as long as its content is in no way modified and this statement is not  
CC removed.  
CC Amphibian defense peptide; Antibiotic; Antimicrobial;  
KW Direct protein sequencing.  
SQ SEQUENCE 20 AA; 1977 MW; EC7541AD6B2F949 CRC64;  
Query Match 31.3%; Score 21; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.7e+04;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 9 ILGP 12  
DB 1 ILGP 4

DB 1 ILGP 4  
RESULT 74  
Q4YU5\_PLABE PRELIMINARY; PRT; 20 AA.  
ID Q4YU5\_PLABE  
AC Q4YU5;  
DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
DE Hypothetical protein (Fragment).  
GN ORFNames=PB105963.00.0;  
OS Plasmodium berghei.  
OC Eukaryota; Alveolata; Apicomplexa; Haemosporidia; Plasmodium.  
OX NCBI\_Taxid=5821;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Hall N., Kairas M., Raine J.D., Carlton J.M., Kool J.T.W.A.,  
RA Bertram M., Florens L., Janssen C.S., Pain A., Christophides G.K.,  
RA James K., Rutherford K., Harris B., Harris D., Churcher C.,  
RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,  
RA Bidwell S.L., Rajadream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,  
RA Janse C.J., Bartell B., Turner C.M.R., Waters A.P., Sinden R.S.;  
RT "A comprehensive survey of the Plasmodium life cycle by genomic,  
RT transcriptomic, and proteomic analyses";  
RL Science 307:82-86(2005).  
CC -1- CAUTION: The sequence shown here is derived from an  
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
CC preliminary data.  
DR EMBL; CA01002380; CAH98362.1; -; Genomic\_DNA.  
KW Hypothetical protein.  
FT NON\_TER 1  
SQ SEQUENCE 20 AA; 2265 MW; 1322E950F0B057BF CRC64;  
Query Match 31.3%; Score 21; DB 2; Length 20;  
Best Local Similarity 37.5%; Pred. No. 1.7e+04;  
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
QY 3 KNSPECIL 10  
DB 1 KXHMOCIT 8  
RESULT 75  
Q49448\_MYCGE PRELIMINARY; PRT; 20 AA.  
ID Q49448\_MYCGE  
AC Q49448;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Uncertain (Fragment).  
OS Mycoplasma genitalium.  
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.  
OX NCBI\_Taxid=2097;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=94075230; PubMed=8253680;  
RA Peterson S.N., Hu P.-C., Bort R.F., Hutchison C.A. III;  
RT "A survey of the Mycoplasma genitalium genome by using random  
RT sequencing";  
RL J. Bacteriol. 175:7918-7930(1993).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RA Peterson S.N.;  
RT "Characterization and analysis of the Mycoplasma genitalium genome.";  
RL Thesis (1992), Microbiology and Immunology, University of North  
Carolina Medical School.  
DR EMBL; U01744; AAD10557.1; -; Genomic\_DNA.  
FT NON\_TER 1  
SQ SEQUENCE 20 AA; 2424 MW; BF8CE399592F014 CRC64;  
Query Match 31.3%; Score 21; DB 2; Length 20;

Best Local Similarity 57.1%; Pred. No. 1.7e+04;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 3 KNSPECI 9  
Db 14 KVSFLCV 20

## RESULT 76

04GZP1\_MYCTU  
ID 04GZP1\_MYCTU PRELIMINARY; PRT; 20 AA.  
AC 04GZP1;  
DT 13-SEP-2005 (TReMBLrel. 31, Created)  
DT 13-SEP-2005 (TReMBLrel. 31, Last sequence update)  
DT 13-SEP-2005 (TReMBLrel. 31, Last annotation update)  
DE Hypothetical protein RV3136 (Fragment).  
GN Name=RV3136;  
OS Mycobacterium tuberculosis.  
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium;  
OC Mycobacterium tuberculosis complex.  
OX NCBI\_TaxID=1773;  
RN  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=ATCC 35811;  
RA Menendez M.C.; Buxton R.S.; Stavropoulos E.; Evans J.;  
RA Gascogne-Binzi D.; Barlow R.E.L.; Hawkey P.M.; Colston M.;  
RT "Genomic characterization by DNA microarray analysis of prevalent  
RT clinical strains of Mycobacterium tuberculosis in the South Asian  
RL community of the UK indicates a common evolutionary origin."  
RL Submitted (JUL-2005) to the EMBL/GenBank/DBJ databases.  
RN  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=ATCC 35811;  
RA Menendez M.C.;  
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AJ879178; CA51329.1; -; Genomic\_DNA.  
KM Hypothetical protein.  
FT NON\_TER 20  
SQ SEQUENCE 20 AA; 2166 MW; B6D1A559B33CA2F CRC64;

Query Match 31.3%; Score 21; DB 2; Length 20;  
Best Local Similarity 45.5%; Pred. No. 1.7e+04;  
Matches 5; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 2 EKXSPECILCP 12  
Db 9 EVNSARMYTCP 19

## RESULT 77

06TH87\_MOUSE  
ID 06TH87\_MOUSE PRELIMINARY; PRT; 20 AA.  
AC 06TH87;  
DT 05-JUL-2004 (TReMBLrel. 27, Created)  
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)  
DE Mu oploid receptor variant S (Fragment).  
GN Name=Opml; Synonym=Opnm;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Eumarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN  
RP NUCLEOTIDE SEQUENCE.  
RC T18SUB=Whole brain;  
RX PubMed=1499152; DOI=10.1007/s00109-003-0514-z;  
RA Kram T.M.; Baar C.; Rakvag T.T.; Kaasa S.; Krokan H.B.; Skorpen F.;  
RT "Genetic analysis of the murine micro oploid receptor: increased  
RT complexity of Opnm gene splicing."  
RL J. Mol. Med. 82:250-255(2004).  
DR EMBL; AY397681; AAR28085.1; -; mRNA.

DR MGI; MGI:97441; Opml.  
DR GO; GO:0016021; C:integral to membrane, TAS.  
DR GO; GO:0005624; C:membrane fraction; IDA.  
DR GO; GO:0004988; F:mu-opioid receptor activity; IDA.  
DR GO; GO:0007610; P:behavior; IMP.  
DR GO; GO:0007191; P:dopamine receptor, adenylate cyclase activa. . .; IDA.  
DR GO; GO:0007193; P:G-protein signaling, adenylate cyclase inh. . .; IDA.  
KW Receptor.  
FT NON\_TER 1  
SQ SEQUENCE 20 AA; 2160 MW; EBD8381A9DE5B0B CRC64;

Query Match 31.3%; Score 21; DB 2; Length 20;  
Best Local Similarity 42.9%; Pred. No. 1.7e+04;  
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 5 SFECLIG 11  
Db 1 SIVCVG 7

## RESULT 78

07L297\_RANCA  
ID 07L297\_RANCA PRELIMINARY; PRT; 20 AA.  
AC 07L297;  
DT 01-MAR-2004 (TReMBLrel. 26, Created)  
DT 01-MAR-2004 (TReMBLrel. 26, Last sequence update)  
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)  
DE Gamma crystallin V (Fragment).  
OS Rana catesbeiana (Bull frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana;  
OC Aquarana.  
OX NCBI\_TaxID=8400;  
RN  
RP PROTEIN SEQUENCE.  
RX MEDLINE=89351593; PubMed=3255376;  
RA Chlou S.H.;  
RT "The protein sequence homology of gamma-crystallins among major  
RT vertebrate classes and their DNA sequence homology to heat-shock  
RT protein genes."  
RL J. Protein Chem. 7:527-534(1988).  
DR HSP; P08209; 1BLP.  
DR PIR; D60894; D60894.  
DR InterPro; IPR01064; Crystallin.  
DR Pfam; PF00030; Crystall; 1.  
DR PROSITE; PSS0915; CRYSTALLIN\_BETAGAMMA; 1.  
FT NON\_TER 1  
FT NON\_TER 20  
SQ SEQUENCE 20 AA; 2386 MW; E24FBA30914FB23 CRC64;

Query Match 31.3%; Score 21; DB 2; Length 20;  
Best Local Similarity 75.0%; Pred. No. 1.7e+04;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 5 SFECL 8  
Db 15 SYEC 18

## RESULT 79

012036\_CAVY  
ID 012036\_CAVY PRELIMINARY; PRT; 12 AA.  
AC 012036;  
DT 01-JUL-1997 (TReMBLrel. 04, Created)  
DT 01-JUL-1997 (TReMBLrel. 04, Last sequence update)  
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN Name=env;  
OS Caprine arthritis encephalitis virus (CAEV).  
OC Viruses; Retroviridae; Retroviridae; Lentivirus;  
OC Ovis/caprine lentivirus.  
OX NCBI\_TaxID=11660;  
RN  
[1]

```

RP NUCLEOTIDE SEQUENCE.
RX MEDLINE-97296261; PubMed=9151845;
RA Turelli P., Guiguen P., Mornex J.F., Vigne R., Querat G.;
RT "dUTPase-minus caprine arthritis-encephalitis virus is attenuated for
RL pathogenesis and accumulates G-to-A substitutions.";
DR J. Virol. 71:4522-4530(1997).
DR EMBL; U81390; AAC57905.1; -; Genomic RNA.
DR GO; GO:0019031; C: viral envelope; IEA.
KW Envelope protein.
FT NON_TER
SQ SEQUENCE 12 AA; 1398 MW; 8D24228CA3733455 CRC64;

Query Match 29.9%; Score 20; DB 2; Length 12;
Best Local Similarity 42.9%; Pred. No. 1.6e+04;
Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 EKNSPEC 8
DB 4 ESNKWTCT 10

RESULT 80
Q6LCK3 HUMAN PRELIMINARY; PRT; 14 AA.
AC Q6LCK3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Amloride-sensitive epithelial sodium channel gamma subunit
DE (Fragment).
OS Name=SCNN1G;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE-96415159; PubMed=8824247; DOI=10.1074/jbc.271.42.26062;
RA Thomas C.P., Doggett N.A., Fisher R., Stokes J.B.;
RT "Genomic organization and the 5' flanking region of the gamma subunit
of the human amloride-sensitive epithelial sodium channel.";
DR J. Biol. Chem. 271:26062-26066(1996).
DR EMBL; U53853; AAC50761.1; -; Genomic DNA.
DR GO; GO:0005216; F: ion channel activity; IEA.
KW Ion channel.
FT NON_TER
SQ SEQUENCE 14 AA; 1536 MW; 97F3F771ACD52945 CRC64;

Query Match 29.9%; Score 20; DB 2; Length 14;
Best Local Similarity 57.1%; Pred. No. 1.8e+04;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 NSPECIT 10
DB 6 NSIEMML 12

RESULT 81
Q9Y429 HUMAN PRELIMINARY; PRT; 15 AA.
AC Q9Y429;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE PANCA protein (Fragment).
OS Name=PCNA;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;

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RN [1]
RP NUCLEOTIDE SEQUENCE.
RA D'Apollito M., Ianzano L., Savino M., Rommens J., Zelante L.,
RA Savota A.;
RT Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ131189; CAB46099.1; -; Genomic DNA.
FT NON_TER
SQ SEQUENCE 15 AA; 1590 MW; 8732D75A24DCA4F0 CRC64;

Query Match 29.9%; Score 20; DB 2; Length 15;
Best Local Similarity 60.0%; Pred. No. 2e+04;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 CILGP 12
DB 6 CTCGP 10

RESULT 82
Q7M2P4 PIG PRELIMINARY; PRT; 16 AA.
AC Q7M2P4;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Annexin 36k chain (Fragment).
OS Sus scrofa domestica (domestic pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC Sus.
OX NCBI_TaxID=9825;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE-86203621; PubMed=2422556;
RA Geisow M.J., Fritsche U., Hexham J.M., Dash B., Johnson T.;
RT "A consensus amino-acid sequence repeat in Torpedo and mammalian
RT Ca(2+)-dependent membrane-binding proteins.";
RL Nature 320:636-638(1986).
DR PIR; A26393; A26393.
FT NON_TER
SQ SEQUENCE 16 AA; 1801 MW; A7554408D57CF129 CRC64;

Query Match 29.9%; Score 20; DB 2; Length 16;
Best Local Similarity 50.0%; Pred. No. 2.1e+04;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 DEKNSPECIT 10
DB 7 DEDRLIBITL 16

RESULT 83
Q5BIH5 EMENI PRELIMINARY; PRT; 17 AA.
AC Q5BIH5;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Hypothetical protein.
OS ORFNames=AN5605.2;
OS Apeerygillus nidulans FGSC A4.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiiales; Trichocomaceae; Emericella.
OX NCBI_TaxID=227321;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FGSC A4;
RA Birren B., Nusbaum C., Abouelleil A., Allen N., Anderson S.,
RA Arachchi H.M., Barna N., Baatien V., Bloom T., Boguslavsky L.,
RA Boukhalter B., Butler J., Calvo S.E., Camarata J., Chang J.,
RA Choepel Y., Collimore A., Cook A., Cooke P., Corum B., Deatellano K.,
RA Diaz J.S., Dodge S., Dooley K., Dorris L., Elkins T., Engels R.,
RA Erickson J., Faro S., Ferreira P., Fitzgerald M., Gage D., Galagan J.,

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RA Gardyna S., Gnerre S., Graham L., Grand-Pierre N., Hafez N.,  
 RA Hagopian D., Hagos R., Hall J., Horton L., Hulme W., Iliev I.,  
 RA Jaffe D., Johnson R., Jones C., Kamal M., Kamat A., Karakas A.,  
 RA Kellis C., Landers T., Levine R., Lindblad-Toh K., Liu G., Lui A.,  
 RA Ma L.-J., Mabbitt R., Maclean C., MacDonald P., Major J., Manning J.,  
 RA Matthews C., Mauceli E., McCarthy M., Meldrum J., Menes L.,  
 RA Mhova T., Mienna V., Murphy T., Naylor J., Nguyen C., Nicol R.,  
 RA Nielsen C.B., Norbu C., O'Connor T., O'Donnell P., O'Neill D.,  
 RA Oliver J., Peterson K., Phunkhang P., Pierre N., Purcell S.,  
 RA Raghupathi A., Ramasamy U., Raymond C., Reta R., Rise C., Rogov P.,  
 RA Roman J., Schauer S., Schupbach R., Seaman S., Severy P., Smirnov S.,  
 RA Smith C., Spencer B., Stange-Thomann N., Stojanovic N., Stubbs M.,  
 RA Tatham J., Tesfaye S., Theodore J., Topham K., Travers M.,  
 RA Vesiliev H., Venkatarman V.S., Viel R., Vo A., Wang S., Wilson B.,  
 RA Wu X., Wyman D., Young G., Zainoun J., Zembek U., Zimmer A., Zody M.,  
 RA Zander B.,  
 RT "genome sequence of Aspergillus nidulans."  
 RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.  
 CC -1- CAUTION: The sequence shown here is derived from an  
 EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
 CC preliminary data.  
 DR EMBL, AACD0100097; EAA62195.1; -; Genomic\_DNA.  
 KW Hypothetical protein.  
 SQ SEQUENCE 17 AA; 1874 MW; B279D1966C71F967 CRC64;

Query Match 29.9%; Score 20; DB 2; Length 17;  
 Best Local Similarity 60.0%; Pred. No. 2.2e+04;  
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 6 FECL 10  
 Db 4 FDCAL 8

RESULT 84  
 Q4XMI0\_PLACH PRELIMINARY; PRT; 17 AA.  
 ID Q4XMI0\_PLACH PRELIMINARY; PRT; 17 AA.  
 AC Q4XMI0; 13-SEP-2005 (TrEMBLrel. 31, Created)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
 DE Hypothetical protein (fragment).  
 GN ORFNames=PC108836.00.0;  
 OS Plasmodium chabaudi.  
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporidia; Plasmodium.  
 OX NCBI\_TaxID=5825;  
 OX NCBI\_TaxID=5825;  
 RP NUCLEOTIDE SEQUENCE.  
 RA Hall N., Karras M., Raine J.D., Carlton J.M., Kool J.T.W.A.,  
 RA Bertman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,  
 RA James K., Rutherford K., Harris B., Harris D., Churcher C.,  
 RA Quail M.A., Ormond D., Doggett J., Truman H.B., Mendoza J.,  
 RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,  
 RA Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.,  
 RT "A comprehensive survey of the Plasmodium life cycle by genomic,  
 RT transcriptomic, and proteomic analyses."  
 RL Science 307:82-86 (2005).  
 CC -1- CAUTION: The sequence shown here is derived from an  
 EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
 CC preliminary data.  
 DR EMBL, CAJ01004645; CAH81882.1; -; Genomic\_DNA.  
 KW Hypothetical protein.  
 FT NON\_TER 1  
 SQ SEQUENCE 17 AA; 2068 MW; F407DD2F398B1E09 CRC64;

Query Match 29.9%; Score 20; DB 2; Length 17;  
 Best Local Similarity 60.0%; Pred. No. 2.2e+04;  
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 NSPEC 8  
 Db 10 NNFCV 14

RESULT 85  
 Q704V9\_BOVIN PRELIMINARY; PRT; 17 AA.  
 ID Q704V9\_BOVIN PRELIMINARY; PRT; 17 AA.  
 AC Q704V9; 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Signal transducer and activator of transcription 3 (fragment).  
 GN Name=Stat3;  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;  
 OC Pecora; Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 OX NCBI\_TaxID=9913;  
 RP NUCLEOTIDE SEQUENCE.  
 RA Seyfert H.M., Wheeler T.T., Molenaar A., Pitra C.,  
 RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL, AJ220667; CAF06194.1; -; Genomic\_DNA.  
 FT NON\_TER 1  
 SQ SEQUENCE 17 AA; 1863 MW; AA9BCCEFCDC255F CRC64;

Query Match 29.9%; Score 20; DB 2; Length 17;  
 Best Local Similarity 33.3%; Pred. No. 2.2e+04;  
 Matches 4; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 DEKNSPECIAGP 12  
 Db 5 DMEITSECATSP 16

RESULT 86  
 Q712K0\_CAPI PRELIMINARY; PRT; 17 AA.  
 ID Q712K0\_CAPI PRELIMINARY; PRT; 17 AA.  
 AC Q712K0; 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Alpha s2-casein precursor (fragment).  
 GN Name=csn1s2;  
 OS Capra hircus (Goat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;  
 OC Pecora; Bovidae; Caprinae; Capra.  
 OX NCBI\_TaxID=9925;  
 OX NCBI\_TaxID=9925;  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Blood;  
 RX MEDLINE=33216130; PubMed=8462880; DOI=10.1016/0378-1119(93)90336-2;  
 RA Boudol C.;  
 RT "Sequence of the goat alpha s2-casein-encoding cDNA."  
 RL Gene 125:235-236 (1993).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Blood;  
 RX MEDLINE=21313038; PubMed=11419340;  
 RA Ramunno L., Longobardi E., Pappalardo M., Rando A., Di Gregorio P.,  
 RA Cosenza G., Mariani P., Pastore N., Marina P.;  
 RT "An allele associated with a non detectable amount of as2 casein in  
 RT goat milk."  
 RL Anim. Genet. 32:19-26 (2001).  
 DR EMBL, AJ242924; CAB44499.1; -; Genomic\_DNA.  
 DR GO: GO:0005576; Extracellular region; IEA.  
 DR GO: GO:0005215; F:transporter activity; IEA.  
 DR InterPro: IPR001588; Casein.  
 DR PROSITE: PS00306; CASIN\_ALPHA\_BETA; 1.  
 KW Signal.  
 FT SIGNAL 1 15  
 FT CHAIN 16 >17 Potential.  
 FT NON\_TER 17 alpha s2-casein.  
 SQ SEQUENCE 17 AA; 1953 MW; C76CC285A9B94551 CRC64;

Query Match 29.9%; Score 20; DB 2; Length 17;  
 Best Local Similarity 60.0%; Pred. No. 2.2e+04;  
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 PECTL 10  
 | | |  
 | | |  
 DB 6 PCTCL 10

RESULT 87  
 HSTR ECOLI STANDARD; PRT; 18 AA.  
 AC P01560;  
 DT 21-UTL-1986 (Rel. 01, Created)  
 DT 21-UTL-1986 (Rel. 01, Last sequence update)  
 DT 05-UTL-2004 (Rel. 44, Last annotation update)  
 DE Heat-stable enterotoxin ST-2 (ST-B).  
 OS Escherichia coli.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Escherichia.  
 OX NCBI\_TaxID=562;  
 [1]  
 RP PROTEIN SEQUENCE.  
 RC STRAIN=O42:K86:H37 / 18D / ETBC;  
 RX MEDLINE=81264141; PubMed=7021541;  
 RA Chan S.-K., Giamella R.A.;  
 RT "Amino acid sequence of heat-stable enterotoxin produced by  
 Escherichia coli pathogenic for man."  
 RL J. Biol. Chem. 256:7744-7746(1981).  
 RN [2]  
 RP DISULFIDE BONDS.  
 RX MEDLINE=87191003; PubMed=3552731; DOI=10.1016/0014-5793(87)80134-5;  
 RA Shimomishi Y., Hida Y., Koizumi M., Hane M., Almoto S., Takeda T.,  
 RA Miwatani T., Takeda Y.;  
 RT "Mode of disulfide bond formation of a heat-stable enterotoxin (STh)  
 produced by a human strain of enterotoxigenic Escherichia coli."  
 RL FEBS Lett. 215:165-170(1987).  
 CC -1- FUNCTION: Toxin which activates the particulate form of guanylate  
 cyclase and increases cyclic GMP levels within the host intestinal  
 epithelial cells.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- SIMILARITY: Belongs to the heat-stable enterotoxin family.  
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 the European Bioinformatics Institute. There are no restrictions on its  
 use as long as its content is in no way modified and this statement is not  
 removed.

DR PIR; A01823; QHEC2.  
 DR HSSP; P01559; 1BTN.  
 DR InterPro; IPR001489; Enterotoxin HS.  
 DR Pfam; PF02048; Enterotoxin HS; 1.  
 DR PROSITE; PS00273; ENTEROTOXIN\_H\_STABLE; 1.  
 KM Direct protein sequencing; Enterotoxin; Toxin.  
 FT DISULFID 5 10  
 FT DISULFID 6 14  
 FT DISULFID 9 17  
 SQ SEQUENCE 18 AA; 1978 MW; DDC975F49D600650 CRC64;

Query Match 29.9%; Score 20; DB 1; Length 18;  
 Best Local Similarity 60.0%; Pred. No. 2.4e+04;  
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 NSPEC 8  
 | | |  
 | | |  
 DB 1 NTFFC 5

RESULT 88  
 Q7M532 HALMA PRELIMINARY; PRT; 18 AA.

AC Q7M532;  
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Ribosomal protein HS25 (fragment).  
 OS Halobaculum marismortui (Halobacterium marismortui).  
 OC Archaea; Euryarchaeota; Halobacteria; Halobacteriales;  
 OC Halobacteriaceae; Halobaculum.  
 OX NCBI\_TaxID=2238;  
 [1]  
 RP PROTEIN SEQUENCE.  
 RA Engemann S., Herfurth E., Briesemeister U., Grell G.,  
 RA Wittmann-Liebold B.;  
 RL Submitted (NOV-1994) to the PIR data bank.  
 RN [2]  
 RP PROTEIN SEQUENCE.  
 RX MEDLINE=96096717; PubMed=8529646;  
 RA Engemann S., Noelle R., Herfurth E., Briesemeister U., Grell G.,  
 RA Wittmann-Liebold B.;  
 RT "Cartography of ribosomal proteins of the 30S subunit from the  
 halophilic Halobaculum marismortui and complete sequence analysis of  
 protein HS26."  
 RL Eur. J. Biochem. 234:24-31(1995).  
 DR PIR; S49026; S49026.  
 FT NON TER 1 1  
 FT NON TER 18 18  
 SQ SEQUENCE 18 AA; 2008 MW; F66720F002BAEDCD CRC64;

Query Match 29.9%; Score 20; DB 2; Length 18;  
 Best Local Similarity 75.0%; Pred. No. 2.4e+04;  
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 9 ILGP 12  
 | | |  
 | | |  
 DB 12 VLGP 15

RESULT 89  
 Q7S364 NEUCR PRELIMINARY; PRT; 18 AA.  
 ID Q7S364;  
 AC Q7S364;  
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Predicted protein.  
 GN Name=NC008586.1;  
 OS Neurospora crassa.  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.  
 OX NCBI\_TaxID=5141;  
 [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=OR74A;  
 RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,  
 RA Jaffe D., Fitzhugh W., Ma L.-J., Smirnov S., Purcell S., Rehm B.,  
 RA Blythe T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,  
 RA Qui D., Ianklev P., Pedersen D., Nelson M., Washburne M.,  
 RA Selitrenikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,  
 RA Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte B., Greenberg D.,  
 RA Roy A., Foley K., Naylor J., Thomann N., Barrett R., Greer S.,  
 RA Kamal M., Kamyssele M., Mauceli E., Bielke C., Rudd S., Friedman D.,  
 RA Kryzofova S., Rasmussen C., Metznerberg R.L., Perkins D.D., Kroken S.,  
 RA Cogoni C., Macino G., Catchside D., Li W., Pratt R.J., Omani S.A.,  
 RA Desouza C.C., Glaser L., Orbach M.U., Berglund U., Voelker R.,  
 RA Yarden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,  
 RA Natvig D.O., Alex L.A., Mannhaupt G., Ebdole D.J., Freitag M.,  
 RA Paulsen I., Sachs M.S., Lander E.S., Nussbaum C., Birren B.;  
 RT "The Genome Sequence of the Filamentous Fungus Neurospora crassa."  
 RL Nature 0:0-0(2003).  
 CC -1- CAUTION: The sequence shown here is derived from an  
 EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
 preliminary data.  
 CC EMBL; AABX01000413; EAA29868.1; -; Genomic\_DNA.



8Q SEQUENCE 18 AA; 2108 MW; 015DD9CC527B1B7 CRC64;

Query Match 29.9%; Score 20; DB 2; Length 18;  
Best Local Similarity 80.0%; Pred. No. 2.4e+04;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DEKNS 5  
DB 10 DPKNS 14

## RESULT 90

Q7M0U3\_CITFR PRELIMINARY; PRT; 18 AA.  
AC Q7M0U3;  
DT 01-MAR-2004 (TrEMBLrel. 26, Created)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Heat-stable enterotoxin ST-1a.  
OS Citrobacter freundii.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Citrobacter.  
OX NCBI\_TaxID=546;  
RN [1]  
RP PROTEIN SEQUENCE.  
RX MEDLINE=89108617; PubMed=2912902;  
RA Guarino A., Giannella R., Thompson M.R.;  
RT "Citrobacter freundii produces an 18-amino-acid heat-stable  
RT enterotoxin identical to the 18-amino-acid Escherichia coli heat-  
RL stable enterotoxin (ST 1a)."  
RL Infect. Immun. 57:649-652(1989).  
DR PIR; A60103; A60103.  
DR HSSP; P01559; 1ETN.  
DR CO; GO:0005576; C:extracellular region; IEA.  
DR GO; GO:0009405; P:pathogenesis; IEA.  
DR InterPro; IPR001489; Enterotoxin\_HS.  
DR Pfam; PF02048; Enterotoxin\_HS; 1.  
DR PROSITE; PS00273; ENTEROTOXIN\_H\_STABLE; 1.  
SQ SEQUENCE 18 AA; 1978 MW; D4D975F49D60064F CRC64;

Query Match 29.9%; Score 20; DB 2; Length 18;  
Best Local Similarity 60.0%; Pred. No. 2.4e+04;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 NSPEC 8  
DB 1 NTPYC 5

## RESULT 91

Q7M076\_RAT PRELIMINARY; PRT; 18 AA.  
AC Q7M076;  
DT 01-MAR-2004 (TrEMBLrel. 26, Created)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Enkephalin-degrading aminopeptidase (EC 3.4.-.-), puromycin-sensitive  
DE (fragment).  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP PROTEIN SEQUENCE.  
RX MEDLINE=90132681; PubMed=2299352;  
RA Dyer S.H., Slaughter C.A., Orth K., Moomaw C.R., Heresh L.B.;  
RT "Comparison of the soluble and membrane-bound forms of the puromycin-  
RT sensitive enkephalin-degrading aminopeptidases from rat."  
RL J. Neurochem. 54:547-554(1990).  
DR PIR; A60915; A60915.  
FT NON\_TER 1 1  
FT NON\_TER 16 16

8Q SEQUENCE 18 AA; 2172 MW; 100BA0863239CC3 CRC64;

Query Match 29.9%; Score 20; DB 2; Length 18;  
Best Local Similarity 66.7%; Pred. No. 2.4e+04;  
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 EKNSFE 7  
DB 2 EKRPFE 7

## RESULT 92

DURA\_STRGV STANDARD; PRT; 19 AA.  
AC P36504;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 13-SEP-2005 (Rel. 48, Last annotation update)  
DE Lantibiotic duramycin (Leucopentin) (Antibiotic PA48009).  
OS Streptococcus thermophilus griseovercillium.  
OC Bacteria; Actinobacteria; Actinobacteriales; Actinomycetales;  
OC Streptococcaceae; Streptococcaceae; Streptomyces.  
OX NCBI\_TaxID=68215;  
RN [1]  
RP PROTEIN SEQUENCE, AND STRUCTURE BY NMR.  
RC STRAIP=PA-48009;  
RX MEDLINE=9107438; PubMed=2272918;  
RA Hayaishi F., Nagashima K., Terui Y., Kawamura Y., Matsumoto K.,  
RA Itazaki H.;  
RT "The structure of PA48009, the revised structure of duramycin."  
RL J. Antibiot. 43:1421-1430(1990).  
RN [2]

PROTEIN SEQUENCE.  
RX MEDLINE=9107436; PubMed=2125590;  
RA Fiedenhagen A., Fendrich G., Marki F., Marki W., Gruner J.,  
RA Raschdorf F., Peter H.H.;  
RT "Duramycin B and C, two new lantibiotics containing antibiotics as  
RT inhibitors of phospholipase A2. Structural revision of duramycin and  
RT cinnamycin."  
RL J. Antibiot. 43:1403-1412(1990).  
CC -1- FUNCTION: Acts as inhibitor of phospholipase A2.  
CC -1- PFM: Maturation of lantibiotics involves the enzymic conversion of  
CC Thr, and Ser into dehydrated AA and the formation of thioether  
CC bonds with cysteine and the formation of dialkylamine bonds with  
CC lysine. This is followed by membrane translocation and cleavage of  
CC the modified precursor.  
CC -1- SIMILARITY: Belongs to the type B lantibiotic family.

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CC the European Bioinformatics Institute. There are no restrictions on its  
CC use as long as its content is in no way modified and this statement is not  
CC removed.

CC Antitibiotic; Antimicrobial; Bacteriocin; Direct protein sequencing;  
KW Lantibiotic; Thioether bond.  
FT CROSSLINK 1 18 Beta-methylanthionine (Cys-Thr).  
FT CROSSLINK 4 14 Lanthionine (Ser-Cys).  
FT CROSSLINK 5 11 Beta-methylanthionine (Cys-Thr).  
FT CROSSLINK 6 19 Lysinoalanine (Ser-Lys).  
SQ SEQUENCE 19 AA; 2069 MW; 012951AE27362F00 CRC64;

Query Match 29.9%; Score 20; DB 1; Length 19;  
Best Local Similarity 60.0%; Pred. No. 2.5e+04;  
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 CILGP 12  
DB 5 CSFGP 9

## RESULT 93

DURB\_STRGW

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ID DURB_STRGM STANDARD; PRT; 19 AA.
AC P36502;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Lanthibiotic duramycin B.
OS Streptococcicillium sp. (strain R2075).
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomycetes.
OK NCBI_TaxID=35759;
RN (1)
RP PROTEIN SEQUENCE.
RX MEDLINE=91107436; PubMed=2125590;
RA Fredenhagen A., Fendrich G., Markl F., Markl W., Gruner J.,
RA Raschdorf F., Peter H.H., Jung G.,
RT "Duramycin B and C, two new lanthionine containing antibiotics as
RT inhibitors of phospholipase A2. Structural revision of duramycin and
RT cinamycin.",
RL J. Antibiot. 43:1403-1412(1990).
RN (2)
RP STRUCTURE BY NMR.
RA Zimmermann N., Freund S., Fredenhagen A., Jung G.,
RT "Solution structure of the lanthibiotics duramycin B and C.",
RL (in) Schneider C.H., Eberle A.N. (eds.),
RL Peptides 1992, pp.519-520, Bescm Science Publishers, Leiden (1993).
RN (3)
RP STRUCTURE BY NMR.
RX MEDLINE=93387292; PubMed=8375380;
RA Zimmermann N., Freund S., Fredenhagen A., Jung G.,
RT "Solution structures of the lanthibiotics duramycin B and C.",
RL Bur. J. Biochem. 216:419-428(1993).
CC -1- FUNCTION: Acts as inhibitor of phospholipase A2.
CC -1- FUNCTION: Acts as inhibitor of phospholipase A2.
CC Thr. and Ser into dehydrated AA and the formation of thioether
CC bonds with cysteine or the formation of dialkylamine bonds with
CC lysine. This is followed by membrane translocation and cleavage of
CC the modified precursor.
CC -1- SIMILARITY: Belongs to the type B lanthibiotic family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
KW Antibiotic; Antimicrobial; Bacteriocin; Direct protein sequencing;
KM Lanthibiotic; Thioether bond.
FT CROSSLINK 1 18 Beta-methylanthionine (Cys-Thr).
FT CROSSLINK 4 14 Lanthionine (Ser-Cys).
FT CROSSLINK 5 11 Beta-methylanthionine (Cys-Thr).
FT CROSSLINK 6 19 Lysinoalanine (Ser-Lys).
SQ SEQUENCE 19 AA; 2063 MW; 0133445B27362F00 CRC64;

Query Match 29.9%; Score 20; DB 1; Length 19;
Best Local Similarity 60.0%; Pred. No. 2.5e+04;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 CILGP 12
DB 5 CSFGP 9

```

```

OK NCBI_TaxID=72591;
RN (1)
RP PROTEIN SEQUENCE.
RA Wakamiya T., Ueki Y., Shiba T., Kido Y., Moroki Y.,
RT "The structure of ancoventin, a new peptide inhibitor of angiotensin I
RT converting enzyme.",
RL Tetrahedron Lett. 26:665-668(1985).
CC -1- FUNCTION: Acts as an inhibitor of angiotensin I converting enzyme.
CC -1- FUNCTION: Acts as an inhibitor of angiotensin I converting enzyme.
CC Thr. and Ser into dehydrated AA and the formation of thioether
CC bonds with cysteine or the formation of dialkylamine bonds with
CC lysine. This is followed by membrane translocation and cleavage of
CC the modified precursor.
CC -1- SIMILARITY: Belongs to the type B lanthibiotic family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
KW PIR; A61284; EWSMAN.
KM Antibiotic; Antimicrobial; Bacteriocin; Direct protein sequencing;
KM Lanthibiotic; Thioether bond.
FT CROSSLINK 1 18 Beta-methylanthionine (Cys-Thr).
FT CROSSLINK 4 14 Lanthionine (Ser-Cys).
FT CROSSLINK 5 11 Beta-methylanthionine (Cys-Thr).
FT CROSSLINK 6 19 Lysinoalanine (Ser-Lys).
SQ SEQUENCE 19 AA; 2033 MW; F434299E2736286A CRC64;

Query Match 29.9%; Score 20; DB 1; Length 19;
Best Local Similarity 60.0%; Pred. No. 2.5e+04;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 CILGP 12
DB 5 CSFGP 9

RESULT 95
Q9TWS8_9TRYP PRELIMINARY; PRT; 19 AA.
AC Q9TWS8;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE Hapoglobin-related protein beta subunit (Fragment).
OS Trypanosoma brucei.
OC Eukaryota; Euzlenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OK NCBI_TaxID=5691;
RN (1)
RP PROTEIN SEQUENCE.
RX MEDLINE=95232503; PubMed=7716520;
RA Smith A.B., Bako J.D., Hajduk S.L.,
RT "Killing of trypanosomes by the human hapoglobin-related protein.",
RL Science 268:284-286(1995).
SQ SEQUENCE 19 AA; 2055 MW; 65BD135667C94056 CRC64;

Query Match 29.9%; Score 20; DB 2; Length 19;
Best Local Similarity 66.7%; Pred. No. 2.5e+04;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 DEKNSP 6
DB 7 DAKGSP 12

```

```

RESULT 96
Q4XA82_PLACH PRELIMINARY; PRT; 19 AA.
AC Q4XA82;
DT 13-SEP-2005 (TREMBLrel. 31, Created)
DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)

```

DE 13-SEP-2005 (TrEMBLrel. 31, last annotation update)  
DT Hypothetical protein (Fragment).  
GN ORFNames=PC401441.00.0,  
OS Plasmodium chabaudi.  
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
OX NCBI\_TaxID=5825;  
RN (1)  
RP NUCLEOTIDE SEQUENCE.  
RA Hall N., Karras M., Raine J.D., Carlton J.M., Kool J.T.W.A.,  
RA Berriman M., Plorens L., Janssen C.S., Pain A., Christophides G.K.,  
RA James K., Rutherford K., Harris B., Harris D., Churcher C.,  
RA Quail M.A., Omond D., Doggett J., Trueman H.E., Mendoza C.,  
RA Bitwell S.J., Randleham M.A., Carucci D.J., Yates J.R., Kafatos F.C.,  
RA Jansse C.L., Barrall B., Turner C.M.R., Waters A.P., Sinden R.S.;  
RT "A comprehensive survey of the Plasmodium life cycle by genomic,  
RT transcriptomic, and proteomic analyses."  
RL Science 307:83-86(2005).  
CC -!- CAUTION: The sequence shown here is derived from an  
CC EMBL/GenBank/DBD whole genome shotgun (WGS) entry which is  
CC preliminary data.  
CC EMBL; CA070100094; CAH88371.1; -; Genomic\_DNA.  
KW Hypothetical protein.  
FT NON TER 1  
SQ SEQUENCE 19 AA; 2254 MW; 3C19399D8033FC753 CRC64;

Query Match	29.9%	Score 20	DB 2	Length 19
Best Local Similarity	42.9%	Pred. NO. 2.5e+04		
Matches	3	Conservative	2	Mismatches 2
				Indels 0
				Gaps 0
Q7	3	KNSPECT 9		
	:	:		
Db	13	KNNITCL 19		

```

RESULT 97
Q04904_PLABE
ID Q04904_PLABE PRELIMINARY; PRT; 19 AA.
AC Q04904;
DT 13-SEP-2005 (TRENBLUREL. 31, Created)
DT 13-SEP-2005 (TRENBLUREL. 31, Last sequence update)
DT 13-SEP-2005 (TRENBLUREL. 31, Last annotation update)
DE Hypothetical protein (Fragment).
GN ORFNames=PB403980.00.0;
OS Plasmodium berghei.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5621;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Hall N., Karras M., Raine J.D., Carlton J.W., Kool J.T.W.A.,
RA Bertram M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Chritchey C.,
RA Quail M.A., Ormond D., Doggett J., Trueman H.B., Mendoza J.,
RA Bidwell S.L., Rajadream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
RA Jansse C.J., Barrett B., Turner C.M.R., Waters A.P., Sinden R.S.;
RT "A comprehensive survey of the plasmodium life cycle by genomic,
RT transcriptomic, and proteomic analyses.";
RL Sequence 307:82-86(2005).

```

CC	-	CAUTION:	The sequence shown here is derived from an EMBL/Genbank/DBJ whole genome shotgun (WGS) entry which is preliminary data.
CC	EMBL:	CAI01007305:	CA105554.1; - / Genomic_DNA.
DR	EMBL:	CAI01007305:	CA105554.1; - / Genomic_DNA.
KM	Hypothetical protein.	1	
PT	NON TER	1	
SQ	SEQUENCE	19 AA;	2106 MW; P29GCEABED8DC461A CRC64;

Query Match	29.9%	Score 20	DB 2	Length 19
Best Local Similarity	75.0%	Pred. No. 2.5e+04		
Matches	3	Conservative	1	Mismatches 0, Gaps 0
Qy	8 CILG 11			
db	1 CMLG 4			

RESULT 98	09GI97_9PHAE	PRELIMINARY;	PRT;	19 AA.
ID	09GI97_9PHAE	PRELIMINARY;	PRT;	19 AA.
AC	09GI97;			
DT	01-MAR-2001 (TrEMBLrel. 16, Created)			
DT	01-MAR-2001 (TrEMBLrel. 16, Last sequence update)			
DT	01-JUN-2003 (TrEMBLrel. 24, Last annotation update)			
DE	Ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (Fragment).			
GN	Name=ZbcL;			
OS	Sargassum polycystum.			
OG	Chloroplast.			
OC	Eukaryote; stramenopiles; Phaeophyceae; Fucales; Sargassaceae;			
CC	Sargassum.			
OX	NCBI_TaxID=127578;			
RN	[1]			
RP	NCLEOTIDE SEQUENCE.			
RC	STRAIN=nepl27;			
RA	Phillips N.E.;			
RT	"Molecular phylogenetic analysis of the pan-pacific genus Sargassum (Fucales, Phaeophyceae).";			
RL	Theste (1998), University of Hawaii.			
RN	[2]			
RP	NCLEOTIDE SEQUENCE.			
RC	STRAIN=nepl27;			
RA	Phillips N.E., Smith C.M., Morden C.W.;			
RL	Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AF244344; AAF98113.1; -; Genomic_DNA.			
GO	GO:0009507; Chloroplast; IEA.			
KW	Chloroplast.			
FT	NON TER			
SEQUENCE	19 AA; 2108 MW; A02FD2B6DD68A57 CRC64;			

Query Match	29.9%	Score 20;	DB 2;	Length 19;
Best Local Similarity	100.0%	Pred. No. 2.5e+04;		
Matches	3;	Conservative	0;	Mismatches 0;
				Indels 0;
Gaps				
Qy	6	FEC	8	
Db	1	FEC	3	

RESULT 99	0570L9_ARATH	PRT;	19 AA.
ID	Q570L9_ARATH PRELIMINARY;		
AC	Q570L9;		
DT	10-MAY-2005 (TrEMBLrel. 30, Created)		
DT	10-MAY-2005 (TrEMBLrel. 30, Last sequence update)		
DT	10-MAY-2005 (TrEMBLrel. 30, Last annotation update)		
DE	Hypothetical protein (Fragment).		
OS	Arabidopsis thaliana (Mouse-ear cress).		
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;		
OC	eurosid II; Brassicales; Brassicaceae; Arabidopsids.		
OX	NCBI_TaxId=3702;		
RN	[1]		
RP	NUCLEOTIDE SEQUENCE.		
RA	Totoaki Y., Seki M., Ishida J., Nakajima M., Enju A., Kamiya A.,		
RA	Narusaka M., Shin-I T., Nakagawa M., Sakamoto N., Oishi K., Kohara Y.,		
RA	Kobayashi M., Toyoda A., Sakaki Y., Sakurai T., Iida K., Akiyama K.,		
RA	Saitou M., Toyoda T., Konagaya A., Carninci P., Kawai J.,		
RA	Hayashizaki Y., Shinozaki K.;		
RT	"Large-scale analysis of RIKEN Arabidopsis full-length (RAFL) cDNAs."		
RL	Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; ACZ20689; BAD95761.1; -, mRNA.		
FW	Hypothetical protein.		

PT	NON	TER	1	1	
SEQ	SEQUENCE	19	AA; 2146	NW; 5DC5F79C9FPA6C37	CRC64;
Query Match		29.94;	Score 2;	DB 2;	Length 19;
Best Local Similarity		60.08;	Pred. No. 2.5e+04;		
Matches	3;	Conservative	1;	Mismatches	1;
				Indels	0;
				Gaps	0;

QY 5 SPECI 9  
: |||  
Db 3 TPSCI 7

RESULT 100  
016129 HUMAN  
ID 016129 HUMAN PRELIMINARY; PRT; 20 AA.  
AC 016129  
DT 01-NOV-1996 (TRMBLrel. 01, Created)  
DT 01-NOV-1996 (TRMBLrel. 01, last sequence update)  
DT 01-NOV-1998 (TRMBLrel. 08, last annotation update)  
DE Protein tyrosine phosphatase (Fragment).  
GN Name=PTPGL;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=94156037; PubMed=7509295; DOI=10.1016/0014-5793(94)80420-6;  
RA Takekawa M., Itoh F., Hinoda Y., Adachi M., Ariyama T., Inazawa J.,  
RA Imai K., Yachi A.;  
RT "Chromosomal localization of the protein tyrosine phosphatase G1 gene  
RT and characterization of the aberrant transcripts in human colon cancer  
RT cells."  
RL FEBS Lett. 339:222-228(1994).  
DR EMBL, S69183; AAB30046.1; -; mRNA.  
FT NON TER 20 20  
SQ SEQUENCE 20 AA; 2428 MW; 473AB954F158A78B CRC64;  
Query Match 29.9%; Score 20; DB 2; Length 20;  
Best Local Similarity 44.4%; Pred. No. 2.6e+04;  
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
QY 2 EKNSPECTL 10  
: |||  
Db 2 KKNRYKDL 10

Search completed: January 20, 2006, 19:11:10  
Job time : 41.9231 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 20, 2006, 18:54:14 ; Search time 68.0192 Seconds  
(without alignments)  
116.273 Million cell updates/sec

Title: US-09-662-293-6

Perfect score: 96

Sequence: 1 DABPHGYLLTAASPCK 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 243163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 880474

Minimum DB seq length: 0  
Maximum DB seq length: 20

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 100 summaries

Database : A\_Geneseq\_21:\*

1: geneseqp19808:\*

2: geneseqp19808:\*

3: geneseqp20008:\*

4: geneseqp20018:\*

5: geneseqp20028:\*

6: geneseqp20038:\*

7: geneseqp20038:\*

8: geneseqp20048:\*

9: geneseqp20058:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	96	100.0	18	3	AAV52515
2	96	100.0	18	3	AAU96319
3	38	39.6	10	2	AAV47095
4	35.5	37.0	19	9	ADM43819
5	34	35.4	15	5	ABJ14737
6	34	35.4	15	5	ABJ14493
7	34	35.4	15	5	ABJ14856
8	34	35.4	15	5	ABJ14620
9	34	35.4	15	5	ABJ14316
10	34	35.4	15	5	ABJ14777
11	34	35.4	15	8	ADL21730
12	34	35.4	15	8	ADL22014
13	34	35.4	15	8	ADL21857
14	34	35.4	15	8	ADL21553
15	34	35.4	15	8	ADL21974
16	34	35.4	15	8	ADL22093
17	34	35.4	15	8	ADL22093
18	34	35.4	15	8	ADL22093
19	34	35.4	15	8	ADL22093
20	34	35.4	15	8	ADL22093
21	34	35.4	15	8	ADL22093
22	34	35.4	15	8	ADL22093
23	34	35.4	15	8	ADL22093
24	34	35.4	15	8	ADL22093

25	33	34.4	17	5	ABG67141	ADG67141 HCV pepti
26	33	34.4	18	2	AAW45412	AAW45412 N-termina
27	32	33.3	12	5	AAE26395	AAE26395 Human GPR
28	32	33.3	16	2	AAW45125	AAW45125 Human car
29	31	32.3	9	5	AAU74686	AAU74686 Human can
30	31	32.3	9	7	ABR82211	ABR82211 Human can
31	31	32.3	15	2	AAV13274	AAV13274 Naturally
32	31	32.3	18	7	ADR40482	ADR40482 KDR & VEG
33	31	32.3	18	8	ADR40700	ADR40700 Cyclic KD
34	31	32.3	20	5	ADK57606	ADK57606 HLA-DR as
35	31	32.3	18	5	AAU73345	AAU73345 Human pro
36	31	32.3	20	9	ADZ25579	ADZ25579 Pig 3-ali
37	31	32.3	20	9	ADZ68008	ADZ68008 Peptide f
38	30	31.2	11	4	AAE26657	AAE26657 Beta-ahoe
39	30	31.2	11	6	ABU79065	ABU79065 Amyloid f
40	30	31.2	11	6	ABW00199	ABW00199 Control p
41	30	31.2	12	5	AAE26397	AAE26397 Human GPR
42	30	31.2	14	8	ADU04328	ADU04328 Human imm
43	30	31.2	19	2	AAE04059	AAE04059 Reagent o
44	30	31.2	20	2	AAV29388	AAV29388 Rinal 3D
45	30	31.2	20	8	ADU04264	ADU04264 Human imm
46	29	30.2	6	8	ADK37698	ADK37698 Binding p
47	29	30.2	6	8	ADK28220	ADK28220 Capture s
48	29	30.2	6	8	ADR50397	ADR50397 6-mer pep
49	29	30.2	6	8	ADR56043	ADR56043 Tagged po
50	29	30.2	6	9	ADZ46403	ADZ46403 Antigenic
51	29	30.2	11	5	AEK30513	AEK30513 Therapeut
52	29	30.2	11	5	AAE80180	AAE80180 HER-2 mim
53	29	30.2	11	8	ADJ67980	ADJ67980 T. thermo
54	29	30.2	11	8	ADJ68192	ADJ68192 T. thermo
55	29	30.2	11	8	ADK01270	ADK01270 DNA polym
56	29	30.2	11	8	ADU79489	ADU79489 T. thermo
57	29	30.2	11	8	ADU78492	ADU78492 Bacterial
58	29	30.2	11	8	ADM77717	ADM77717 DNA polym
59	29	30.2	11	8	ADM66384	ADM66384 T. thermo
60	29	30.2	11	8	ADP82514	ADP82514 Conserved
61	29	30.2	11	8	ADP82514	ADP82514 DNA polym
62	29	30.2	11	8	ADJ15721	ADJ15721 Peptide f
63	29	30.2	11	9	ADY55212	ADY55212 T. thermo
64	29	30.2	11	9	ADZ76788	ADZ76788 T. thermo
65	29	30.2	11	9	AEK424796	AEK424796 Thermus t
66	29	30.2	11	9	AEK424796	AEK424796 Thermus t
67	29	30.2	11	9	AEK51623	AEK51623 DNA polym
68	29	30.2	12	5	AAE26390	AAE26390 Human will
69	29	30.2	12	5	AAE26398	AAE26398 Human GPR
70	29	30.2	13	7	ADM35713	ADM35713 HLA bindi
71	29	30.2	13	7	ADM34480	ADM34480 HLA bindi
72	29	30.2	13	7	ADM34479	ADM34479 HLA bindi
73	29	30.2	13	7	ADM34479	ADM34479 HLA bindi
74	29	30.2	13	8	ADN30473	ADN30473 Kinase pe
75	29	30.2	15	2	AAV13276	AAV13276 Naturally
76	29	30.2	15	5	ABJ14633	ABJ14633 Human 125
77	29	30.2	15	5	ABJ14367	ABJ14367 Human 125
78	29	30.2	15	5	ABJ14669	ABJ14669 Human 125
79	29	30.2	15	8	ADJ38549	ADJ38549 HSV-2 maj
80	29	30.2	15	8	ADJ38547	ADJ38547 HSV-2 maj
81	29	30.2	15	8	ADL21906	ADL21906 125P5C8 p
82	29	30.2	15	8	ADL21870	ADL21870 125P5C8 p
83	29	30.2	15	8	ADL21604	ADL21604 125P5C8 p
84	29	30.2	17	4	ABH14772	ABH14772 Human net
85	29	30.2	17	4	ABH11968	ABH11968 Salmonell
86	29	30.2	17	9	ABH11815	ABH11815 Salmonell
87	29	30.2	17	9	AEK52660	AEK52660 Peptide f
88	29	30.2	17	9	AEK53031	AEK53031 Salmonell
89	29	30.2	18	6	ABU09114	ABU09114 C. elegans
90	29	30.2	19	7	ADH37053	ADH37053 Nylon sut
91	29	30.2	20	2	AAW21835	AAW21835 KMTL-cont
92	29	30.2	16	6	ADK83646	ADK83646 Rat insul
93	28	29.2	6	8	ADK37172	ADK37172 Binding p
94	28	29.2	6	8	ADK37180	ADK37180 Binding p
95	28	29.2	6	8	ADK37694	ADK37694 Capture s
96	28	29.2	6	8	ADK37702	ADK37702 Capture s
97	28	29.2	6	8	ADR49879	ADR49879 6-mer pep

98	28	29.2	6	8	ADR49871	6-mer pep
99	28	29.2	6	8	ADS95517	Tagged po
100	28	29.2	6	8	ADS95525	Tagged po

## ALIGNMENTS

## RESULT 1

ID AAY52515 standard; peptide, 18 AA.

XX AAY52515/

DT 22-FEB-2000 (first entry)

XX House dust mite allergen protein (map) A/B fragment map(5).

DE Mite allergen protein; map; high molecular weight; HMW-map; allergy;

KM house dust mite; IGE; immunoglobulin E; allergen; mapA; mapB;

KM hypersensitivity reaction; therapy; treatment; diagnosis; human; feline;

XX canine; veterinary; antibody; vaccine; immunisation.

OS Dermatophagoides farinae.

XX WO954349-A2.

XX 28-OCT-1999.

PF 16-APR-1999; 99WO-US008524.

PR 17-APR-1998; 98US-00062013.

PR 13-MAY-1998; 98US-0085295P.

PR 02-SEP-1998; 98US-0098909P.

XX (HESK-) HESKA CORP.

XX Mccall CA, Hunter SW, Weber ER;

XX WPI; 2000-052700/04.

XX Novel high molecular weight Dermatophagoides nucleic acid polypeptides

XX used to modify an animal's hypersensitivity to mite allergens.

XX Claim 3; Page 69; 154pp; English.

XX Sequences AAY5510-Y53522 represent proteolytic fragments of

XX Dermatophagoides farinae high molecular weight mite allergen protein (HMW

XX -map) composition. The HMW-map composition was isolated from a D. farinae

XX homogenate by gel filtration, with each fraction being analysed for the

XX presence of proteins that bound to IGB present in mite-allergic dog

XX antiserum. The HMW-map composition comprises mapA (a 109 kD protein) and

XX mapB (98 kD). Mite allergenic proteins and peptides, and nucleic acids

XX encoding them, may be used in therapeutic compositions to modify an

XX animal's hypersensitivity reaction to mite allergens. Animals that may be

XX created include mammals and birds, especially felines, canines, equines,

XX humans, other pets, and work or domestic animals. The proteins or

XX fragments may also be used to diagnose allergies via a skin test. The

XX proteins and peptides can also be used to raise antibodies, which have a

XX variety of potential uses. For example, they can be used as vaccines to

XX passively immunise animals against dust mite hypersensitivity, as

XX positive controls in test kits and as tools to recover desired dust mite

XX allergens from a mixture of proteins

XX Sequence 18 AA;

SQ

Query Match 100.0%; Score 96; DB 3; Length 18;

Best Local Similarity 100.0%; Pred. No. 1.6e-09;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAFEPHGYLLTAAVSPGK 18

DB 1 DAFEPHGYLLTAAVSPGK 18

RESULT 2

ID AAU96319 standard; peptide, 18 AA.

XX AAU96319/

DT 15-JUL-2002 (first entry)

XX Der HMW-map polypeptide #6.

KM Der HMW-map; American house dust mite; anti-allergic; mite; IGE;

KM mite allergenic protein; immunoglobulin E; hypersensitivity;

XX immunocomplex formation.

XX Dermatophagoides farinae.

XX WO200222807-A2.

XX 21-MAR-2002.

PF 14-SEP-2001; 2001WO-US028730.

PR 14-SEP-2000; 2000US-00662293.

XX (HESK-) HESKA CORP.

XX Mccall CA, Hunter SW, Weber ER;

XX WPI; 2002-351888/38.

XX New mite allergenic protein isolated from Dermatophagoides, designated

XX Der HMW-map protein, useful as a vaccine for treating mite allergy.

XX Claim 12; Page 70; 161pp; English.

XX The invention relates to an isolated mite allergenic protein of

XX Dermatophagoides, designated Der HMW-map protein, and its related nucleic

XX acid. The Der HMW-map protein is useful for eliciting an immune response

XX against Der HMW-map protein. The protein or a reagent comprising a non-

XX proteinaceous epitope is useful for identifying an animal (e.g., dog,

XX cat) susceptible to or having an allergic response to a mite. A

XX therapeutic composition is useful for desensitising a host animal to an

XX allergic response to a mite. The DNA and protein can be used in the

XX detection of anti-Der HMW-map antibodies in animal fluids, and inhibition

XX of immunoglobulin (Ig)E or Der HMW-map protein activity associated with a

XX disease. Antibodies that bind to Der HMW-map are useful for inhibiting

XX binding of proteins to IGB, to prevent immunocomplex formation, thus

XX reducing hypersensitivity responses to mite allergens, and as vaccines

XX against mite allergen hypersensitivity. Sequences AAU96314-AAU96342

XX represent Der HMW-map polypeptides of the invention

XX Sequence 18 AA;

SQ

Query Match 100.0%; Score 96; DB 5; Length 18;

Best Local Similarity 100.0%; Pred. No. 1.6e-09;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAFEPHGYLLTAAVSPGK 18

DB 1 DAFEPHGYLLTAAVSPGK 18

RESULT 3

ID AAAY47095 standard; peptide, 10 AA.

XX AAAY47095/

AC AAAY47095;

DT 01-DEC-1999 (first entry)

XX Immunogenic peptide having a human leukocyte antigen binding motif #1706.

XX Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA;  
 KW immune response; T cell activation; major histocompatibility complex;  
 KW cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer;  
 KW prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;  
 KW vaccine; immunisation.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 XX  
 PN MO9945954-A1.  
 PD 16-SEP-1999.  
 XX  
 PF 13-MAR-1998; 98WO-US005039.  
 XX  
 PR 13-MAR-1998; 98WO-US005039.  
 XX  
 PA (EPIM-) EPIMMUNE INC.  
 PI Sette A, Kubo RT, Sidney J, Cella E, Grey HM, Southwood S;  
 DR WPI; 1999-551214/46.  
 XX  
 PT New immunogenic peptides with HLA binding motif, useful in treatment and  
 PT diagnosis of cancers and viral diseases.  
 XX  
 PS Claim 1, Page 93; 150pp; English.  
 XX  
 CC AA45390 to AA48224 represent specifically claimed immunogenic peptides  
 CC having a human major histocompatibility complex (MHC) Class I (also known  
 CC as human leukocyte antigen (HLA)) binding motif. The immunogenic peptides  
 CC can bind to a specific HLA allele (i.e. HLA-A subtypes HLA-A2.1, A1, A3.2  
 CC or A24.1 or HLA-B or C) and induce a cytotoxic T cell response against  
 CC the antigen from which the peptide is derived. Cytotoxic T lymphocytes  
 CC (CTLs) which destroy antigen-bearing cells are normally induced by an  
 CC antigen in the form of a peptide fragment bound to a HLA molecule, rather  
 CC than the intact foreign antigen itself, and are particularly important in  
 CC tumour rejection and in fighting viral infections. The peptides are  
 CC therefore useful therapeutically to treat or prevent viral infections and  
 CC cancers in mammals (especially humans) e.g. prostate cancer, hepatitis B  
 CC and C, AIDS, and renal carcinoma. They can be administered as vaccines to  
 CC elicit an immune response in individuals susceptible or otherwise at risk  
 CC of viral infection or cancer, or used to treat chronic or acute  
 CC conditions. They are also useful diagnostically, and can be used to  
 CC induce a cytotoxic T cell response, by contacting a cytotoxic T cell with  
 CC the peptide e.g. to produce CTLs ex vivo for infusion back into a  
 CC patient. The polynucleotides encoding the immunogenic peptides are also  
 CC useful therapeutically and for immunisation as above  
 XX  
 SQ Sequence 10 AA;  
 Query Match 39.6%; Score 38; DB 2; Length 10;  
 Best Local Similarity 75.0%; Pred. No. 12;  
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 DAREPGCY 8  
 Db 3 DGEFNGY 10  
 RESULT 4  
 ADW43819  
 ID ADW43819 standard; peptide; 19 AA.  
 AC  
 XX  
 AC ADW43819;  
 XX  
 DT 24-MAR-2005 (first entry)  
 XX  
 DE Mouse chemerin peptide SEQ ID NO 43.  
 XX  
 KW gene therapy; diagnosis; cell signaling; gene therapy;  
 KW lymphoproliferative disease; dermatological disease; dermatological;

KW demostatic; inflammation; antiinflammatory; hematological disease;  
 KW immune disorder; neoplasm; cardiovascular-gen.; can-gen.;  
 KW neurological disease; hyperproliferative disorders; cytostatic; chemerin.  
 XX  
 OS Mus musculus.  
 XX  
 PN MO200500875-A2.  
 PD 06-JAN-2005.  
 XX  
 PF 25-JUN-2004; 2004WO-EP006945.  
 XX  
 PR 25-JUN-2003; 2003US-00603566.  
 XX  
 PA (EURO-) EUROSCREEN SA.  
 PI Wltamer V, Communi D, Dethaux M, Parmentier M, Lohson C;  
 PI Ooms FDR;  
 XX  
 DR WPI; 2005-058121/06.  
 XX  
 PT New Chemerin polypeptides, useful for diagnosing and treating a disease,  
 PT e.g. neoplasms, hypergammaglobulinemia, paraproteinemia, purpura,  
 PT sarcoidosis, Sezary Syndrome, Waldenstrom's Macroglobulinemia, Gaucher's  
 PT Disease, or histiocytosis.  
 XX  
 PS Example 2; SEQ ID NO 43; 183pp; English.  
 XX  
 CC The invention describes a polypeptide (I) of up to 50 amino acids where  
 CC the polypeptide binds specifically to a chemerin polypeptide. Also  
 CC described are: a nucleic acid sequence encoding (I); an expression vector  
 CC comprising the coding sequence of the nucleic acid; a transgenic animal  
 CC transduced with the expression vector; a (therapeutic) composition  
 CC comprising (I) and an isolated Chemerin polypeptide or a nucleic acid  
 CC sequence of (I); an antibody that selectively binds to (I); identifying  
 CC an agent that modulates the interaction between a Chemerin polypeptide  
 CC and a Chemerin polypeptide; detecting the presence, in a sample, of an  
 CC agent that modulates the interaction between a Chemerin polypeptide and a  
 CC Chemerin polypeptide in a sample; identifying an agent that modulates  
 CC the function of Chemerin polypeptide; detecting the presence, in a  
 CC sample, of an agent that modulates the function of Chemerin polypeptide;  
 CC diagnosing a disease or disorder characterized by dysregulation of  
 CC Chemerin (polypeptide) signaling; a kit, for screening agents that  
 CC modulate the signaling activity of Chemerin polypeptide or for  
 CC diagnosing a disease or disorder characterized by dysregulation of  
 CC Chemerin polypeptide signaling, comprising an isolated Chemerin  
 CC polypeptide, (I), an isolated polynucleotide encoding (I), a cell  
 CC transformed with a polynucleotide encoding (I), and its packaging  
 CC materials; a non-human mammal transgenic for a Chemerin polynucleotide  
 CC encoding (I); identifying an antibody inhibiting Chemerin activation;  
 CC and an in vitro method of inhibiting cell proliferation. The  
 CC (therapeutic) composition or expression vector is useful for preparing a  
 CC medicament for ex vivo gene therapy or for in vivo gene therapy or a  
 CC medicament for inhibiting cell proliferation, where the medicament is  
 CC used for treating a disease, e.g. neoplasms, hypergammaglobulinemia,  
 CC lymphoproliferative diseases, disorders, and/or conditions,  
 CC paraproteinemias, purpura, sarcoidosis, Sezary Syndrome, Waldenstrom's  
 CC Macroglobulinemia, Gaucher's Disease, histiocytosis, and any other  
 CC hyperproliferative disease. The polypeptides and polynucleotides and  
 CC methods are useful for diagnosing and treating the cited diseases. This  
 CC is the amino acid sequence of a mouse chemerin peptide used to analyse  
 CC processing of immature chemerin.  
 XX  
 SQ Sequence 19 AA;  
 Query Match 37.0%; Score 35.5; DB 9; Length 19;  
 Best Local Similarity 46.7%; Pred. No. 69;  
 Matches 7; Conservative 2; Mismatches 1; Indels 5; Gaps 1;  
 QY 4 EPHGYLTAAVSPGK 18  
 Db 6 DPHGYLT-----PGQ 15

```
RESULT 5
ABJ14737
ID ABJ14737 standard; peptide; 15 AA.
XX
AC ABJ14737;
XX
DT 10-DEC-2002 (first entry)
XX
DE Human 125P5C8 epitope #3363.
XX
KW Human; 125P5C8; cancer; cytostatic; breast cancer; prostate cancer;
XX bladder cancer; kidney cancer; colon cancer; ovarian cancer; epitope.
XX
OS Homo sapiens.
XX
PN WO200272785-A2.
XX
PD 19-SEP-2002.
XX
PF 13-MAR-2002; 2002WO-US007855.
XX
PR 14-MAR-2001; 2001US-00809638.
XX
PA (AGEN-) AGENSYS INC.
XX
PI Faris M, Challita-Bid PM, Hubert RS, Afar DEH, Raitano AB, Ge W;
XX Morrison RK, Morrison K, Jakobovits A;
XX
DR WPI; 2002-713510/77.
XX
PT New composition comprising a substance that modulates the status of
PT 125P5C8 gene or a molecule that is modulated by 125P5C8, useful for
PT treating or preventing cancer that expresses or over expresses 125P5C8.
XX
PS Disclosure; Page 208; 274pp; English.
XX
CC The present invention relates to compositions comprising a substance that
CC modulates the status of 125P5C8 or a molecule that is modulated by
CC 125P5C8. The status of a cell that expresses 125P5C8 is modulated. The
CC composition is useful for treating cancer, particularly prostate,
CC bladder, kidney, colon, ovary or breast cancer. The 125P5C8 protein
CC and/or a nucleotide sequence encoding the protein is useful for
CC immunising a mammal against cancer. The present sequence is a 125P5C8
CC epitope shown in the exemplification of the invention
XX
SQ Sequence 15 AA;
XX
Query Match 35.4%; Score 34; DB 5; Length 15;
Best Local Similarity 41.7%; Pred. No. 95;
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
QY 7 GYLITRAVSPGK 18
DB 1 GHILINGTNP GK 12
XX
RESULT 6
ABJ14493
ID ABJ14493 standard; peptide; 15 AA.
XX
AC ABJ14493;
XX
DT 10-DEC-2002 (first entry)
XX
DE Human 125P5C8 epitope #3119.
XX
KW Human; 125P5C8; cancer; cytostatic; breast cancer; prostate cancer;
XX bladder cancer; kidney cancer; colon cancer; ovarian cancer; epitope.
XX
OS Homo sapiens.
XX
PN WO200272785-A2.
XX
```

```
XX
PD 19-SEP-2002.
XX
PF 13-MAR-2002; 2002WO-US007855.
XX
PR 14-MAR-2001; 2001US-00809638.
XX
PA (AGEN-) AGENSYS INC.
XX
PI Faris M, Challita-Bid PM, Hubert RS, Afar DEH, Raitano AB, Ge W;
XX Morrison RK, Morrison K, Jakobovits A;
XX
DR WPI; 2002-713510/77.
XX
PT New composition comprising a substance that modulates the status of
PT 125P5C8 gene or a molecule that is modulated by 125P5C8, useful for
PT treating or preventing cancer that expresses or over expresses 125P5C8.
XX
PS Disclosure; Page 203; 274pp; English.
XX
CC The present invention relates to compositions comprising a substance that
CC modulates the status of 125P5C8 or a molecule that is modulated by
CC 125P5C8. The status of a cell that expresses 125P5C8 is modulated. The
CC composition is useful for treating cancer, particularly prostate,
CC bladder, kidney, colon, ovary or breast cancer. The 125P5C8 protein
CC and/or a nucleotide sequence encoding the protein is useful for
CC immunising a mammal against cancer. The present sequence is a 125P5C8
CC epitope shown in the exemplification of the invention
XX
SQ Sequence 15 AA;
XX
Query Match 35.4%; Score 34; DB 5; Length 15;
Best Local Similarity 41.7%; Pred. No. 95;
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
QY 7 GYLITRAVSPGK 18
DB 2 GHILINGTNP GK 13
XX
RESULT 7
ABJ14856
ID ABJ14856 standard; peptide; 15 AA.
XX
AC ABJ14856;
XX
DT 10-DEC-2002 (first entry)
XX
DE Human 125P5C8 epitope #3482.
XX
KW Human; 125P5C8; cancer; cytostatic; breast cancer; prostate cancer;
XX bladder cancer; kidney cancer; colon cancer; ovarian cancer; epitope.
XX
OS Homo sapiens.
XX
PN WO200272785-A2.
XX
PD 19-SEP-2002.
XX
PF 13-MAR-2002; 2002WO-US007855.
XX
PR 14-MAR-2001; 2001US-00809638.
XX
PA (AGEN-) AGENSYS INC.
XX
PI Faris M, Challita-Bid PM, Hubert RS, Afar DEH, Raitano AB, Ge W;
XX Morrison RK, Morrison K, Jakobovits A;
XX
DR WPI; 2002-713510/77.
XX
PT New composition comprising a substance that modulates the status of
PT 125P5C8 gene or a molecule that is modulated by 125P5C8, useful for
PT treating or preventing cancer that expresses or over expresses 125P5C8.
XX
```



XX Disclosure; Page 211; 274pp; English.  
 PS  
 XX  
 CC The present invention relates to compositions comprising a substance that  
 CC modulates the status of 125P5C8 or a molecule that is modulated by  
 CC 125P5C8. The status of a cell that expresses 125P5C8 is modulated. The  
 CC composition is useful for treating cancer, particularly prostate,  
 CC bladder, kidney, colon, ovary or breast cancer. The 125P5C8 protein  
 CC and/or a nucleotide sequence encoding the protein is useful for  
 CC immunising a mammal against cancer. The present sequence is a 125P5C8  
 CC epitope shown in the exemplification of the invention  
 XX  
 SQ Sequence 15 AA;  
 XX  
 Query Match 35.4%; Score 34; DB 5; Length 15;  
 Best Local Similarity 41.7%; Pred. No. 95;  
 Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;  
 QY 7 GYLTTAAVSPGK 18  
 DB 2 GHLSNGTNPGR 13  
 XX  
 RESULT 8  
 ABJ14620  
 ID ABJ14620 standard; peptide; 15 AA.  
 AC ABJ14620;  
 DT 10-DEC-2002 (first entry)  
 XX  
 DE Human 125P5C8 epitope #3246.  
 XX  
 KW Human; 125P5C8; cancer; cytostatic; breast cancer; prostate cancer;  
 KW bladder cancer; kidney cancer; colon cancer; ovarian cancer; epitope.  
 OS Homo sapiens.  
 XX  
 PN WO200272785-A2.  
 XX  
 PD 19-SEP-2002.  
 XX  
 PP 13-MAR-2002; 2002MO-US007855.  
 XX  
 PR 14-MAR-2001; 2001US-00809638.  
 XX  
 PA (AGEN-) AGENSYS INC.  
 PI Faris M, Challita-Bid PM, Hubert RS, Afar DEH, Raicano AB, Ge W;  
 PI Morrison RK, Morrison K, Jakobovits A;  
 PI WPI; 2002-713510/77.  
 DR  
 XX  
 PT New composition comprising a substance that modulates the status of  
 PT 125P5C8 gene or a molecule that is modulated by 125P5C8, useful for  
 PT treating or preventing cancer that expresses or over expresses 125P5C8.  
 XX  
 PS Disclosure; Page 206; 274pp; English.  
 XX  
 CC The present invention relates to compositions comprising a substance that  
 CC modulates the status of 125P5C8 or a molecule that is modulated by  
 CC 125P5C8. The status of a cell that expresses 125P5C8 is modulated. The  
 CC composition is useful for treating cancer, particularly prostate,  
 CC bladder, kidney, colon, ovary or breast cancer. The 125P5C8 protein  
 CC and/or a nucleotide sequence encoding the protein is useful for  
 CC immunising a mammal against cancer. The present sequence is a 125P5C8  
 CC epitope shown in the exemplification of the invention  
 XX  
 SQ Sequence 15 AA;  
 XX  
 Query Match 35.4%; Score 34; DB 5; Length 15;  
 Best Local Similarity 41.7%; Pred. No. 95;  
 Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 7 GYLTTAAVSPGK 18  
 DB 1 GHLSNGTNPGR 12  
 XX  
 RESULT 9  
 ABJ14316  
 ID ABJ14316 standard; peptide; 15 AA.  
 AC ABJ14316;  
 DT 10-DEC-2002 (first entry)  
 XX  
 DE Human 125P5C8 epitope #2942.  
 XX  
 KW Human; 125P5C8; cancer; cytostatic; breast cancer; prostate cancer;  
 KW bladder cancer; kidney cancer; colon cancer; ovarian cancer; epitope.  
 OS Homo sapiens.  
 XX  
 PN WO200272785-A2.  
 XX  
 PD 19-SEP-2002.  
 XX  
 PP 13-MAR-2002; 2002MO-US007855.  
 XX  
 PR 14-MAR-2001; 2001US-00809638.  
 XX  
 PA (AGEN-) AGENSYS INC.  
 PI Faris M, Challita-Bid PM, Hubert RS, Afar DEH, Raicano AB, Ge W;  
 PI Morrison RK, Morrison K, Jakobovits A;  
 PI WPI; 2002-713510/77.  
 DR  
 XX  
 PT New composition comprising a substance that modulates the status of  
 PT 125P5C8 gene or a molecule that is modulated by 125P5C8, useful for  
 PT treating or preventing cancer that expresses or over expresses 125P5C8.  
 XX  
 PS Disclosure; Page 199; 274pp; English.  
 XX  
 CC The present invention relates to compositions comprising a substance that  
 CC modulates the status of 125P5C8 or a molecule that is modulated by  
 CC 125P5C8. The status of a cell that expresses 125P5C8 is modulated. The  
 CC composition is useful for treating cancer, particularly prostate,  
 CC bladder, kidney, colon, ovary or breast cancer. The 125P5C8 protein  
 CC and/or a nucleotide sequence encoding the protein is useful for  
 CC immunising a mammal against cancer. The present sequence is a 125P5C8  
 CC epitope shown in the exemplification of the invention  
 XX  
 SQ Sequence 15 AA;  
 XX  
 Query Match 35.4%; Score 34; DB 5; Length 15;  
 Best Local Similarity 41.7%; Pred. No. 95;  
 Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;  
 QY 7 GYLTTAAVSPGK 18  
 DB 3 GHLSNGTNPGR 14  
 XX  
 RESULT 10  
 ABJ14777  
 ID ABJ14777 standard; peptide; 15 AA.  
 AC ABJ14777;  
 DT 10-DEC-2002 (first entry)  
 XX  
 DE Human 125P5C8 epitope #3403.  
 XX  
 KW Human; 125P5C8; cancer; cytostatic; breast cancer; prostate cancer;

KW bladder cancer; kidney cancer; colon cancer; ovarian cancer; epitope.  
 XX Homo sapiens.  
 OS  
 XX WO200272785-A2.  
 PN  
 XX  
 PD 19-SEP-2002.  
 XX  
 PP 13-MAR-2002; 2002WO-US007855.  
 XX  
 PR 14-MAR-2001; 2001US-00809638.  
 XX  
 PA (AGEN-) AGENSYS INC.  
 XX  
 PI Paris M, Challita-Bid PM, Hubert RS, Afar DEH, Raitano AB, Ge W,  
 PI Morrison RK, Morrilson K, Jakobovits A;  
 XX  
 DR WPI; 2002-713510/77.  
 XX  
 PT New composition comprising a substance that modulates the status of  
 PT 125P5C8 gene or a molecule that is modulated by 125P5C8, useful for  
 PT treating or preventing cancer that expresses or over expresses 125P5C8.  
 XX  
 XX Disclosure; Page 209; 274pp; English.  
 PS  
 CC The present invention relates to compositions comprising a substance that  
 CC modulates the status of 125P5C8 or a molecule that is modulated by  
 CC 125P5C8. The status of a cell that expresses 125P5C8 is modulated. The  
 CC composition is useful for treating cancer, particularly prostate,  
 CC bladder, kidney, colon, ovary or breast cancer. The 125P5C8 protein  
 CC and/or a nucleotide sequence encoding the protein is useful for  
 CC immunising a mammal against cancer. The present sequence is a 125P5C8  
 CC epitope shown in the exemplification of the invention  
 XX  
 SQ Sequence 15 AA;  
 Query Match 35.4%; Score 34; DB 5; Length 15;  
 Best local Similarity 41.7%; Pred. No. 95;  
 Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;  
 QY 7 GYLITRAVSPGK 18  
 DB 4 GHILINGTNPBK 15  
 RESULT 11  
 ADL21730  
 ID ADL21730 standard; peptide; 15 AA.  
 XX  
 AC ADL21730;  
 XX  
 DT 20-MAY-2004 (first entry)  
 XX  
 DE 125P5C8 protein-related peptide #2978.  
 XX  
 KM 125P5C8; cancer-associated gene; cancer-associated protein; cancer.  
 XX  
 OS Unidentified.  
 XX  
 PN US2003219444-A1.  
 XX  
 PD 27-NOV-2003.  
 XX  
 PP 13-MAR-2002; 2002US-00099460.  
 XX  
 PR 14-MAR-2001; 2001US-00809638.  
 XX  
 PA (FARI/) FARI M.  
 PA (CHAL/) CHALLITA-BID P M.  
 PA (HUBE/) HUBERT R S.  
 PA (AFAR/) AFAR D E H.  
 PA (RAIT/) RAITANO A B.  
 PA (GEWM/) GE W.

PA (MORR/) MORRISON R K.  
 PA (MORR/) MORRISON K J M.  
 PA (JAKO/) JAKOBOVITS A.  
 XX  
 PI Paris M, Challita-Bid PM, Hubert RS, Afar DEH, Raitano AB, Ge W,  
 PI Morrison RK, Morrilson KJM, Jakobovits A;  
 XX  
 DR WPI; 2004-021932/02.  
 XX  
 PT New composition comprising a substance that modulates the status of  
 PT 125P5C8 gene or a molecule that is modulated by 125P5C8, useful for  
 PT diagnosing or treating cancer.  
 XX  
 PS Example 51; Page 124; 183pp; English.  
 XX  
 CC The invention comprises a composition which contains a substance that can  
 CC modulate the status of 125P5C8 (125P5C8 is a novel cancer-associated  
 CC gene/protein), or a molecule that is modulated by 125P5C8. The  
 CC composition of the invention is useful for diagnosing or treating cancer.  
 CC The present amino acid sequence represents a 125P5C8-related peptide  
 CC which was used in an example of the invention.  
 XX  
 SQ Sequence 15 AA;  
 Query Match 35.4%; Score 34; DB 8; Length 15;  
 Best local Similarity 41.7%; Pred. No. 95;  
 Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;  
 QY 7 GYLITRAVSPGK 18  
 DB 2 GHILINGTNPBK 13  
 RESULT 12  
 ADL22014  
 ID ADL22014 standard; peptide; 15 AA.  
 XX  
 AC ADL22014;  
 XX  
 DT 20-MAY-2004 (first entry)  
 XX  
 DE 125P5C8 protein-related peptide #3262.  
 XX  
 KM 125P5C8; cancer-associated gene; cancer-associated protein; cancer.  
 XX  
 OS Unidentified.  
 XX  
 PN US2003219444-A1.  
 XX  
 PD 27-NOV-2003.  
 XX  
 PP 13-MAR-2002; 2002US-00099460.  
 XX  
 PR 14-MAR-2001; 2001US-00809638.  
 XX  
 PA (FARI/) FARI M.  
 PA (CHAL/) CHALLITA-BID P M.  
 PA (HUBE/) HUBERT R S.  
 PA (AFAR/) AFAR D E H.  
 PA (RAIT/) RAITANO A B.  
 PA (GEWM/) GE W.  
 PA (MORR/) MORRISON R K.  
 PA (MORR/) MORRISON K J M.  
 PA (JAKO/) JAKOBOVITS A.  
 XX  
 PI Paris M, Challita-Bid PM, Hubert RS, Afar DEH, Raitano AB, Ge W,  
 PI Morrison RK, Morrilson KJM, Jakobovits A;  
 XX  
 DR WPI; 2004-021932/02.  
 XX  
 PT New composition comprising a substance that modulates the status of  
 PT 125P5C8 gene or a molecule that is modulated by 125P5C8, useful for  
 PT diagnosing or treating cancer.

XX Example 51, Page 128, 183pp, English.  
PS  
XX The invention comprises a composition which contains a substance that can  
CC modulate the status of 125P5C8 (125P5C8 is a novel cancer-associated  
CC gene/protein), or a molecule that is modulated by 125P5C8. The  
CC composition of the invention is useful for diagnosing or treating cancer.  
CC The present amino acid sequence represents a 125P5C8-related peptide  
CC which was used in an example of the invention.  
XX  
SQ Sequence 15 AA,  
Query Match 35.4%; Score 34; DB 8; Length 15;  
Best Local Similarity 41.7%; Pred. No. 95;  
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;  
QY 7 GYLTTAAVSPGK 18  
DB 4 GHLLNSGTNPCK 15  
RESULT 13  
ADL21857  
XX ADL21857 standard; peptide; 15 AA.  
XX  
AC ADL21857,  
XX  
DT 20-MAY-2004 (first entry)  
XX  
DE 125P5C8 protein-related peptide #3105.  
XX  
KM 125P5C8; cancer-associated gene; cancer-associated protein; cancer.  
XX  
OS Unidentified.  
XX  
PN US2003219444-A1.  
XX  
PD 27-NOV-2003.  
XX  
PF 13-MAR-2002; 2002US-00099460.  
XX  
PR 14-MAR-2001; 2001US-00809638.  
XX  
PI (PARI/) PARIS M.  
XX  
PI (CHAL/) CHALLITA-BID P M.  
XX  
PA (HUBE/) HUBERT R S.  
XX  
PA (AFAR/) AFAR D E H.  
XX  
PA (RAIT/) RAITANO A B.  
XX  
PA (GEWW/) GE W.  
XX  
PA (MORR/) MORRISON R K.  
XX  
PA (MORR/) MORRISON K J M.  
XX  
PA (JAKO/) JAKOBOVITS A.  
XX  
PI Faris M, Challita-Bid PM, Hubert RS, Afar DEH, Raitano AB, Ge W,  
PI Morrison RK, Morrison KM, Jakobovits A;  
PI MPI, 2004-021932/02.  
XX  
PT New composition comprising a substance that modulates the status of  
PT 125P5C8 gene or a molecule that is modulated by 125P5C8, useful for  
PT diagnosing or treating cancer.  
XX  
PS Example 51, Page 126, 183pp, English.  
XX  
CC The invention comprises a composition which contains a substance that can  
CC modulate the status of 125P5C8 (125P5C8 is a novel cancer-associated  
CC gene/protein), or a molecule that is modulated by 125P5C8. The  
CC composition of the invention is useful for diagnosing or treating cancer.  
CC The present amino acid sequence represents a 125P5C8-related peptide  
CC which was used in an example of the invention.  
XX  
SQ Sequence 15 AA,

Query Match 35.4%; Score 34; DB 8; Length 15;  
Best Local Similarity 41.7%; Pred. No. 95;  
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;  
QY 7 GYLTTAAVSPGK 18  
DB 1 GHLLNSGTNPCK 12  
RESULT 14  
ADL21553  
XX ADL21553 standard; peptide; 15 AA.  
XX  
AC ADL21553;  
XX  
DT 20-MAY-2004 (first entry)  
XX  
DE 125P5C8 protein-related peptide #2801.  
XX  
KM 125P5C8; cancer-associated gene; cancer-associated protein; cancer.  
XX  
OS Unidentified.  
XX  
PN US2003219444-A1.  
XX  
PD 27-NOV-2003.  
XX  
PF 13-MAR-2002; 2002US-00099460.  
XX  
PR 14-MAR-2001; 2001US-00809638.  
XX  
PI (PARI/) PARIS M.  
XX  
PI (CHAL/) CHALLITA-BID P M.  
XX  
PA (HUBE/) HUBERT R S.  
XX  
PA (AFAR/) AFAR D E H.  
XX  
PA (RAIT/) RAITANO A B.  
XX  
PA (GEWW/) GE W.  
XX  
PA (MORR/) MORRISON R K.  
XX  
PA (MORR/) MORRISON K J M.  
XX  
PA (JAKO/) JAKOBOVITS A.  
XX  
PI Faris M, Challita-Bid PM, Hubert RS, Afar DEH, Raitano AB, Ge W,  
PI Morrison RK, Morrison KM, Jakobovits A;  
PI MPI, 2004-021932/02.  
XX  
PT New composition comprising a substance that modulates the status of  
PT 125P5C8 gene or a molecule that is modulated by 125P5C8, useful for  
PT diagnosing or treating cancer.  
XX  
PS Example 51, Page 123, 183pp, English.  
XX  
CC The invention comprises a composition which contains a substance that can  
CC modulate the status of 125P5C8 (125P5C8 is a novel cancer-associated  
CC gene/protein), or a molecule that is modulated by 125P5C8. The  
CC composition of the invention is useful for diagnosing or treating cancer.  
CC The present amino acid sequence represents a 125P5C8-related peptide  
CC which was used in an example of the invention.  
XX  
SQ Sequence 15 AA,  
Query Match 35.4%; Score 34; DB 8; Length 15;  
Best Local Similarity 41.7%; Pred. No. 95;  
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;  
QY 7 GYLTTAAVSPGK 18  
DB 3 GHLLNSGTNPCK 14  
RESULT 15  
ADL21974  
XX ADL21974 standard; peptide; 15 AA.

```
XX AC ADL21974;
XX DT 20-MAY-2004 (first entry)
XX DE 12SP5C8 protein-related peptide #3222.
XX KM 12SP5C8; cancer-associated gene; cancer-associated protein; cancer.
XX OS Unidentified.
XX PN US2003219444-A1.
XX PD 27-NOV-2003.
XX PF 13-MAR-2002; 2002US-00099460.
XX PR 14-MAR-2001; 2001US-00809638.
XX PA (FARI/) FARIS M.
XX PA (CHAL/) CHALLITA-BID P M.
XX PA (HUBE/) HUBERT R S.
XX PA (AFAR/) AFAR D E H.
XX PA (RAIT/) RAITANO A B.
XX PA (GEWW/) GE W.
XX PA (MORR/) MORRISON R K.
XX PA (MORR/) MORRISON K J M.
XX PA (JAKO/) JAKOBOVITS A.
XX PI Faris M, Challita-Bid PM, Hubert RS, Afar DEH, Raitano AB, Ge W,
XX PI Morrison RK, Morrison KM, Jakobovits A;
XX DR MPI; 2004-021932/02.
XX PT New composition comprising a substance that modulates the status of
XX PT 12SP5C8 gene or a molecule that is modulated by 12SP5C8, useful for
XX PT diagnosing or treating cancer.
XX PS Example 51; Page 127; 183pp; English.
XX CC The invention comprises a composition which contains a substance that can
XX CC modulate the status of 12SP5C8 (12SP5C8 is a novel cancer-associated
XX CC gene/protein), or a molecule that is modulated by 12SP5C8. The
XX CC composition of the invention is useful for diagnosing or treating cancer.
XX CC The present amino acid sequence represents a 12SP5C8-related peptide
XX CC which was used in an example of the invention.
XX SQ Sequence 15 AA;
XX
XX Query Match 35.4%; Score 34; DB 8; Length 15;
XX Best Local Similarity 41.7%; Pred. No. 95;
XX Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
XX
XX QY 7 GYLTRAAVSPGK 18
XX |.: : :|||
XX 1 GHLSNGTNPGR 12
XX
XX Db
XX
XX RESULT 16
XX ADL22093
XX ID ADL22093 standard; peptide; 15 AA.
XX AC ADL22093;
XX DT 20-MAY-2004 (first entry)
XX DE 12SP5C8 protein-related peptide #3341.
XX KM 12SP5C8; cancer-associated gene; cancer-associated protein; cancer.
XX OS Unidentified.
XX PN US2003219444-A1.
XX PI
```

```
XX PD 27-NOV-2003.
XX PF 13-MAR-2002; 2002US-00099460.
XX PR 14-MAR-2001; 2001US-00809638.
XX PA (FARI/) FARIS M.
XX PA (CHAL/) CHALLITA-BID P M.
XX PA (HUBE/) HUBERT R S.
XX PA (AFAR/) AFAR D E H.
XX PA (RAIT/) RAITANO A B.
XX PA (GEWW/) GE W.
XX PA (MORR/) MORRISON R K.
XX PA (MORR/) MORRISON K J M.
XX PA (JAKO/) JAKOBOVITS A.
XX PI Faris M, Challita-Bid PM, Hubert RS, Afar DEH, Raitano AB, Ge W,
XX PI Morrison RK, Morrison KM, Jakobovits A;
XX DR MPI; 2004-021932/02.
XX PT New composition comprising a substance that modulates the status of
XX PT 12SP5C8 gene or a molecule that is modulated by 12SP5C8, useful for
XX PT diagnosing or treating cancer.
XX PS Example 51; Page 129; 183pp; English.
XX CC The invention comprises a composition which contains a substance that can
XX CC modulate the status of 12SP5C8 (12SP5C8 is a novel cancer-associated
XX CC gene/protein), or a molecule that is modulated by 12SP5C8. The
XX CC composition of the invention is useful for diagnosing or treating cancer.
XX CC The present amino acid sequence represents a 12SP5C8-related peptide
XX CC which was used in an example of the invention.
XX SQ Sequence 15 AA;
XX
XX Query Match 35.4%; Score 34; DB 8; Length 15;
XX Best Local Similarity 41.7%; Pred. No. 95;
XX Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
XX
XX QY 7 GYLTRAAVSPGK 18
XX |.: : :|||
XX 2 GHLSNGTNPGR 13
XX
XX Db
XX
XX RESULT 17
XX ADO37897
XX ID ADO37897 standard; peptide; 6 AA.
XX AC ADO37897;
XX DT 29-JUL-2004 (first entry)
XX DE Binding partner polypeptide of the invention SEQ ID NO:957.
XX KM polypeptide-tagged collection; capture system; tagged polypeptide;
XX KM pharmaceutical; diagnostic.
XX OS Synthetic.
XX PN WO2004039962-A2.
XX PD 13-MAY-2004.
XX PF 30-OCT-2003; 2003WO-US034821.
XX PR 30-OCT-2002; 2002US-042923P.
XX PR 30-OCT-2002; 2002US-0423018P.
XX PA (POIN-) POINTILLISTE INC.
XX PI Aulic-Riche D, Ackinson B, Geyzen MH;
```

XX MPI, 2004-376185/35.  
DR  
XX  
PT Evenly distributing tags among members of a starting library, useful in  
PT developing pharmaceuticals and diagnostics, comprises dividing the  
PT starting library into sub libraries and attaching a tag to members of  
PT each sub library.  
XX  
XX  
PS Claim 141; SEQ ID NO 957; 510pp; English.  
CC  
CC The invention relates to novel methods for producing polypeptide-tagged  
CC collections and capture systems containing the tagged polypeptides. The  
CC method is useful for evenly distributing tags among members of a starting  
CC library. The system, collection, kits and methods are useful in  
CC developing pharmaceuticals and diagnostics. The present sequence is used  
CC in the exemplification of the invention.  
XX  
SQ Sequence 6 AA;  
XX  
XX  
Query Match 34.4%; Score 33; DB 8; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 4 EPHGY 8  
| | | | |  
| | | | |  
Db 1 EPHGY 5  
XX  
XX  
RESULT 18  
AD028419  
ID AD028419 standard; peptide; 6 AA.  
XX  
AC AD028419;  
XX  
DT 12-AUG-2004 (first entry)  
XX  
DE Capture system related peptide, SEQ ID 957.  
XX  
KM Capture system.  
XX  
OS Synthetic.  
XX  
PN WO2004042019-A2.  
XX  
PD 21-MAY-2004.  
XX  
PF 30-OCT-2003; 2003WO-US034693.  
XX  
PR 30-OCT-2002; 2002US-0422923P.  
PR 30-OCT-2002; 2002US-0423018P.  
XX  
PA (POIN-) POINTILLISTE INC.  
PI Ault-Riche D, Atkinson B, Jesaitis L, Kumble KD, Sperinde G;  
PI MPI, 2004-431543/40.  
XX  
DR  
XX  
PT Capturing biological particles, by contacting biological particles with  
PT capture system comprising addressed loci, addressed collection of  
PT polypeptide tagged molecules, capture agents, and polypeptide tag to  
PT which capture agent binds.  
XX  
PS Disclosure; SEQ ID NO 957; 505pp; English.  
XX  
CC The present invention relates to a method for the capture and analysis of  
CC biological particle using a capture system. The method is useful for  
CC capturing biological particles such as cells, portions of cells, cell  
CC membranes, viruses, viral capsids, viral particles, bacterial cells,  
CC subcellular compartments, organelles and micelles, prokaryotic cells,  
CC eukaryotic cells, intracellular particles, nuclei, cell membranes, cell  
CC membrane fragments, nuclear membranes, nuclear membrane fragments, viral  
CC vectors or viral capsids with or without packaged nucleic acid, phage,  
CC phage vectors, phage capsids with or without encapsulated nucleotide

CC acid, liposomes and other micellar agents. The biological particles are  
CC cells chosen from immune cells, neurons, cancer cells, bacterial cells  
CC and infected cells, subcellular compartment, organelles, viral particles  
CC or pathogens. The cells are dendritic cells, T cells, or B cells. The  
CC method is also useful for identifying molecules that interact with  
CC infectious agents, for profiling the surface of a biological particles,  
CC for identifying a modulator of an interaction among proteins in the  
CC biological particle, for identifying molecules that modulates the  
CC trafficking, activity or functional or structural property in the  
CC biological particle, and for mapping epitopes of molecules displayed on  
CC the surface of a biological particles. The method is also useful for  
CC sorting biological particles, for identifying a receptor on the surface  
CC of biological particle that transduces a signal from a polypeptide, and  
CC for identifying the molecule that interacts with an apically-localized  
CC molecule on a biological particle. The present sequence was used to  
CC illustrate the invention.  
XX  
SQ Sequence 6 AA;  
XX  
XX  
Query Match 34.4%; Score 33; DB 8; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 4 EPHGY 8  
| | | | |  
| | | | |  
Db 1 EPHGY 5  
XX  
XX  
RESULT 19  
ADR49685  
ID ADR49685 standard; peptide; 6 AA.  
XX  
AC ADR49685;  
XX  
DT 18-NOV-2004 (first entry)  
XX  
DE 6-mer peptide epitope works as a highly specific capture agent Seq 46.  
XX  
KM self-assembly array; capture agent; epitope; binding partner.  
XX  
OS Synthetic.  
XX  
PN WO2004071641-A2.  
XX  
PD 26-AUG-2004.  
XX  
PF 30-OCT-2003; 2003WO-US034747.  
XX  
PR 10-FEB-2003; 2003US-0446687P.  
XX  
PA (POIN-) POINTILLISTE INC.  
PA (AULT/) AULT-RICHE D.  
PA (KUMB/) KUMBLE K D.  
PA (SCHU/) SCHULTZ R.  
PA (SCHU/) SCHULTZ K.  
XX  
PI Ault-Riche D, Kumble KD, Schultz R, Schultz K;  
PI MPI, 2004-635071/61.  
XX  
DR  
XX  
PT Self-assembled array for monitoring interaction of molecules, comprising  
PT addressable array of capture agents having predetermined binding partners  
PT and conjugates comprising biological particle and/or molecule linked to  
PT binding partners.  
XX  
PS Disclosure; SEQ ID NO 46; 443pp; English.  
XX  
CC This invention relates to novel self-assembly arrays that each comprises  
CC an addressable collection of capture agents that have predetermined  
CC binding partners, as well as reagents for the covalent conjugation of the  
CC binding partners to molecules for display in the array. Specifically, it  
CC refers to the production of a flexible experimental surface, which can be  
CC adapted for use with almost any analytical system. The present invention



PA (GEYS/) GEYSEN M.  
 XX (AULT/) AULT-RICHE D.  
 XX  
 PI Geyesen M, Ault-Riche D;  
 DR WPI, 2005-345019/35.  
 XX  
 PT Collection of antigenic polypeptides useful as binding partners for use  
 PT with capture agents, comprises three antigenic polypeptides that comprise  
 PT unique residues and include critical residues occupying N and C terminal  
 PT positions.  
 XX  
 PS Claim 22; SEQ ID NO 9, 196pp; English.  
 XX  
 CC The present invention relates to a collection (I) of antigenic  
 CC polypeptides (AD245683 - AD246593), which comprises at least three  
 CC antigenic polypeptides that comprise five to eight unique residues and  
 CC include at least four residues, designated critical residues, chosen from  
 CC Glu, Pro, Gln, Asn, Phe, His, Thr, Lys, Ileu, Asp, where the critical  
 CC residues occupy the N and C terminal positions in each polypeptide, and  
 CC no more than three polypeptides in the collection contain the same four  
 CC critical residues. (I) is useful as binding partners for use with capture  
 CC agents which recognize the highly antigenic, highly specific  
 CC polypeptides.  
 CC  
 SQ Sequence 6 AA;  
 XX  
 Query Match 34.4%; Score 33; DB 9; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 EPHGY 8  
 Db 1 EPHGY 5  
 XX  
 RESULT 22  
 AEB29801  
 ID AEB29801 standard; peptide; 6 AA.  
 XX  
 AC AEB29801;  
 XX  
 DT 06-OCT-2005 (first entry)  
 XX  
 DB Therapeutic complex associated antigenic peptide SEQ ID NO 9.  
 XX  
 KW immunomodulatory; cytostatic; antiinflammatory; antimicrobial;  
 KW neuroprotective; nootropic; ophthalmological; antirheumatic;  
 KW antiarthritic; vitruclide; dermatological; immunosuppressive; infection;  
 KW pharmaceutical; cancer; autoimmune disease; neuroprotective; infection;  
 KW neurodegenerative disease; neuroprotective; neurological disease;  
 KW ophthalmological; ocular disease; non-hodgkin lymphoma;  
 KW hematological disease; rheumatoid arthritis; antiarthritic;  
 KW antirheumatic; musculoskeletal disease; multiple sclerosis;  
 KW neuroprotective; immune disorder; neurological disease; melanoma;  
 KW cytostatic; neoplasm; inflammation; viral infection; vitruclide; infection;  
 KW antigen.  
 KW  
 XX  
 OS Synthetic.  
 XX  
 PN WO2005067980-A2.  
 XX  
 PD 28-UTL-2005.  
 XX  
 PP 10-JAN-2005, 2005WO-US000816.  
 XX  
 PR 12-JAN-2004, 2004US-0536184P.  
 PR 29-MAR-2004, 2004US-0557591P.  
 XX  
 PA (POIN-) POINTILLISTE INC.  
 XX  
 PI Ault-Riche D, Levy R;  
 XX

DR WPI, 2005-533851/54.  
 XX  
 XX Complex for treating e.g. cancer, comprises a targeting domain  
 PT specifically binding to a subject-specific target and an effector  
 PT molecule rendering the complex biologically effective.  
 XX  
 PS Disclosure; SEQ ID NO 9, 403pp; English.  
 XX  
 CC The invention describes a therapeutic complex comprising a targeting  
 CC domain that specifically binds to a subject-specific target and an  
 CC effector molecule that renders the resulting therapeutic complex  
 CC biologically effective, where the targeting domain and effector molecule  
 CC are linked by a specific interaction of a binding partner and a capture  
 CC agent. Also described are: preparing (M1) (I) by contacting a targeting  
 CC domain and an effector molecule to form a complex; rendering an antibody  
 CC or fragment therapeutically effective; rendering a target-specific  
 CC polypeptide therapeutically effective; screening test molecules to  
 CC identify effectors for use in (I); and screening test molecules to  
 CC identify targeting domains for use in (I). (I) is used to render an  
 CC antibody or its fragment or target specific polypeptide therapeutically  
 CC effective. (II) is used to treat a disease or condition, by administering  
 CC (II) which comprises a therapeutic complex designed for personalized  
 CC treatment. The disease is chosen from B cell-mediated disease, autoimmune  
 CC disease and T cell-mediated disease, cancers, inflammatory disease,  
 CC autoimmune disease, infectious disease, neurodegenerative disease and  
 CC ophthalmic disease, preferably non-Hodgkin's lymphoma, rheumatoid  
 CC arthritis, lupus, multiple sclerosis, melanoma, posterior intraocular  
 CC inflammation, pathogen and virus infection. The targeting domain and the  
 CC effector are administered as a complex, or administered sequentially,  
 CC simultaneously or intermittently. The targeting domain and effector are  
 CC administered separately and either one or more doses of the targeting  
 CC domain is(are) administered prior to administration of a therapeutic  
 CC complex also comprising the targeting domain, or one or more doses of the  
 CC effector prior is(are) administered prior to administration of a  
 CC therapeutic complex comprising the effector. This is the amino acid  
 CC sequence of an antigenic peptide used in the creation of a therapeutic  
 CC complex of the invention.  
 CC  
 SQ Sequence 6 AA;  
 XX  
 Query Match 34.4%; Score 33; DB 9; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 EPHGY 8  
 Db 1 EPHGY 5  
 XX  
 RESULT 23  
 AAE26394  
 ID AAE26394 standard; peptide; 12 AA.  
 XX  
 AC AAE26394;  
 XX  
 DT 13-DEC-2002 (first entry)  
 XX  
 DB Human GPR10 mutant C-terminal peptide, V266A.  
 XX  
 KW Human; wakefulness; sleep disorder; prolactin releasing peptide receptor;  
 KW FRP; GPR10; therapy; epilepsy; narcolepsy; sleepiness; sleep apnoea;  
 KW insomnia; idiopathic hypersomnia; psychogenic hypersomnia; seizure;  
 KW anticonvulsant; mutant; mutein.  
 KW  
 XX  
 OS Homo sapiens.  
 XX  
 PN Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 8  
 FT /note= "Wild-type Val substituted with Ala; This position  
 FT corresponds to position 366 of the wild-type protein"  
 XX  
 PN US2002037533-A1.

```

XX 28-MAR-2002.
PD 17-AUG-2001; 2001US-00932161.
XX 28-APR-2000; 2000US-00560915.
XX (CIVE/) CIVELLI O.
XX (LINS/) LIN S.
XX CIVELLI O, Lin S;
XX WPI; 2002-403931/43.
XX Screening for compounds useful for promoting wakefulness or sleep, and
XX for treating sleeping disorders, e.g. insomnia, hypersomnia or sleep
XX apnea, comprises administering a prolactin releasing peptide agonist or
XX antagonist.
XX Example 2; Page 23; 35pp; English.
XX The present invention relates to a method of screening for compounds for
XX promoting wakefulness or sleep in a mammal. The method involves
XX administering a prolactin releasing peptide (PrRP) receptor (GPR10)
XX agonist or antagonist respectively and determining the ability of the
XX compound to promote wakefulness or sleep. The compounds identified from
XX the method are used in the therapy of epilepsy and other diseases
XX associated with absence seizures and in promoting wakefulness and sleep
XX in individuals having sleep disorders such as insomnia and narcolepsy.
XX PrRP receptor agonists may be used to treat common disorders which lead
XX to sleepiness, e.g. sleep apnoea, narcolepsy, idiopathic hypersomnia and
XX psychogenic hypersomnia. PrRP receptor antagonists are useful for
XX promoting sleep and for treating insomnia such as adjustment sleep
XX disorder and psychophysiological insomnia. The present sequence is human
XX GPR10 mutant C-terminal peptide
XX
XX Sequence 12 AA;
XX
XX Query Match          34.4%; Score 33; DB 5; Length 12;
XX Best Local Similarity 60.0%; Pred. No. 1.1e+02;
XX Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 5 PHGYLLTAAV 14
XX      |||  :||:|
XX      1 PHGQNMNTASV 10
XX
XX Db
XX
XX RESULT 24
XX AAM97665
XX ID AAM97665 standard; peptide; 14 AA.
XX
XX AC AAM97665;
XX
XX DT 24-JAN-2002 (first entry)
XX
XX DE Human peptide #940 encoded by a SNP oligonucleotide.
XX
XX XX Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
XX neuroprotective; antimicrobial; gene therapy; vaccine; amyase; cancer;
XX amyloid protein; angiotensin; apoptosis related protein; cadherin;
XX cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
XX complement related protein; cytochrome; kinesin; cytokine; interferon;
XX interleukin; G-protein coupled receptor; thioesterase; inflammation;
XX multifactorial disease; autoimmune disease; infection;
XX nervous system disease.
XX
XX OS Homo sapiens.
XX
XX PN WO200147944-A2.
XX
XX PD 05-JUL-2001.
XX
XX PF 28-DEC-2000; 2000WO-US035498.

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XX 28-DEC-1999; 99US-0173419P.
XX 27-DEC-2000; 2000US-00173419.
XX (CURA-) CURAGEN CORP.
XX Shinketsu RA, Leach M;
XX WPI; 2001-465210/50.
XX Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
XX oncogenes and histones, useful for diagnosing and treating, e.g. cancer,
XX autoimmune diseases and infections.
XX Disclosure; Page 3873; 4143pp; English.
XX
XX PS The present invention relates to oligonucleotides (see AAL26793-AAL34659)
XX encoding polymorphic variants of proteins related to amylases, amyloid
XX proteins, angiotensin, apoptosis related proteins, cadherin, cyclin,
XX polymerase, oncogene, histones, kinases, colony stimulating factors,
XX complement related proteins, cytochromes, kinesins, cytokines,
XX interferons, interleukins, G-protein coupled receptors and thioesterases.
XX The present sequence is a peptide encoded by one such oligonucleotide.
XX The oligonucleotides and the peptides encoded by them may be used in the
XX prevention, diagnosis and treatment of diseases associated with
XX inappropriate expression of the proteins listed above. Disorders that may
XX be prevented, diagnosed and/or treated include multifactorial diseases
XX with a genetic component, such as autoimmune diseases (e.g. rheumatoid
XX arthritis, multiple sclerosis, diabetes, systemic lupus erythematosus
XX and Grave's disease), inflammation, cancer (e.g. cancers of the bladder,
XX brain, breast, colon and kidney, leukaemia), diseases of the nervous
XX system and an infection of pathogenic organisms
XX
XX SQ Sequence 14 AA;
XX
XX Query Match          34.4%; Score 33; DB 4; Length 14;
XX Best Local Similarity 71.4%; Pred. No. 1.3e+02;
XX Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 5 PHGYLLT 11
XX      |||  :|
XX      5 PHGYRMT 11
XX
XX Db
XX
XX RESULT 25
XX ABG67141
XX ID ABG67141 standard; peptide; 17 AA.
XX
XX AC ABG67141;
XX
XX DT 24-SEP-2002 (first entry)
XX
XX DE HCV peptide FRI having reactivity with human monoclonal antibodies.
XX
XX XX Hepatitis C virus; hepatitis B; antibody; helper T-lymphocyte;
XX cytotoxic T-lymphocyte; HCV infection; virulence.
XX
XX OS Hepatitis C virus.
XX
XX PN WO200245743-A2.
XX
XX PD 13-JUN-2002.
XX
XX PF 07-DEC-2001; 2001WO-GB005421.
XX
XX XX 09-DEC-2000; 2000GB-00030102.
XX PR 18-DEC-2000; 2000GB-00030769.
XX
XX XX (ALLA/) ALLAIN J.
XX
XX PA Allain J, Li C, Piccolella E;
XX
XX PI

```



DR WPI; 2002-508540/54.

XX Hepatitis C virus (HCV) vaccines able to raise antibodies, helper T

PT lymphocytes and/or cytotoxic T lymphocytes able to bind to the

PT hypervariable 1 region of the infecting HCV strain.

XX

PS Example 4, Page 27; 52pp; English.

XX

CC The present invention relates to a hepatitis C virus (HCV) vaccine

CC comprising different groups of peptides each group being capable of

CC raising, in an infected individual, an antibody able to bind to the

CC hypervariable 1 (HVR1) region of the envelope protein E2 of the infecting

CC HCV strain. The different groups of peptides are administered

CC sequentially to raise antibodies, helper T-lymphocytes, and cytotoxic T-

CC lymphocytes which are cross-reactive to the HVR1 region of the infecting

CC HCV. The vaccines are useful for preventing and treating chronic HCV

CC infections. AB667139-AB667169 represent HCV peptides having reactivity

CC with human monoclonal antibodies

XX

SQ Sequence 17 AA;

QY Query Match 34.4%; Score 33; DB 5; Length 17;

DB Best Local Similarity 70.0%; Pred. No. 1.7e+02;

Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 8 YLTLAAVSPG 17

DB 4 YGLTALUSPG 13

RESULT 26

AAW45412

ID AAW45412 standard; peptide; 18 AA.

AC AAW45412;

AC

DT 14-MAY-1998 (first entry)

XX

DE N-terminal amino acid sequence of (R)-specific acylase, large subunit.

XX

KW Biocatalyst; K1/1 acylase activity; acylamide; stereoselective; racemic;

KW amine acylase; stereoisomer.

XX

OS Archaeobacter aureusens.

OS

PH Key Location/Qualifiers

FT Misc-difference 4 /note= "the identity of this Arg is not certain"

FT

FT Misc-difference 6 /note= "the identity of this Arg is not certain"

FT

FT Misc-difference 9 /note= "amino acid residue unknown"

FT

PN W09741214-A1.

PN

PD 06-NOV-1997.

XX

XX 14-APR-1997; 97WO-EP001866.

XX

PR 25-APR-1996; 96BP-00810266.

XX

XX (NOVS ) NOVARTIS AG.

XX

PI Ghisalba O, Kiltelmann M, Laumen K, Walservolken P;

XX

DR WPI; 1997-549719/50.

XX

PT Bio:catalyst which exhibits amine cyclase enzymatic activity - is

PT obtained from Rhodococcus globervulvis, Rhodococcus equi or Archaeobacter

XX aureusens.

XX

PS Claim 30; Page 48; 67pp; English.

XX

CC This is the N-terminal amino acid sequence of the (R)-specific acylase of

CC Archaeobacter aureusens ACR5b (large subunit) which acts as a biocatalyst

CC exhibiting amine acylase enzymatic activity without added lipase or

CC esterase activity. It is capable of stereoselectively hydrolysing a

CC racemic acylamide which has an aliphatic acyl residue and which is not a

CC derivative of a natural amino acid. The biocatalyst is especially used

CC for the stereoselective hydrolysis of N-acetyl-1-phenylethylamine or N-

CC acetyl-2-amino-1-phenyl-4-pentene, giving one enantiomer of the

CC corresponding phenylamine and leaving the other enantiomer of the

CC starting amide. No end uses are given for the separated enantiomers,

CC although reference is made to the need for enantiomerically pure

CC pharmaceutical and agrochemical drugs

XX

SQ Sequence 18 AA;

QY Query Match 34.4%; Score 33; DB 2; Length 18;

DB Best Local Similarity 41.2%; Pred. No. 1.8e+02;

Matches 7; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 2 AFEPHGILTLAAVSPGK 18

DB 2 AIRIRGYXDTPSVAPG 18

RESULT 27

AAE26395

ID AAE26395 standard; peptide; 12 AA.

AC AAE26395;

AC

DT 13-DEC-2002 (first entry)

XX

DE Human GPR10 mutant C-terminal peptide, S367A.

XX

KW Human; wakefulness; sleep disorder; prolactin releasing peptide receptor;

KW PRP; GPR10; therapy; epilepsy; narcolepsy; sleepiness; sleep apnoea;

KW insomnia; idiopathic hypersomnia; psychogenic hypersomnia; seizure;

KW anticonvulsant; mutant; mutcin.

XX

OS Homo sapiens.

OS

OS Synthetic.

OS

PH Key Location/Qualifiers

FT Misc-difference 9 /note= "Wild-type Ser substituted with Ala; This position

FT corresponds to position 367 of the wild-type protein"

FT

PN US2002037533-A1.

PN

PD 28-MAR-2002.

XX

XX 17-AUG-2001; 2001US-00932161.

XX

PR 28-APR-2000; 2000US-00560915.

XX

XX (CIVE/) CIVELLI O.

XX

XX (LINS/) LIN S.

XX

PI Civelli O, Lin S;

XX

DR WPI; 2002-403931/43.

XX

XX Screening for compounds useful for promoting wakefulness or sleep, and

PT for treating sleeping disorders, e.g. insomnia, hypersomnia or sleep

PT apnea, comprises administering a prolactin releasing peptide agonist or

PT antagonist.

XX

XX Example 2, Page 23; 35pp; English.

XX

CC The present invention relates to a method of screening for compounds for

CC promoting wakefulness or sleep in a mammal. The method involves

CC administering a prolactin releasing peptide (PRP) receptor (GPR10)

CC agonist or antagonist respectively and determining the ability of the

CC compound to promote wakefulness or sleep. The compounds identified from  
 CC the method are used in the therapy of epilepsy and other diseases  
 CC associated with absence seizures and in promoting wakefulness and sleep  
 CC in individuals having sleep disorders such as insomnia and narcolepsy.  
 CC PRP receptor agonists may be used to treat common disorders which lead  
 CC to sleepiness, e.g. sleep apnoea, narcolepsy, idiopathic hypersomnia and  
 CC psychogenic hypersomnia. PRP receptor antagonists are useful for  
 CC promoting sleep and for treating insomnia such as adjustment sleep  
 CC disorder and psychophysilogic insomnia. The present sequence is human  
 CC GPR10 mutant C-terminal peptide

XX Sequence 12 AA;

Query Match 33.3%; Score 32; DB 5; Length 12;  
 Best Local Similarity 60.0%; Pred. No. 1.6e+02;  
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 5 PHGYLLTAAV 14  
 ||| : |||  
 Db 1 PHGQNMVTAV 10

RESULT 28

AAW45125 standard; peptide; 16 AA.

XX AAW45125;

XX 28-APR-1998 (first entry)

XX Human cartilage glycoprotein 39 derived peptide #26.

XX Articular cartilage; immunosuppressive therapy; antigen; autoantigen;

XX immunological tolerance; T-cell; human cartilage glycoprotein 39;

XX HC gp-39; rheumatoid arthritis; epitope.

XX Synthetic.

XX Homo sapiens.

XX WO9740068-A1.

XX 30-OCT-1997.

XX 22-APR-1997; 97MO-EP002051.

XX 24-APR-1996; 96EP-00201106.

XX (ALKU ) AKZO NOBEL NV.

XX Boots AMH, Verheijden GFW;

XX WPI; 1997-535775/49.

XX Disclosure; Page 16; 82pp; English.

XX The present sequence represents a peptide which resembles or mimics an  
 CC epitope present on human cartilage glycoprotein 39 (HC gp-39), an  
 CC autoantigen in rheumatoid arthritis. The invention relates to peptides  
 CC consisting of 16-55 amino acid residues comprising at least one of the  
 CC following 19 sequences: LVCYVTSMS; FLCHHYS; IISPNIS; LKTLISVG;  
 CC FLSKPPPE; PDGLDLML; LYGRKQ; YDIKISQ; LDFISMTY; FISTMTDF;  
 CC FKGQDAS; YAVGIMRL; MTRGAPAS; LAYELCDF; LRGAVHRT; YLKORLAG;  
 CC LAGAVWML; VWALDLDF; or LDLDFFQS. They can be used medicially in antigen  
 CC specific immunosuppressive therapy, particularly the treatment of T-cell  
 CC mediated destruction of articular cartilage in autoimmune diseases (e.g.  
 CC rheumatoid arthritis). They can also be used to detect activated  
 CC autoreactive T cells in an individual. The peptides have a specific  
 CC effect on the autoreactive T cells, thus leaving the other components of  
 CC the immune system intact, unlike the non-specific suppressive effect of

CC immunosuppressive drugs, and do not cause toxic side effects. The  
 CC peptides are predominantly recognised by autoreactive T cells from  
 CC rheumatoid arthritis patients, but rarely by those from healthy donors

XX Sequence 16 AA;

Query Match 33.3%; Score 32; DB 2; Length 16;  
 Best Local Similarity 70.0%; Pred. No. 2.3e+02;  
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 9 LITAAVSPK 18  
 ||| : |||  
 Db 2 LLSAALSAGK 11

RESULT 29

AAU74686 standard; peptide; 9 AA.

XX AAU74686;

XX 09-APR-2002 (first entry)

XX Human cancer antigen ATP4/CREB-2 natural immunogenic ligand.

XX Human; cancer antigen; ATP4; CREB-2; vaccine; cytostatic;

XX immunogenic ligand; gene therapy; MHC; major histocompatibility complex;

XX adoptive immunotherapy; cancer; ovarian cancer.

XX Homo sapiens.

XX WO200192306-A2.

XX 06-DEC-2001.

XX 30-MAY-2001; 2001WO-US017454.

XX 31-MAY-2000; 2000US-0209388P.

XX PR 20-DEC-2000; 2000US-0257007P.

XX (GEN2 ) GENZYME CORP.

XX Nicolette CA;

XX WPI; 2002-097764/13.

XX Claim 6; Page 56; 68pp; English.

XX The invention relates to compounds comprising an immunogenic ligand whose  
 CC sequence is based in part on residues 42-50 of human cancer antigen  
 CC ATP4/CREB-2 (not defined) and the polynucleotides encoding them. Also  
 CC included are an antibody that specifically recognises and binds the  
 CC compound, a method for inducing an immune response in a subject by  
 CC delivering the compound, a method of immunotherapy comprising  
 CC administering to a subject the antibody, an immune effector cell that has  
 CC been raised in vitro or in vivo in the presence and at the expense of an  
 CC antigen presenting cell that presents the immunogenic compound in the  
 CC context of an MHC (major histocompatibility complex) molecule and a  
 CC method of adoptive immunotherapy comprising administering the immune  
 CC effector cell. The compounds are useful for modulating an immune response  
 CC to the synthetic and naturally occurring compounds. The compounds are  
 CC especially useful in gene therapy or as components of anti-cancer  
 CC vaccines. The compounds are useful for treating cancer, particularly  
 CC ovarian cancer. The compounds are also useful for generating antibodies  
 CC that specifically recognise and bind to these molecules. These antibodies  
 CC are further useful for immunotherapy when administered to a subject. The  
 CC peptides, polypeptides and polynucleotides are useful in diagnostic  
 CC methods, for the detection and purification of antibodies, or as  
 CC immunogens for the production of antibodies. The present sequence

CC represent a human cancer antigen ATP4/CREB-2 based immunogenic ligand of  
 CC the invention. Note: Immunogenic ligands AAU74681-AAU74686 are stated to  
 CC be encoded by the degenerate DNA sequences AAS20120-AAS20125 respectively  
 CC but have not been cross-referenced or CDS features put in due to the  
 CC degeneracy of the DNA sequences

XX Sequence 9 AA;

Query Match 32.3%; Score 31; DB 5; Length 9;  
 Best Local Similarity 66.7%; Pred. No. 2e+06;  
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PEPHGY 8  
 |||||  
 Db 3 FKPHGP 8

RESULT 30

ABR82211  
 ID ABR82211 standard; peptide; 9 AA.

XX ABR82211;

DT 13-OCT-2003 (first entry)

XX Human cancer antigen ATP4/CREB-2 epitope.

KW ATP4/CREB-2; neoplasia; cytosolic; cancer; antigen; human.

OS Homo sapiens.

PN W02003050307-A1.

PD 19-JUN-2003.

PF 05-DEC-2001; 2001WO-US048123.

PR 05-DEC-2001; 2001WO-US048123.

PA (GENZ ) GENZYME CORP.

PI Nicotinic CA;

DR WPI, 2003-532922/50.

DR N-PSDB; ACCB5028.

PT Aiding in the diagnosis of a neoplastic condition or susceptibility to a  
 PT neoplastic condition of an animal cell or tissue comprises determining an  
 PT amount of expression of an ATP4/CREB-2 protein in a test sample from the  
 PT cell or tissue.

XX Claim 6; Page 31; 81pp; English.

XX The invention relates to aiding in the diagnosis of a neoplastic  
 CC condition or susceptibility to a neoplastic condition of an animal cell  
 CC or tissue. The method involves determining an amount of expression of an  
 CC ATP4/CREB-2 protein in a test sample isolated from the cell or tissue,  
 CC and diagnosing a neoplastic condition or susceptibility to the neoplastic  
 CC condition based on the amount of expression of the ATP4/CREB-2 protein.  
 CC The method and kit are useful in detecting, diagnosing, prognosing,  
 CC treating and monitoring the progress of ATP4/CREB-2-related cancers and  
 CC malignancies. The method may also be used in screening agonists and  
 CC antagonists of cancer antigens associated with ATP4/CREB-2-related  
 CC cancers and malignancies. The present sequence represents a human cancer  
 CC antigen ATP4/CREB-2 peptide epitope

XX Sequence 9 AA;

Query Match 32.3%; Score 31; DB 7; Length 9;  
 Best Local Similarity 66.7%; Pred. No. 2e+06;  
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PEPHGY 8

Db |||||  
 3 FKPHGP 8

RESULT 31

AAV13274  
 ID AAV13274 standard; peptide; 15 AA.

XX AAV13274;

DT 21-JUN-1999 (first entry)

XX Naturally occurring variant of the glutenin epitope Y13221.

KW Gluten; variant; gliadin; glutenin; gluten-sensitive T-cell; vaccine;  
 KW gluten tolerance; gluten-sensitivity; celiac disease; CD; celiac sprue;  
 KW tropical sprue; childhood food allergy; dermatitis herpetiformis; DH.

OS Synthetic.

PN EP905518-A1.

PD 31-MAR-1999.

PF 23-SEP-1997; 97EP-00202909.

PR 23-SEP-1997; 97EP-00202909.

PA (ZIEK-) ACAD ZIEKENHUIS LEIDEN.

PA (VYLE-) RIJDSUNTIV LEIDEN.

PI Konig F, Van De Wal Y, Drijfhout JW, Kooy-Winkeljaar EMC;

DR WPI; 1999-192792/17.

PT New antigenic peptides of gluten and methods for isolating them, useful  
 PT as diagnostic agents and for treatment of gluten sensitivity i.e. Celiac  
 PT disease (CD).

PS Disclosure; Page 28; 58pp; English.

XX Peptides AAV13220-13343 represents gluten derived peptides, and their  
 CC variants. The specification describes a method to find and characterize  
 CC peptides that are recognized by an intestinally derived gluten-sensitive  
 CC T-cells. The method comprises establishing and contacting at least one  
 CC gluten-sensitive T-cell clone with a mixture of gluten-derived peptides,  
 CC and fractionating the mixture to select peptides that stimulate the  
 CC clonal cells from bioactive fractions. Peptides AAV13220 (gliadin derived  
 CC peptide) and AAV13221 (glutenin derived peptide) were identified using  
 CC these methods, and can be used in pharmaceuticals/medicines (vaccines)  
 CC for inducing tolerance to gluten, or to treat gluten-sensitivity, i.e.  
 CC celiac disease (CD) or celiac sprue, tropical sprue, childhood food  
 CC allergies and dermatitis herpetiformis (DH). The peptides are also useful  
 CC for elimination of a group of gluten-sensitive T-cells, and for  
 CC generating antibodies, T-cell receptors, anti-idiotypic B- or T-cells by  
 CC immunization of a mammal with the peptide

XX Sequence 15 AA;

Query Match 32.3%; Score 31; DB 2; Length 15;  
 Best Local Similarity 50.0%; Pred. No. 3.2e+02;  
 Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 7 GYLTLTAIVSPGX 18  
 |||||  
 Db 4 GYPTSAQPRQ 15

RESULT 32

ADK40482  
 ID ADK40482 standard; peptide; 18 AA.

AC ADK40482;

XX 06-MAY-2004 (first entry)  
 DT KDR & VEGF/KDR complex binding peptide of the TN12 peptide library ID133.  
 XX  
 XX endotheelial cell; vacular endotheelial growth factor; VEGF;  
 XX receptor tyrosine kinase; VEGF-2; kinase domain region; KDR;  
 XX foetal liver kinase-1; flk-1; VEGF/KDR complex; angiogenesis;  
 XX neoplastic tumour; radiotherapeutic; malaria; HIV; SIV infection;  
 XX simian haemorrhagic fever virus;  
 XX enterohaemorrhagic Escherichia coli infection; protozoacidal; anti-HIV;  
 XX virucidal; antibacterial; cytostatic.  
 XX  
 OS Synthetic.  
 XX  
 XX WO2003074005-A2.  
 XX  
 XX 12-SEP-2003.  
 XX  
 XX 03-MAR-2003; 2003WO-US006731.  
 XX  
 XX 01-MAR-2002; 2002US-0360851P.  
 XX 15-JAN-2003; 2003US-0440411P.  
 XX  
 XX (DYAX-) DYAX CORP.  
 XX (BRAC) BRACCO INT BV.  
 XX  
 XX Sato AK, Sexton DJ, Ladhner RC, Dransfield DT, Swenson RE;  
 XX Martineili ER, Ramalingam K, Nunn AD, Von Wronski MA, Shrivastava A,  
 XX Pochon S, Bussat P, Arbogast C, Pillai R, Fan H, Linder KE, Song B;  
 XX Nanjappan P;  
 XX  
 XX WPI; 2003-779009/73.  
 XX  
 PT New polypeptide that binds to vacular endotheelial growth factor receptor  
 PT -2, usefull for diagnosis and treatment of e.g. tumors, and its conjugates  
 PT with therapeutic or imaging agents.  
 XX  
 XX Claim 79; SEQ ID NO 133; 350pp; English.  
 XX  
 CC This invention relates to novel peptides useful for detecting and  
 CC targeting primary receptors on endotheelial cells that bind vacular  
 CC endotheelial growth factor (VEGF). Specifically, it refers to detecting  
 CC the receptor tyrosine kinase identified as VEGF-2, which is also known as  
 CC kinase domain region (KDR) and foetal liver kinase-1 (flk-1). The present  
 CC invention describes the involvement of the VEGF/KDR complex as important  
 CC in angiogenesis, and that VEGF/KDR complex binding or KDR binding  
 CC polypeptides can be used for imaging neoplastic tumours. Furthermore,  
 CC these compositions are usefull for targeting radiotherapeutics to specific  
 CC sites for treating diseases associated with KDR activation, which include  
 CC malaria, HIV, SIV infection, simian haemorrhagic fever virus and  
 CC enterohaemorrhagic Escherichia coli infection. Accordingly, these  
 CC compositions exhibit various activities including protozoacidal, anti-  
 CC HIV, virucidal, antibacterial and cytostatic. This peptide sequence is a  
 CC high affinity binding peptide of KDR and the VEGF/KDR complex, part of  
 CC the TN12 peptide library of the invention.  
 XX  
 XX Sequence 18 AA;  
 SQ  
 Query Match 32.3%; Score 31; DB 7; Length 18;  
 Best Local Similarity 55.6%; Pred. No. 4e+02;  
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

XX 21-OCT-2004 (first entry)  
 DT Cyclic KDR/ VEGF binding peptide of the secondary TN12 library Seq 133.  
 XX  
 XX  
 XX kinase domain region; KDR; vacular endotheelial growth factor; VEGF;  
 XX VEGF receptor 2; VEGFR2; foetal liver kinase 1; flk-1; angiogenesis;  
 XX neoplastic tumour; malaria; HIV infection; SIV infection;  
 XX simian haemorrhagic fever virus infection;  
 XX enterohaemorrhagic Escherichia coli infection; cytostatic;  
 XX antiangiogenic; antimalarial; anti-HIV; virucidal; antibacterial;  
 XX TN12 library; cyclic.  
 XX  
 OS Synthetic.  
 XX  
 XX  
 XX Key Location/Qualifiers  
 XX Disulfide-bond 4..15  
 XX  
 XX WO2004065621-A1.  
 XX  
 XX 05-AUG-2004.  
 XX  
 XX 11-SEP-2003; 2003WO-US028787.  
 XX  
 XX 15-JAN-2003; 2003US-0440411P.  
 XX 03-MAR-2003; 2003US-00382082.  
 XX 03-MAR-2003; 2003WO-US006731.  
 XX  
 XX (DYAX-) DYAX CORP.  
 XX (BRAC) BRACCO INT BV.  
 XX  
 XX Sato AK, Sexton DJ, Dransfield DT, Ladhner RC, Arbogast C;  
 XX Bussat P, Fan H, Kourana S, Linder KE, Martineili ER, Nanjappan P;  
 XX Nunn AD, Pillai R, Pochon S, Ramalingam K, Shrivastava A, Song B;  
 XX Swenson RE, Von Wronski MA;  
 XX  
 XX WPI; 2004-580734/56.  
 XX  
 PT Novel isolated polypeptide having ability to bind to kinase domain region  
 PT or vacular endotheelial growth factor/kinase domain region complex,  
 PT usefull in inhibiting vacular endotheelial growth factor activation of  
 PT kinase domain region.  
 XX  
 XX Claim 11; SEQ ID NO 133; 470pp; English.  
 XX  
 CC This invention relates to novel isolated peptides that can bind to a  
 CC kinase domain region (KDR) or vacular endotheelial growth factor  
 CC (VEGF)/KDR complex. Specifically, it refers to polypeptides, peptide  
 CC dimers and multimeric complexes that bind with high affinity to KDR (also  
 CC known as the VEGF receptor 2 (VEGFR2) and foetal liver kinase 1 (flk-1))  
 CC or the VEGF/KDR complex, and as such due to the involvement of VEGF and  
 CC KDR in angiogenesis these binding peptides can be used for imaging  
 CC important sites of angiogenesis, as well as in targeting therapeutics to  
 CC such sites. The present invention describes these peptides as usefull for  
 CC promoting or inhibiting angiogenesis and pathogenic conditions associated  
 CC thereof such as neoplastic tumours. Furthermore, these binding peptides  
 CC are usefull for treating malaria, HIV infection, SIV infection, simian  
 CC haemorrhagic fever virus infection and enterohaemorrhagic Escherichia  
 CC coli infection. Accordingly, they exhibit cytostatic, antiangiogenic,  
 CC antimalarial, anti-HIV, virucidal and antibacterial activities. In  
 CC particular, they inhibit VEGF activation of its receptor (i.e. KDR), and  
 CC enable efficient detection, imaging and localisation of activated  
 CC endotheelial cells exhibiting upregulated KDR expression. This peptide  
 CC sequence is a high affinity KDR and VEGF/KDR cyclic binding peptide  
 CC belonging to the secondary TN12 library of the invention.  
 XX  
 XX Sequence 18 AA;  
 SQ  
 Query Match 32.3%; Score 31; DB 8; Length 18;  
 Best Local Similarity 55.6%; Pred. No. 4e+02;  
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;



PN US2005085630-A1.  
 PD 21-APR-2005.  
 XX  
 XX 16-OCT-2003; 2003US-00687297.  
 PF  
 XX 16-OCT-2003; 2003US-00687297.  
 PR  
 XX (AMBE-) AMBERGEN INC.  
 PA  
 XX Olejnik J, Rothschild KJ;  
 PI  
 XX WPI; 2005-314004/32.  
 DR PIR; A42912.  
 XX  
 PT Photocleavable compound useful to detect and isolate component e.g.  
 PT protein from biological sample comprises affinity moiety attached via  
 PT linker to photoreactive group, which in turn attached via second linker  
 PT to protein reactive group.  
 XX  
 XX Disclosure; SEQ ID NO 63; 86pp; English.  
 PS  
 CC The invention relates to photocleavable isotope-coded affinity tags which  
 CC can be used to detect and isolate target proteins and protein fragments  
 CC from biological samples. The photocleavable isotope-coded affinity tags  
 CC comprise an affinity capable of binding to a capture reagent attached via  
 CC a first linker to a photoreactive group, which is in turn attached via a  
 CC second linker labeled with one or more stable isotopes to a protein.  
 CC reactive group which reacts with functional groups on polypeptides. The  
 CC invention also relates to methods of preparing the photocleavable  
 CC affinity tags, and to a method of providing information about a mixture  
 CC of proteins. This method comprises conjugating photocleavable affinity  
 CC tags to the proteins, subjecting these protein conjugates to proteolysis  
 CC to yield affinity tagged peptides, capturing these affinity tagged  
 CC peptides on a solid support, and releasing the peptides by exposing the  
 CC affinity tagged peptides to electromagnetic radiation to cleave the  
 CC photocleavable group of the tag. The method optionally further involves  
 CC analyzing the released peptides using mass spectrometry. The  
 CC photocleavable affinity tags of the invention can be used to detect and  
 CC isolate target components, especially polypeptides, from heterogeneous  
 CC mixtures such as biological samples, proteinaceous compositions, nucleic  
 CC acids, biomass, cell cultures, cellular extracts, vesicles or in vivo  
 CC sources. The target components that can be isolated include immune system  
 CC modulators, cytokines, agents of the hematopoietic system, proteins,  
 CC nucleic acid, hormones, gene products, antigens, cells, toxins, bacteria,  
 CC membrane vesicles, virus particles or combinations of the above. The tags  
 CC may be used to screen for changes in the expression or state  
 CC of enzymatic activity of specific proteins, or to implement a variety of  
 CC clinical and diagnostic analyses to detect the presence, absence,  
 CC deficiency or excess of a given protein or protein function in a  
 CC biological fluid (e.g. blood) or in cells or tissues. For example, they  
 CC can be used for the detection of disorders such as bacterial, viral or  
 CC parasitic infections, genetic disorders (e.g., enzyme overproduction or  
 CC deficiency), or neoplasias (e.g., tumors) in a sample from a patient.  
 CC Additionally, the photocleavable tags are envisaged for use in the  
 CC controlled release of a therapeutic agent at a selected site for the  
 CC treatment of the above disorders. Use of the photocleavable affinity tag  
 CC in protein analysis is rapid and efficient, and proteins can be isolated  
 CC and identified without the interference of steric hindrance and other  
 CC prior art problems before down-stream analysis and processing. Sequences  
 CC AD225576-AD225580 represent peptide sequences identified from database searches as  
 CC the top 5 matches for a peptide AD225581 whose mass spectrum was  
 CC determined in an illustration of the invention.  
 XX  
 XX Sequence 20 AA;  
 SQ  
 Query Match 32.3%; Score 31; DB 9; Length 20;  
 Best Local Similarity 54.5%; Pred. No. 4.6e+02;  
 Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 DAFEPHGVLIT 11  
 DB 8 DAFEPHGQFVT 18

RESULT 37  
 AD268008  
 ID AD268008 standard; peptide; 20 AA.  
 XX  
 XX AD268008;  
 AC  
 XX  
 DT 14-UTL-2005 (first entry)  
 XX  
 DE Peptide fragment.  
 XX  
 KM Protein purification.  
 XX  
 OS Unidentified.  
 XX  
 PN WO2005037210-A2.  
 XX  
 PD 28-APR-2005.  
 XX  
 XX 14-OCT-2004; 2004WO-US033819.  
 PF  
 XX 16-OCT-2003; 2003US-00687297.  
 PR  
 XX (AMBE-) AMBERGEN INC.  
 PA  
 XX Olejnik J, Rothschild KJ;  
 PI  
 XX WPI; 2005-333195/34.  
 DR  
 XX  
 PT New photocleavable isotope-coded tag used to detect and isolate target  
 PT components from complex mixtures e.g. cells.  
 XX  
 PS Disclosure; SEQ ID NO 63; 241pp; English.  
 XX  
 CC The invention relates to agents and conjugates that can be used to detect  
 CC and isolate target components from complex mixtures such as proteins and  
 CC protein fragments from biological samples from in vivo and in vitro  
 CC sources. The agents comprise a detectable group bound to a photoreactive  
 CC group. The conjugates comprise agents coupled to substrates by covalent  
 CC bonds which can be selectively cleaved with the administration of  
 CC electromagnetic radiation. Target substances labeled with detectable  
 CC molecules can be easily identified and separated from a heterogeneous  
 CC mixture of substances. Exposure of the conjugate to radiation releases  
 CC the target in a functional form and completely unaltered. Using  
 CC photocleavable molecular precursors as the conjugates, labels can be  
 CC incorporated into macromolecules, the nascent macromolecules isolated and  
 CC the label completely removed. The invention also relates to targets  
 CC isolated with these conjugates which may be useful as pharmaceutical  
 CC agents or compositions that can be administered to humans and other  
 CC mammals. The present sequence is of a peptide fragment that was used to  
 CC identify a glyceraldehyde-3-phosphate dehydrogenase peptide fragment  
 CC AD268005 identified by the method of the invention.  
 XX  
 XX Sequence 20 AA;  
 SQ  
 Query Match 32.3%; Score 31; DB 9; Length 20;  
 Best Local Similarity 54.5%; Pred. No. 4.6e+02;  
 Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 DAFEPHGVLIT 11  
 DB 8 DAFEPHGQFVT 18  
 RESULT 38  
 AAG62667  
 ID AAG62667 standard; peptide; 11 AA.  
 XX  
 AC AAG62667;  
 XX  
 DT 17-SBP-2001 (first entry)  
 XX



PR 07-JUN-1995; 95US-00478326.  
 PR 10-APR-1996; 96US-00630645.  
 PR 12-DEC-1996; 96US-00766596.  
 XX  
 PA (UNYNY ) UNIV NEW YORK STATE.  
 PI Soto-Jara C, Baumann MH, Frangione B;  
 XX WPI; 2003-616149/58.  
 DR  
 XX  
 PT New inhibitory peptide, useful for preparing a composition for  
 PT diagnosing, preventing or treating disorders associated with amyloid-like  
 PT fibril deposits, e.g. Alzheimer's disease, or prion related  
 PT encephalopathies.  
 XX  
 PS Example 1; Page 28; 52pp; English.  
 XX  
 CC The invention relates to inhibitory peptide comprising a portion of at  
 CC least three amino acid residues and a sequence predicted not to adopt a  
 CC beta-sheet structure that associates with a hydrophobic beta-sheet  
 CC cluster on a protein or peptide involved in the abnormal folding into a  
 CC beta-sheet structure, to structurally block the abnormal folding of the  
 CC protein or peptide. The inhibitory peptide is useful for preparing a  
 CC composition for preventing, treating or detecting disorders or diseases  
 CC associated with amyloid-like fibril deposits e.g. Alzheimer's disease and  
 CC prion related encephalopathies. The invention is also useful in gene  
 CC therapy. The present sequence is a control peptide used in the invention  
 CC  
 SQ Sequence 11 AA;  
 Query Match 31.2%; Score 30; DB 7; Length 11;  
 Best Local Similarity 63.6%; Pred. No. 3.3e+02;  
 Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 OY 7 GYLTAAVSPG 17  
 DB 1 GYLTAAVFRG 11  
 RESULT 41  
 AAE26397  
 ID AAE26397 standard; peptide; 12 AA.  
 XX  
 AC AAE26397;  
 XX  
 DT 13-DEC-2002 (first entry)  
 XX  
 DE Human GPR10 mutant C-terminal peptide, V369A.  
 XX  
 XX Human; wakefulness; sleep disorder; prolactin releasing peptide receptor;  
 KM P-PRP; GPR10; therapy; epilepsy; narcolepsy; sleepiness; sleep apnoea;  
 KM insomnia; idiopathic hypersomnia; psychogenic hypersomnia; seizure;  
 KM anticonvulsant; mutant; mutain.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 OS  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 11  
 FT /note= "Wild-type Val substituted with Ala; this position  
 FT corresponds to position 369 of the wild-type protein"  
 XX  
 PN US2002037533-A1.  
 XX  
 PD 28-MAR-2002.  
 XX  
 PF 17-AUG-2001; 2001US-00932161.  
 XX  
 PR 28-APR-2000; 2000US-00560915.  
 XX  
 PA (CIVE/) CIVELLI O.  
 PA (LINS/) LIN S.  
 XX

PI Civelli O, Lin S;  
 XX WPI; 2002-403931/43.  
 DR  
 XX  
 PT Screening for compounds useful for promoting wakefulness or sleep, and  
 PT for treating sleeping disorders, e.g. insomnia, hypersomnia or sleep  
 PT apnea, comprises administering a prolactin releasing peptide agonist or  
 PT antagonist.  
 XX  
 PS Example 2; Page 23; 35pp; English.  
 XX  
 CC The present invention relates to a method of screening for compounds for  
 CC promoting wakefulness or sleep in a mammal. The method involves  
 CC administering a prolactin releasing peptide (PrRP) receptor (GPR10)  
 CC agonist or antagonist respectively and determining the ability of the  
 CC compound to promote wakefulness or sleep. The compounds identified from  
 CC the method are used in the therapy of epilepsy and other diseases  
 CC associated with absence seizures and in promoting wakefulness and sleep  
 CC in individuals having sleep disorders such as insomnia and narcolepsy.  
 CC PrRP receptor agonists may be used to treat common disorders which lead  
 CC to sleepiness, e.g. sleep apnoea, narcolepsy, idiopathic hypersomnia and  
 CC psychogenic hypersomnia. PrRP receptor antagonists are useful for  
 CC promoting sleep and for treating insomnia such as adjustment sleep  
 CC disorder and psychophysilogic insomnia. The present sequence is human  
 CC GPR10 mutant C-terminal peptide  
 XX  
 SQ Sequence 12 AA;  
 Query Match 31.2%; Score 30; DB 5; Length 12;  
 Best Local Similarity 45.5%; Pred. No. 3.7e+02;  
 Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;  
 OY 5 PHGYLTAAVS 15  
 DB 1 PHGQNMVTSVA 11  
 RESULT 42  
 ADU04328  
 ID ADU04328 standard; peptide; 14 AA.  
 XX  
 AC ADU04328;  
 XX  
 DT 13-JAN-2005 (first entry)  
 XX  
 DE Human immunoglobulin light chain (IgVL) FRI peptide 12.  
 XX  
 XX viral infection; virucide; autoimmune disease;  
 KM lymphoproliferative disorder; vaccine; gene therapy; immunoglobulin;  
 KM antibody.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2004090544-A2.  
 XX  
 PD 21-OCT-2004.  
 XX  
 PF 13-APR-2004; 2004WO-CA000544.  
 XX  
 PR 09-APR-2003; 2003US-0461137P.  
 PR 30-SEP-2003; 2003US-0506779P.  
 XX  
 PA (CABL-) CANADIAN BLOOD SERVICES.  
 XX  
 PI Hu Y, Brown E;  
 PI  
 DR WPI; 2004-766498/75.  
 XX  
 PT Characterizing a viral infection in a host, for developing treatment for  
 PT severe acute respiratory syndrome-coronavirus (SARS-CoV), by determining  
 PT homology profile of a viral-based sequence element with an endogenous  
 PT host element.  
 XX



PS Example 1, Fig 5A, 16pp; English.

XX The invention relates to a novel method for characterizing a viral

CC infection in a host. The method comprises identifying at least one viral-

CC based sequence element in a biological sample obtained from the host,

CC determining a homology profile of the viral-based sequence element with

CC at least one endogenous host element and characterizing the viral

CC infection based on the homology profile, where the homology profile is

CC indicative of a viral behaviour of the viral infection in the host. The

CC method of the invention demonstrates virucide applications and may be

CC useful for preparing a medicament for detecting and/or treating a viral

CC infection or related condition, such as an autoimmune disease e.g. type

CC I cryoglobulinemia, or lymphoproliferative disorder. The viral

CC infection may be due to HCV (Hepatitis C virus), HIV or a member of a

CC Retroviridae, Flaviviridae, Herpesviridae, Papillomaviridae or

CC Coronaviridae virus family. Treatment of the infection may utilise

CC vaccine or gene therapy. The target compound of the invention may be

CC useful for detecting the presence of a virus in a biological sample or

CC for manufacturing a medicament for treating SARS coronavirus (SARS-CoV)

CC and/or Human T-lymphotropic virus 1 (HTLV-I) infection. The methods are

CC further useful for developing treatment regimes to target genotype-

CC specific viral variants. The current sequence is that of a human

CC immunoglobulin light chain (IgVL) FR peptide of the invention.

CC

XX Sequence 14 AA;

SO

Query Match 31.2%; Score 30; DB 8; Length 14;

Best Local Similarity 66.7%; Pred. No. 4.4e+02;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 10 LTAASPQK 18

Db 6 LTAATSPQK 14

RESULT 43

AA04059

ID AAR04059 standard; peptide; 19 AA.

AC AAR04059;

XX 17-MAR-1993 (first entry)

DT

XX Reagent of GTP-binding protein (14).

DE

XX G-protein; signal transducing protein; cell proliferation; cancer;

KW dementia; receptor; transmembrane.

KM

XX Synthetic.

OS

XX JP02069665-A.

PN

XX 08-MAR-1990.

PD

XX 06-SEP-1988; 88JP-00221446.

PF

XX 06-SEP-1988; 88JP-00221446.

PR

XX (NISHI/) NISHIMOTO I.

PA

XX WPI, 1990-119771/16.

DR

XX Reagent of GTP-binding protein - consists of polypeptide of less than 33

PT aminoacid residues where 4 are basic aminoacid residues, etc.

PT

XX Disclosure; Fig 1; 4pp; Japanese.

PS

XX A reagent for activating GTP-binding protein (G-protein) consists of a

CC polypeptide of less than 33 amino acids, of which more than 4 are basic,

CC and more than 20% are hydrophobic. The reagent is useful for the

CC purification, identification, functional examination, etc. of G-protein,

CC a signal transducing protein. It will be possible to study the mechanism

CC of cell proliferation, anticancer action, prevention of dementia, by

CC activating/inhibiting the G-protein, using the reagent. The peptides

CC given in AAR04048-59, AAR05848, AAR09313 and indicated in the Features

CC table bind selectively, activating the G-protein. The peptides have the

CC same config. as the part of the receptor which binds to G-protein and is

CC effective for the transmission of signal information into the cell. The

CC reagent can be used in the form of powder or soln. Affinity purification

CC can be simply carried out by using ion-exchange resin beads such as

CC Sepharose. For example, the reagent is stuck onto the beads and

CC homogenate is passed through a column packed with the beads to obtain a

CC given G-binding protein

CC

XX Sequence 19 AA;

SO

Query Match 31.2%; Score 30; DB 2; Length 19;

Best Local Similarity 54.5%; Pred. No. 6.4e+02;

Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 6 HGVLTAASP 16

Db 2 HGVEDAAVTP 12

RESULT 44

AA29388

ID AAY29388 standard; peptide; 20 AA.

AC AAY29388;

XX 01-OCT-1999 (first entry)

DT

XX Final 3D profile with myoglobin backbone structure peptide #22.

DE

XX Myoglobin; Mb; sperm whale; protein design; function; property;

KW stereo structure; globular protein; detection.

KM

XX Synthetic.

OS

XX Physeter sp.

PN

XX JP11193297-A.

PD

XX 21-JUL-1999.

PF

XX 06-OCT-1998; 98JP-00283852.

PR

XX 06-OCT-1997; 97JP-00272431.

PA

XX (RIKA ) RIKAGAKU KENKYUSHO.

XX

XX WPI, 1999-462430/39.

DR

XX Method for designing artificial protein - useful for producing proteins

PT with required functions.

PT

XX Example; Page 4; 10pp; Japanese.

PS

XX The present invention describes a method for producing an ideal amino

CC acid sequence. The method comprises: (1) preparation of one initial amino

CC acid sequence corresponding to the structure of a protein; (2) selecting

CC the amino acid residues optimal to each site; (3) repeating the steps of

CC selecting the amino acid residues optimum to each sites of the total

CC amino acid residues constituting the N-order amino acid sequence

CC integer not less than 2) to give an N+1-order amino acid sequence

CC consisting of the selected amino acid residues until the N-order amino

CC acid sequence comes to be same as the N+1-order amino acid sequence; and

CC (4) selecting the resultant N-order amino acid sequence as the optimum

CC amino acid sequence of said protein. The method can design a protein with

CC desired functions and properties. AAY29343 to AAY29367 represent peptides

CC used in an example from the present invention where the stereo structure

CC of sperm whale myoglobin was targeted as a globular protein to detect an

CC amino acid sequence best fit to the structure of the main chain of the

CC sperm whale myoglobin

XX

SO Sequence 20 AA;

Query Match 31.2%; Score 30; DB 2; Length 20;  
Best Local Similarity 80.0%; Pred. No. 6.8e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 PHGYL 9  
:||||:  
Db 10 PHGYM 14

RESULT 45  
ADU04264  
ID ADU04264 standard; peptide; 20 AA.  
XX  
AC ADU04264;  
XX

DT 13-JAN-2005 (first entry)  
XX

DE Human immunoglobulin light chain (IgVL) FR1 peptide 3.  
XX

KM viral infection; viraemia; autoimmune disease;  
KM lymphoproliferative disorder; vaccine; gene therapy; immunoglobulin,  
antibody.  
XX

OS Homo sapiens.  
XX

PN WO2004090544-A2.  
XX

PD 21-OCT-2004.  
XX

PF 13-APR-2004; 2004WO-CA000544.  
XX

PR 09-APR-2003; 2003US-0461137P.  
XX

PR 30-SEP-2003; 2003US-0506779P.  
XX

PA (CABL-) CANADIAN BLOOD SERVICES.  
XX

PI Hu Y, Brown E;  
XX

DR WPI; 2004-766498/75.  
XX

PT Characterizing a viral infection in a host, for developing treatment for  
severe acute respiratory syndrome-coronavirus (SARS-CoV), by determining  
PT host element.  
PT host element.

PS Example 1; Fig 1C; 166pp; English.  
XX

CC The invention relates to a novel method for characterizing a viral  
infection in a host. The method comprises identifying at least one viral-  
based sequence element in a biological sample obtained from the host,  
determining a homology profile of the viral-based sequence element with  
at least one endogenous host element and characterizing the viral  
infection based on the homology profile, where the homology profile is  
indicative of a viral behaviour of the viral infection in the host. The  
method of the invention demonstrates viraemia applications and may be  
useful for preparing a medicament for detecting and/or treating a viral  
infection or related condition, such as an autoimmune disease e.g. type  
II cryoglobulinaemia, or lymphoproliferative disorder. The viral  
infection may be due to HCV (Hepatitis C virus), HIV or a member of a  
CC Retroviridae, Flaviviridae, Herpesviridae, Papillomaviridae or  
Coronaviridae virus family. Treatment of the infection may utilize  
CC vaccine or gene therapy. The target compound of the invention may be  
useful for detecting the presence of a virus in a biological sample or  
for manufacturing a medicament for treating SARS coronavirus (SARS-CoV)  
and/or Human T-lymphotropic virus 1 (HTLV-1) infection. The methods are  
further useful for developing treatment regimes to target genotype-  
CC specific viral variants. The current sequence is that of a human  
immunoglobulin light chain (IgVL) FR1 peptide of the invention.

CC Sequence 20 AA;  
XX

Query Match 31.2%; Score 30; DB 8; Length 20;

Best Local Similarity 66.7%; Pred. No. 6.8e+02;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 10 LTRAVSPGK 18  
:||||:  
Db 9 LTRAVSPGQ 17

RESULT 46  
ADO37698  
ID ADO37698 standard; peptide; 6 AA.  
XX  
AC ADO37698;  
XX

DT 29-JUL-2004 (first entry)  
XX

DE Binding partner polypeptide of the invention SEQ ID NO: 758.  
XX

KM polypeptide-tagged collection; capture system; tagged polypeptide;  
KM pharmaceutical; diagnostic.  
XX

OS Synthetic.  
XX

PN WO2004039962-A2.  
XX

PD 13-MAY-2004.  
XX

PF 30-OCT-2003; 2003WO-US034821.  
XX

PR 30-OCT-2002; 2002US-0422923P.  
XX

PR 30-OCT-2002; 2002US-0423018P.  
XX

PA (POIN-) POINTILLISTE INC.  
XX

PI Aul-Riche D, Atkinson B, Geysen MH;  
XX

DR WPI; 2004-376185/35.  
XX

PT Evenly distributing tags among members of a starting library, useful in  
PT developing pharmaceuticals and diagnostics, comprises dividing the  
PT starting library into sub libraries and attaching a tag to members of  
each sub library.  
XX

PS Claim 14; SEQ ID NO 758; 510pp; English.  
XX

CC The invention relates to novel methods for producing polypeptide-tagged  
CC collections and capture systems containing the tagged polypeptides. The  
CC method is useful for evenly distributing tags among members of a starting  
CC library. The system, collection, kits and methods are useful in  
developing pharmaceuticals and diagnostics. The present sequence is used  
in the exemplification of the invention.

CC Sequence 6 AA;  
XX

Query Match 30.2%; Score 29; DB 8; Length 6;  
Best Local Similarity 80.0%; Pred. No. 2e+06;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 EPRGY 8  
:||||:  
Db 1 KPRGY 5

RESULT 47  
ADO28220  
ID ADO28220 standard; peptide; 6 AA.  
XX  
AC ADO28220;  
XX

DT 12-AUG-2004 (first entry)  
XX

DE Capture system related peptide, SEQ ID 758.  
XX

KM Capture system.  
 XX  
 OS Synthetic.  
 XX  
 PN WO2004042019-A2.  
 XX  
 PD 21-MAY-2004.  
 XX  
 PF 30-OCT-2003; 2003WO-US034693.  
 XX  
 PR 30-OCT-2002; 2002US-0422923P.  
 XX 30-OCT-2002; 2002US-0423018P.  
 PA (POIN-) POINTILLISTE INC.  
 PI Ault-Riche D, Atkinson B, Jesaitis L, Kumble KD, Sperinde G,  
 XX WPI; 2004-431543/40.  
 DR  
 XX  
 PT Capturing biological particles, by contacting biological particles with  
 PT capture system comprising addressed loci, addressed collection of  
 PT polypeptide tagged molecules, capture agents, and polypeptide tag to  
 PT which capture agent binds.  
 PS Disclosure; SEQ ID NO 758; 505bp; English.  
 XX  
 CC The present invention relates to a method for the capture and analysis of  
 CC biological particle using a capture system. The method is useful for  
 CC capturing biological particles such as cells, portions of cells, cell  
 CC membranes, viruses, viral capsids, viral particles, bacterial cells,  
 CC eukaryotic cells, intracellular particles, nuclei, cell membranes, cell  
 CC membrane fragments, nuclear membranes, nuclear membrane fragments, viral  
 CC vectors or viral capsids with or without packaged nucleic acid, phage,  
 CC phage vectors, phage capsids with or without encapsulated nucleotide  
 CC acid, liposomes and other micellar agents. The biological particles are  
 CC cells chosen from immune cells, neurons, cancer cells, bacterial cells  
 CC and infected cells, subcellular compartment, organelles, viral particles  
 CC or pathogens. The cells are dendritic cells, T cells, or B cells. The  
 CC method is also useful for identifying molecules that interact with  
 CC infectious agents, for profiling the surface of a biological particles,  
 CC for identifying a modulator of an interaction among proteins in the  
 CC biological particle, for identifying molecules that modulates the  
 CC trafficking, activity or functional or structural property in the  
 CC biological particle, and for mapping epitopes of molecules displayed on  
 CC the surface of a biological particles. The method is also useful for  
 CC sorting biological particles, for identifying a receptor on the surface  
 CC of biological particle that transduces a signal from a polypeptide, and  
 CC for identifying the molecule that interacts with an aptically-localized  
 CC molecule on a biological particle. The present sequence was used to  
 CC illustrate the invention.  
 XX  
 SQ Sequence 6 AA;  
 XX  
 Query Match 30.2%; Score 29; DB 8; Length 6;  
 Best Local Similarity 80.0%; Pred. No. 2e+06; 0; Indels 0; Gaps 0;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 EPHGY 8  
 :||||  
 :||||  
 Db 1 KPHGY 5  
 RESULT 48  
 ADS96043  
 ID ADS96043 standard; peptide; 6 AA.  
 XX  
 AC ADS96043;  
 XX  
 DT 18-NOV-2004 (first entry)  
 XX  
 DE 6-mer peptide epitope works as a highly specific capture agent Seq 758.  
 XX

KM self-assembly array; capture agent; epitope; binding partner.  
 XX  
 OS Synthetic.  
 XX  
 PN WO2004071641-A2.  
 XX  
 PD 26-AUG-2004.  
 XX  
 PF 30-OCT-2003; 2003WO-US034747.  
 XX  
 PR 10-FEB-2003; 2003US-0446687P.  
 XX  
 PA (POIN-) POINTILLISTE INC.  
 PA (AULT/) AULT-RICHE D.  
 PA (KOMB/) KUMBLE K D.  
 PA (SCHU/) SCHULZ R.  
 PA (SCHU/) SCHULZ K.  
 PI Ault-Riche D, Kumble KD, Schulz R, Schulz K;  
 XX WPI; 2004-635071/61.  
 DR  
 XX  
 PT Self-assembled array for monitoring interaction of molecules, comprising  
 PT addressable array of capture agents having predetermined binding partners  
 PT and conjugates comprising biological particle and/or molecule linked to  
 PT binding partners.  
 PS Disclosure; SEQ ID NO 758; 443bp; English.  
 XX  
 CC This invention relates to novel self-assembly arrays that each comprises  
 CC an addressable collection of capture agents that have predetermined  
 CC binding partners, as well as reagents for the covalent conjugation of the  
 CC binding partners to molecules for display in the array. Specifically, it  
 CC refers to the production of a flexible experimental surface, which can be  
 CC adapted for use with almost any analytical system. The present invention  
 CC describes apparatus useful for monitoring an interaction of an exogenous  
 CC molecule with a capture agent of the array both in the presence and  
 CC absence of candidate compounds, identifying molecules that modulate  
 CC trafficking in biological particles or modulate activity, functional or  
 CC structural properties of the biological particle. As such, it can be used  
 CC for elucidating biological pathways and their reactions that occur either  
 CC simultaneously or sequentially, disease processes, inhibitors and  
 CC enhancers of a molecular system or for understanding receptor-signal  
 CC recognition. In particular, it enables assaying one or more biological  
 CC samples having one or more targets per sample on a single array, such  
 CC that it is cost effective and specific. This peptide sequence is an  
 CC exemplary 6-mer peptide epitope that provides a highly specific capture  
 CC agent of the invention.  
 XX  
 SQ Sequence 6 AA;  
 XX  
 Query Match 30.2%; Score 29; DB 8; Length 6;  
 Best Local Similarity 80.0%; Pred. No. 2e+06;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 EPHGY 8  
 :||||  
 :||||  
 Db 1 KPHGY 5  
 RESULT 49  
 ADS96043  
 ID ADS96043 standard; peptide; 6 AA.  
 XX  
 AC ADS96043;  
 XX  
 DT 13-JAN-2005 (first entry)  
 XX  
 DE Tagged polypeptide-associated peptide #544.  
 XX  
 KM Peptide tag; epitope; antibody; single-chain antibody fragment; ScFv.  
 XX  
 OS Synthetic.

XX US2004209282-A1.  
 PN 21-OCT-2004.  
 PD 30-OCT-2003; 2003US-00699088.  
 XX 30-OCT-2002; 2002US-0422923P.  
 PR 30-OCT-2002; 2002US-0423018P.  
 PA (AULT/) AULT-RICHE D.  
 PA (ATKI/) ATKINSON B.  
 PI Ault-Riche D, Atkinson B;  
 DR WPI; 2004-756825/74.  
 XX  
 PT Evenly distributing tags among members of starting library by dividing  
 PT starting library into sublibraries, attaching tag to members of  
 PT sublibrary, mixing tagged sublibraries and splitting mixed library into  
 PT array libraries.  
 PS Disclosure; SEQ ID NO 758; 293pp; English.  
 XX  
 CC The invention relates to evenly distributing tags (e.g. epitopes) or  
 CC nucleic acid molecules encoding polypeptide tags among members of a  
 CC starting library, involving optionally adjusting the diversity of a  
 CC starting library so that the diversity is within an order of magnitude  
 CC of the number of molecules in the library, dividing the starting library  
 CC into n sublibraries designated 1-n, where n is equal to or less than the  
 CC number of unique tags (where each unique tag specifically binds to a  
 CC different capture agent), attaching a tag to several members of each  
 CC sublibrary to produce n tagged sublibraries containing tagged members  
 CC (where each member has the same tag, and the tag is unique to each  
 CC sublibrary), mixing some or all of the tagged sublibraries to produce a  
 CC mixed library (where the number of tagged molecules added from each  
 CC sublibrary is the same), and splitting the mixed library into q array  
 CC libraries, where q is from 1 up to a predetermined number of arrays. Also  
 CC included are a collection of tagged molecules produced by the method, a  
 CC capture system comprising the tagged polypeptides and an addressable  
 CC collection of capture agent (where each locus in the collection contains  
 CC capture agents that specifically bind to the same tag, and the tagged  
 CC molecules are specifically bound to capture agents), capturing molecules  
 CC (involving connecting a capture system with molecules under conditions,  
 CC where molecules bind to the capture system, and the capture system  
 CC comprises several of addressed loci with an addressed collection of  
 CC polypeptide-tagged molecules bound to addressed capture agents at each  
 CC locus, the capture agents at each locus bind to the same polypeptide tag,  
 CC the polypeptide tag to which the capture agent binds is different among  
 CC the loci, each locus in capture system contains a several of different  
 CC molecules, each with the same tag bound to the capture agents, and the  
 CC polypeptide tags are evenly distributed among the tagged molecules such  
 CC that the diversity of tagged molecules at each locus in the capture  
 CC system is within one order of magnitude), sorting molecules or reducing  
 CC their diversity, and reducing the diversity of a collection of molecules.  
 CC The starting library encodes antibodies (or their fragments or single-  
 CC chain antibody fragments (ScFvs)) or is comprised of antibodies (or their  
 CC fragments), where the antibodies or their fragments specifically bind to  
 CC antigens. The methods are useful for evenly distributing tags among  
 CC members of starting library, for identifying modulators of interactions  
 CC between capture systems and molecules (which involves adding/exposing a  
 CC test compound to the capture system to a condition before, during or  
 CC after contacting the capture system with molecules or before, during or  
 CC after contacting the capture system with the tagged molecules, and  
 CC identifying a change in an interaction of the molecules with the capture  
 CC system or tagged molecules with the capture agents to identify a test  
 CC compound that modulates the interaction between the molecules and the  
 CC capture system or between tagged molecules and capture agents. The change  
 CC is assessed by detecting a change in binding pattern or a physical or  
 CC chemical change in the bound molecules or a conformational change in the  
 CC bound molecules and/or tagged molecules). The present sequence is a  
 CC peptide included in the sequence listing but not mentioned anywhere else  
 CC in the specification.

XX SQ Sequence 6 AA;  
 Query Match 30.2%; Score 29; DB 8; Length 6;  
 Best Local Similarity 80.0%; Pred. No. 2e+06;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 EPHGY 8  
 :|||||  
 Db 1 KPHGY 5  
 :|||||  
 RESULT 50  
 AD246403  
 ID AD246403 standard; peptide; 6 AA.  
 XX  
 AC AD246403;  
 XX  
 DT 14-JUL-2005 (first entry)  
 XX  
 DE Antigenic peptide, SEQ ID NO: 721.  
 XX  
 KW Antigen; protein purification.  
 XX  
 OS Synthetic.  
 OS  
 PN US2005095648-A1.  
 XX  
 PD 05-MAY-2005.  
 XX  
 PF 22-MAR-2004; 2004US-00806924.  
 XX  
 PR 30-OCT-2003; 2003US-00699088.  
 PR 30-OCT-2003; 2003WO-US034821.  
 XX  
 PA (GEYS/) GEYSEN M.  
 PA (AULT/) AULT-RICHE D.  
 XX  
 PI Geysen M, Ault-Riche D;  
 XX  
 DR WPI; 2005-345019/35.  
 XX  
 CC Collection of antigenic polypeptides useful as binding partners for use  
 CC with capture agents, comprises three antigenic polypeptides that comprise  
 CC unique residues and include critical residues occupying N and C terminal  
 CC positions.  
 PT  
 PS Claim 22; SEQ ID NO 721; 196pp; English.  
 XX  
 CC The present invention relates to a collection (1) of antigenic  
 CC polypeptides (AD245683 - AD246593), which comprises at least three  
 CC antigenic polypeptides that comprise five to eight unique residues and  
 CC include at least four residues, designated critical residues, chosen from  
 CC Glu, Pro, Gln, Asn, Phe, His, Thr, Lys, Leu, Asp, where the critical  
 CC residues occupy the N and C terminal positions in each polypeptide, and  
 CC no more than three polypeptides in the collection contain the same four  
 CC critical residues. (1) is useful as binding partners for use with capture  
 CC agents which recognize the highly antigenic, highly specific  
 CC polypeptides.  
 CC  
 XX SQ Sequence 6 AA;  
 Query Match 30.2%; Score 29; DB 9; Length 6;  
 Best Local Similarity 80.0%; Pred. No. 2e+06;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 EPHGY 8  
 :|||||  
 Db 1 KPHGY 5  
 :|||||  
 RESULT 51  
 AB930513

ID ABB30513 standard; peptide; 6 AA.  
 AC ABB30513;  
 DT 06-OCT-2005 (first entry)  
 XX  
 DE Therapeutic complex associated antigenic peptide SEQ ID NO 721.  
 XX  
 KW immunomodulatory; cytostatic; antiinflammatory; antimicrobial;  
 KW neuroprotective; nootropic; ophthalmological; antirheumatic;  
 KW antiarthritic; virocidic; dermatological; immunomodulatory; therapeutic;  
 KW pharmacological; cancer; autoimmune disease; immunosuppressive; infection;  
 KW neurodegenerative disease; neuroprotective; neurological disease;  
 KW ophthalmological; ocular disease; non-hodgkin lymphoma;  
 KW hematological disease; rheumatoid arthritis; antiallergic;  
 KW antirheumatic; musculoskeletal disease; multiple sclerosis;  
 KW neuroprotective; immune disorder; neurological disease; melanoma;  
 KW cytostatic; neoplasm; inflammation; viral infection; virocidic; infection;  
 KW antigen.  
 XX  
 OS Synthetic.  
 XX  
 PN WO2005067980-A2.  
 PD  
 XX 28-JUL-2005.  
 XX  
 PF 10-JAN-2005; 2005WO-US000816.  
 XX  
 PR 12-JAN-2004; 2004US-0536184P.  
 PR 23-MAR-2004; 2004US-0557591P.  
 XX  
 XX (POIN-) POINTILLISTE INC.  
 PA  
 PI Aulc-Riche D, Levy R;  
 PT WPI; 2005-533851/54.  
 DR  
 XX  
 PT Complex for treating e.g. cancer, comprises a targeting domain  
 PT specifically binding to a subject-specific target and an effector  
 PT molecule rendering the complex biologically effective.  
 PT  
 PS Disclosure; SEQ ID NO 721; 403pp; English.  
 XX  
 CC The invention describes a therapeutic complex comprising a targeting  
 CC domain that specifically binds to a subject-specific target and an  
 CC effector molecule that renders the resulting therapeutic complex  
 CC biologically effective, where the targeting domain and effector molecule  
 CC are linked by a specific interaction of a binding partner and a capture  
 CC agent. Also described are: preparing (M1) (I) by contacting a targeting  
 CC domain and an effector molecule to form a complex; rendering an antibody  
 CC or fragment therapeutically effective; screening a target-specific  
 CC polypeptide therapeutically effective; screening test molecules to  
 CC identify effectors for use in (I); and screening test molecules to  
 CC identify targeting domains for use in (I). (I) is used to render an  
 CC antibody or its fragment or target specific polypeptide therapeutically  
 CC effective. (II) is used to treat a disease or condition, by administering  
 CC (II) which comprises a therapeutic complex designed for personalized  
 CC treatment. The disease is chosen from B cell-mediated disease, autoimmune  
 CC disease and T cell-mediated disease, cancers, inflammatory disease,  
 CC autoimmune disease, preferably non-Hodgkin's lymphoma, rheumatoid  
 CC ophthalmic disease, infectious disease, neurodegenerative disease and  
 CC arthritis, lupus, multiple sclerosis, melanoma, posterior intraocular  
 CC inflammation, pathogen and virus infection. The targeting domain and the  
 CC effector are administered as a complex, or administered sequentially,  
 CC simultaneously or intermittently. The targeting domain and effector are  
 CC administered separately and either one or more doses of the targeting  
 CC domain is(are) administered prior to administration of a therapeutic  
 CC complex also comprising the targeting domain, or one or more doses of the  
 CC effector prior is(are) administered prior to administration of a  
 CC therapeutic complex comprising the effector. This is the amino acid  
 CC sequence of an antigenic peptide used in the creation of a therapeutic  
 CC complex of the invention.

SO Sequence 6 AA;  
 Query Match 30.2%; Score 29; DB 9; Length 6;  
 Best Local Similarity 80.0%; Pred. No. 2e+06;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 BPHGY 8  
 DB 1 KPHGY 5  
 XX  
 RESULT 52  
 ID AAG80180 standard; peptide; 11 AA.  
 AC AAG80180;  
 XX  
 DT 21-JAN-2002 (first entry)  
 XX  
 DE HER-2 mimotope SEQ ID 5.  
 XX  
 KW Mimotope; HER-2; vaccine; cancer; antibody; tumor cell; cytostatic;  
 KW adenocarcinoma; gastrointestinal tract; prostate; breast;  
 KW multiple myeloma; B-lymphoproliferative post-transplant syndrome;  
 KW B-cell malignoma; chronic lymphatic leukemia.  
 XX  
 OS Unidentified.  
 XX  
 PN WO200178766-A1.  
 PD  
 XX 25-OCT-2001.  
 XX  
 PF 12-APR-2001; 2001WO-EP004251.  
 XX  
 PR 13-APR-2000; 2000DE-01018403.  
 PR 23-AUG-2000; 2000DE-01041342.  
 XX  
 PA (BIOL-) BIO LIFE SCI FORSCHUNGS & ENTWICKLUNGSGR.  
 PA  
 PI Zielinski C, Scheiner O, Jensen-Jarolim B, Breiteneder H;  
 PT WPI; 2002-017563/02.  
 DR  
 XX  
 PT Preparing vaccine against cancer, useful for treatment or prevention,  
 PT comprises coupling antibody mimetopes, selected from a phage-display  
 PT library, to macromolecular carrier.  
 PT  
 PS Example 2B; Page 27; 36pp; German.  
 XX  
 CC This invention describes a novel method for preparing a vaccine (A)  
 CC against cancer, comprising conjugating one or more mimetopes of an  
 CC antibody (Ab) to a macromolecular carrier (I). The mimetopes are selected  
 CC from a phage-display library using one or more autogenous or synthetic  
 CC antibodies that are directed against one or more Ag expressed  
 CC specifically on tumor cells. The products of the invention have  
 CC cytostatic activity. (A) is used to prevent, or treat, cancers,  
 CC particularly (adeno)carcinoma of the gastrointestinal tract, prostate or  
 CC breast, multiple myeloma; B-lymphoproliferative post-transplant syndrome,  
 CC B-cell malignoma, and chronic lymphatic leukemia. (A) can be produced  
 CC even when the nature of Ag is not known; are free of phages and  
 CC endotoxins (so well suited for use in humans) and provide active  
 CC immunization before tumors have developed. AAG80176-AAG80182 represent  
 CC peptide mimetopes used to illustrate the method of the invention  
 CC  
 SO Sequence 11 AA;  
 Query Match 30.2%; Score 29; DB 5; Length 11;  
 Best Local Similarity 71.4%; Pred. No. 4.9e+02;  
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 DAFPHG 7  
 DB 4 DPFPHG 10

RESULT 53  
ADJ67980 standard; peptide; 11 AA.  
XX  
AC ADJ67980;  
XX  
DT 20-MAY-2004 (first entry)  
XX  
DE T. thermophilus holB primer peptide #4.  
XX  
KM DNA polymerase; DNA sequencing; DNA amplification.  
XX  
OS Thermus thermophilus.  
XX  
PN US2004038289-A1.  
XX  
PD 26-FEB-2004.  
XX  
PF 25-SEP-2003; 2003US-00671403.  
XX  
PR 08-APR-1997; 97US-0043202P.  
PR 08-APR-1998; 98US-00057416.  
PR 18-AUG-2000; 2000US-00642218.  
PR 21-NOV-2000; 2000US-00716964.  
XX  
PA (ODON/) O'DONNELL M E.  
PA (YUZH/) YUZHAKOV A.  
PA (YURI/) YURIEVA O.  
PA (JERU/) JERUZALMI D.  
PA (BRUC/) BRUCK I.  
PA (KURI/) KURIYAN J.  
XX  
PI O'donnell ME, Yuzhakov A, Yurleva O, Jeruzalmi D, Bruck I;  
PI Kuriyan J;  
XX  
DR WPI; 2004-203218/19.  
DR N-PSDB; ADJ67979.  
XX  
XX  
PT Isolated DNA molecule from Bacillus stearothermophilus encoding a delta  
PT subunit of a DNA polymerase I mul-type, useful for producing DNA  
PT polymerases for use in DNA sequencing and DNA amplification methods.  
XX  
PS Example 14; SEQ ID NO 210; 245pp; English.  
XX  
CC The invention relates to an isolated DNA molecule from Bacillus  
CC stearothermophilus encoding a delta subunit of a DNA polymerase I. The  
CC subunits are useful for producing DNA polymerases for use in DNA  
CC sequencing and DNA amplification methods. The present sequence is used in  
CC the exemplification of the present invention.  
XX  
SQ Sequence 11 AA;  
XX  
Query Match 30.2%; Score 29; DB 8; Length 11;  
Best Local Similarity 100.0%; Pred. No. 4.9e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 6 HGTYL 10  
DB 7 HGTYL 11  
XX  
RESULT 54  
ADJ68192 standard; peptide; 11 AA.  
XX  
ID ADJ68192 standard; peptide; 11 AA.  
XX  
AC ADJ68192;  
XX  
DT 20-MAY-2004 (first entry)  
XX  
XX T. thermophilus holB primer peptide #4.  
XX

KM DNA polymerase; DNA sequencing; DNA amplification.  
XX  
OS Thermus thermophilus.  
XX  
PN US2004038290-A1.  
XX  
PD 26-FEB-2004.  
XX  
PF 25-SEP-2003; 2003US-00671419.  
XX  
PR 08-APR-1997; 97US-0043202P.  
PR 08-APR-1998; 98US-00057416.  
PR 18-AUG-2000; 2000US-00642218.  
PR 21-NOV-2000; 2000US-00716964.  
XX  
PA (ODON/) O'DONNELL M E.  
PA (YUZH/) YUZHAKOV A.  
PA (YURI/) YURIEVA O.  
PA (JERU/) JERUZALMI D.  
PA (BRUC/) BRUCK I.  
PA (KURI/) KURIYAN J.  
XX  
XX O'donnell ME, Yuzhakov A, Yurleva O, Jeruzalmi D, Bruck I;  
PI Kuriyan J;  
XX  
DR WPI; 2004-203219/19.  
DR N-PSDB; ADJ68191.  
XX  
XX  
PT Novel DNA molecule from Thermotoga species encoding delta prime subunit  
PT of DNA polymerase III-type enzyme, useful for producing the enzyme by  
PT recombinant techniques.  
XX  
PS Example 14; SEQ ID NO 210; 245pp; English.  
XX  
CC The invention relates to an isolated DNA molecule from Bacillus  
CC stearothermophilus encoding a delta subunit of a DNA polymerase I. The  
CC subunits are useful for producing DNA polymerases for use in DNA  
CC sequencing and DNA amplification methods. The present sequence is used in  
CC the exemplification of the present invention.  
XX  
SQ Sequence 11 AA;  
XX  
Query Match 30.2%; Score 29; DB 8; Length 11;  
Best Local Similarity 100.0%; Pred. No. 4.9e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 6 HGTYL 10  
DB 7 HGTYL 11  
XX  
RESULT 55  
ADK01270 standard; peptide; 11 AA.  
XX  
ID ADK01270 standard; peptide; 11 AA.  
XX  
AC ADK01270;  
XX  
DT 20-MAY-2004 (first entry)  
XX  
XX DNA polymerase III-type enzyme subunit peptide fragment #25.  
DE DNA polymerase III delta subunit; chromosomal replicase;  
KM DNA polymerase III; enzyme.  
XX  
OS Synthetic.  
XX  
PN US2004043415-A1.  
XX  
PD 04-MAR-2004.  
XX  
PF 25-SEP-2003; 2003US-00671134.  
PR 08-APR-1997; 97US-0043202P.  
XX

PR 08-APR-1998; 98US-00057416.  
PR 18-AUG-2000; 2000US-00642218.  
PR 21-NOV-2000; 2000US-00716964.  
XX  
PA (ODON/) O'DONNELL M E.  
PA (YUZH/) YUZHAKOV A.  
PA (YURI/) YURIEVA O.  
PA (JERU/) JERUZALMI D.  
PA (BRUC/) BRUCK I.  
PA (KURI/) KURIYAN J.  
XX  
PI O'donnelli ME, Yuzhakov A, Yurieva O, Jeruzalmi D, Bruck I;  
PI Kuriyan J;  
XX  
DR WPI; 2004-225698/21.  
XX  
PT New holB DNA molecule derived from an Aquifex species, encoding a delta  
PT prime subunit of a DNA polymerase III-type enzyme, useful for amplifying  
PT or sequencing nucleic acid molecules.  
XX  
PS Example 14; SEQ ID NO 210; 245bp; English.  
XX  
CC The invention relates to an isolated DNA molecule from an Aquifex species  
CC encoding a delta subunit of a DNA polymerase III-type enzyme. The delta  
CC subunit encoded by the DNA molecule is useful as part of a thermostable  
CC DNA polymerase III enzyme complex useful in amplifying or sequencing a  
CC nucleic acid molecule. The polymerase is especially useful as a  
CC chromosomal replicase. This sequence represents a DNA polymerase III-type  
CC enzyme subunit peptide fragment of the invention.  
XX  
SQ Sequence 11 AA;

Query March 30.2%; Score 29; DB 8; Length 11;  
Best Local Similarity 100.0%; Pred. No. 4.9e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 6 HGYYL 10  
Db 7 HGYYL 11

RESULT 56  
ADJ79489  
ID ADJ79489 standard; peptide; 11 AA.  
XX  
AC ADJ79489;  
XX  
DT 20-MAY-2004 (first entry)  
XX  
DE T. thermophilus holB primer peptide #4.  
XX  
KW DNA polymerase; DNA sequencing; DNA amplification.  
XX  
OS Thermus thermophilus.  
XX  
PN US2004043414-A1.  
XX  
PD 04-MAR-2004.  
XX  
PF 25-SEP-2003; 2003US-00670844.  
XX  
PR 08-APR-1997; 97US-0043202P.  
PR 08-APR-1998; 98US-00057416.  
PR 18-AUG-2000; 2000US-00642218.  
PR 21-NOV-2000; 2000US-00716964.  
XX  
PA (ODON/) O'DONNELL M E.  
PA (YUZH/) YUZHAKOV A.  
PA (YURI/) YURIEVA O.  
PA (JERU/) JERUZALMI D.  
PA (BRUC/) BRUCK I.  
PA (KURI/) KURIYAN J.  
XX

PI O'donnelli ME, Yuzhakov A, Yurieva O, Jeruzalmi D, Bruck I;  
PI Kuriyan J;  
XX  
DR WPI; 2004-225698/21.  
DR N-PSDB; ADJ79488.  
XX  
PT Novel isolated DNA molecule from Bacillus stearothermophilus, encoding  
PT tau subunit of DNA polymerase III-type enzyme, useful in amplification  
PT and sequencing reactions.  
XX  
PS Example 14; SEQ ID NO 210; 245bp; English.  
XX  
CC The invention relates to an isolated DNA molecule from Bacillus  
CC stearothermophilus encoding a delta subunit of a DNA polymerase I. The  
CC subunits are useful for producing DNA polymerases for use in DNA  
CC sequencing and DNA amplification methods. The present sequence is used in  
CC the exemplification of the present invention.  
XX  
SQ Sequence 11 AA;

Query Match 30.2%; Score 29; DB 8; Length 11;  
Best Local Similarity 100.0%; Pred. No. 4.9e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 6 HGYYL 10  
Db 7 HGYYL 11

RESULT 57  
ADJ84929  
ID ADJ84929 standard; peptide; 11 AA.  
XX  
AC ADJ84929;  
XX  
DT 03-JUN-2004 (first entry)  
XX  
DE Bacterial DNA polymerase III-associated peptide #5.  
XX  
KW DNA polymerase III; DNA pol III; thermophilic bacteria;  
KW polymerase chain reaction; PCR; thermostable polymerase; DNA sequencing;  
KW dnaX; holA; holB; dnaB; dnaN; dnaQ; dnaB; ssb.  
XX  
OS Unidentified.  
XX  
PN US2004048309-A1.  
XX  
PD 11-MAR-2004.  
XX  
PF 26-SEP-2003; 2003US-00673098.  
XX  
PR 08-APR-1997; 97US-0043202P.  
PR 08-APR-1998; 98US-00057416.  
PR 18-AUG-2000; 2000US-00642218.  
PR 21-NOV-2000; 2000US-00716964.  
XX  
PA (ODON/) O'DONNELL M E.  
PA (YUZH/) YUZHAKOV A.  
PA (YURI/) YURIEVA O.  
PA (JERU/) JERUZALMI D.  
PA (BRUC/) BRUCK I.  
PA (KURI/) KURIYAN J.  
XX  
PI O'donnelli ME, Yuzhakov A, Yurieva O, Jeruzalmi D, Bruck I;  
PI Kuriyan J;  
XX  
DR WPI; 2004-238491/22.  
XX  
PT Novel isolated Thermotoga delta primer subunit of DNA polymerase III-type  
PT enzyme, useful for amplifying and sequencing DNA molecule by polymerase  
PT chain reaction.  
XX  
PS Disclosure; SEQ ID NO 210; 235bp; English.

XX The invention relates to an isolated Thermotoga delta' (prime) subunit of  
CC a DNA polymerase III-type (polIII) enzyme appearing as ADJ84867, encoded  
CC by a nucleic acid molecule hybridizing to the complement of ADJ84866. The  
CC DNA and protein are two of a number of DNAs and proteins from  
CC thermotable bacteria polIII subunits disclosed in the specification  
CC (e.g. the dnaX, holA, holB, dnaH, dnaQ, dnaE, ssb genes). Also  
CC included are a clamp loader complex comprising polIII delta', a DNA  
CC polymerase III-type enzyme complex comprising the clamp loader and a kit  
CC comprising a container that contains either a deoxynucleoside  
CC triphosphate or a dideoxynucleoside triphosphate and a container  
CC containing a DNA polymerase III-type enzyme complex. The polIII delta'  
CC subunits are useful for amplifying and sequencing a DNA molecule by PCR.  
CC The present sequence is a bacterial polIII subunit-associated peptide  
CC included in the sequence listing but not mentioned anywhere else in the  
CC specification.

XX Sequence 11 AA;  
SQ

Query Match 30.2%; Score 29; DB 8; Length 11;  
Best Local Similarity 100.0%; Pred. No. 4.9e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 HGYLE 10  
|||||  
DB 7 HGYLE 11

RESULT 58  
ADM77717  
ID ADM77717 standard; peptide; 11 AA.  
XX ADM77717;  
DT 15-JUL-2004 (first entry)  
XX  
XX DNA polymerase III-type enzyme related peptide #35.  
DE  
XX  
XX Bacillus PolC subunit; DNA polymerase III; dnaX, dnaH; holB;  
KM thermophilic bacterium; enzyme.  
XX  
XX Thermus thermophilus.  
OS  
XX  
XX US2004077012-A1.  
PN  
XX  
XX 22-APR-2004.  
PD  
XX  
XX 26-SEP-2003; 2003US-00672638.  
PP  
XX  
XX 08-APR-1997; 97US-0043202P.  
PR 08-APR-1998; 98US-00057416.  
PR 18-AUG-2000; 2000US-00642218.  
PR 21-NOV-2000; 2000US-00716964.  
XX  
XX (ODON/) O'DONNELL M E.  
PA (YUZH/) YUZHAKOV A.  
PA (YURI/) YURIEVA O.  
PA (JERU/) JERUZALMI D.  
PA (BRUC/) BRUCK I.  
PA (KURI/) KURIYAN J.  
XX  
XX O'donnell ME, Yuzhakov A, Yurieva O, Jeruzalmi D, Bruck I;  
PI Kuriyan J;  
PI  
XX  
XX MPI; 2004-340000/31.  
DR  
XX  
XX Novel isolated Bacillus PolC subunit of DNA polymerase III-type enzyme,  
PT useful for amplifying and sequencing DNA molecules by polymerase chain  
PT reaction.  
XX  
XX Example 14; SEQ ID NO 210; 245pp; English.  
PS  
XX The invention relates to an isolated Bacillus PolC subunit of a DNA

CC polymerase III-type enzyme. The invention also relates to a method of  
CC preparing DNA polymerase III enzymes, DNA molecules obtained by  
CC amplifying and sequencing using the DNA polymerase III enzymes, DNA  
CC probes constructed from the DNA sequences coding for dnaX, dnaH and holB  
CC genes, DNA molecules encoding the DNA polymerase III enzymes, a method of  
CC producing a recombinant thermostable DNA polymerase III enzyme from  
CC thermophilic bacterium and a method of isolating a target DNA fragment  
CC consisting essentially of DNA encoding a DNA polymerase III enzyme. The  
CC Bacillus PolC subunit is useful for amplifying and sequencing a DNA  
CC molecule by PCR. This sequence represents a DNA polymerase III-type  
CC enzyme related peptide of the invention.

XX Sequence 11 AA;  
SQ

Query Match 30.2%; Score 29; DB 8; Length 11;  
Best Local Similarity 100.0%; Pred. No. 4.9e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 HGYLE 10  
|||||  
DB 7 HGYLE 11

RESULT 59  
ADM6384  
ID ADM6384 standard; peptide; 11 AA.  
XX ADM6384;  
AC  
XX  
XX 15-JUL-2004 (first entry)  
DT  
XX  
XX T. thermophilus holB primer peptide #4.  
DE  
XX  
XX DNA polymerase; DNA sequencing; DNA amplification.  
KM  
XX  
XX Thermus thermophilus.  
OS  
XX  
XX US2004081995-A1.  
PN  
XX  
XX 29-APR-2004.  
PD  
XX  
XX 26-SEP-2003; 2003US-00673127.  
PP  
XX  
XX 08-APR-1997; 97US-0043202P.  
PR 08-APR-1998; 98US-00057416.  
PR 18-AUG-2000; 2000US-00642218.  
PR 21-NOV-2000; 2000US-00716964.  
XX  
XX (ODON/) O'DONNELL M E.  
PA (YUZH/) YUZHAKOV A.  
PA (YURI/) YURIEVA O.  
PA (JERU/) JERUZALMI D.  
PA (BRUC/) BRUCK I.  
PA (KURI/) KURIYAN J.  
XX  
XX O'donnell ME, Yuzhakov A, Yurieva O, Jeruzalmi D, Bruck I;  
PI Kuriyan J;  
PI  
XX  
XX MPI; 2004-340140/31.  
DR N-PSDB; ADM6383.  
DR  
XX  
XX Novel isolated Bacillus beta subunit of DNA polymerase III-type enzyme,  
PT useful for amplifying and sequencing DNA molecule by polymerase chain  
PT reaction.  
XX  
XX Example 14; SEQ ID NO 210; 245pp; English.  
PS  
XX The invention relates to an isolated DNA molecule from Bacillus  
CC acetotherophilus encoding a delta subunit of a DNA polymerase I. The  
CC subunits are useful for producing DNA polymerases for use in DNA  
CC sequencing and DNA amplification methods. The present sequence is used in  
CC the exemplification of the present invention.



SO Sequence 11 AA;  
 Query Match 30.2%; Score 29; DB 8; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 4.9e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 6 HGVL 10  
 Db 7 HGVL 11

RESULT 60  
 ADO04437  
 ID ADO04437 standard; peptide; 11 AA.  
 XX  
 AC ADO04437;  
 XX  
 DT 26-AUG-2004 (first entry)  
 XX  
 DE Conserved DNA polymerase III delta' subunit peptide #2.  
 XX  
 KW DNA polymerase III; single-stranded DNA binding protein; ssb;  
 KM chromosomal replicase; secondary structure element; replication.  
 OS Bacteria.  
 XX  
 PN US2004106137-A1.  
 XX  
 PD 03-JUN-2004.  
 XX  
 PF 25-SEP-2003; 2003US-00670817.  
 XX  
 PR 08-APR-1997; 97US-0043202P.  
 PR 08-APR-1998; 98US-00057416.  
 PR 18-AUG-2000; 2000US-00642218.  
 PR 21-NOV-2000; 2000US-00716964.  
 XX  
 PA (ODON/) O'DONNELL M E.  
 PA (YUZH/) YUZHAKOV A.  
 PA (YURI/) YURIEVA O.  
 PA (JERU/) JERUZALMI D.  
 PA (BRUC/) BRUCK I.  
 PA (KURI/) KURIYAN J.  
 PI O'Donnell ME, Yuzhakov A, Yurleva O, Jeruzalmi D, Bruck I,  
 PI Kuriyan J;  
 DR WPI; 2004-419457/39.  
 XX  
 PT Novel isolated DNA derived from *Bacillus stearothermophilus*, encoding  
 PT single-strand DNA binding protein, useful in removing secondary structure  
 PT element from single-stranded DNA during DNA replication.  
 XX  
 PS Example 14; SEQ ID NO 210; 245bp; English.  
 XX  
 CC The invention relates to an isolated DNA molecule from *Bacillus* sp.  
 CC encoding a single-strand DNA binding protein (ssb) appearing as ADO04402  
 CC encoding the protein appearing as ADO04403, and DNAs hybridizing to  
 CC complementary sequence of ADO04402 under hybridization conditions. Also  
 CC included are an expression system comprising an expression vector into  
 CC which the ssb gene is inserted and a host cell comprising a heterologous  
 CC ssb gene. The following are disclosed as new, a kit (comprising a  
 CC container that contains either a deoxynucleoside triphosphate or a  
 CC dideoxynucleoside triphosphate, and a container containing DNA polymerase  
 CC III-type complex), methods and products (for identifying, isolating and  
 CC cloning DNA molecules encoding subunits encoded by genes of DNA  
 CC polymerase III-type enzyme from thermophilic bacteria), preparing DNA  
 CC polymerase III enzymes, DNA molecules obtained by amplifying and  
 CC sequencing using the DNA polymerase III enzymes, recombinant alpha, beta,  
 CC epsilon, tau, gamma, delta and delta' DNA polymerase III subunits, genes  
 CC encoding bacterial chromosomal replicases, and producing a recombinant  
 CC thermostable DNA polymerase III enzyme from a thermophilic bacterium. The  
 CC ssb protein and gene, derived from *Bacillus stearothermophilus*, are

CC useful in producing a recombinant thermostable single-strand binding  
 CC protein useful in removing secondary structure element from ssDNA during  
 CC replication. The present sequence is a bacterial DNA polymerase III  
 CC subunit derived peptide (or consensus motif) used to design PCR primers  
 CC for isolation of the DNA polIII genes.  
 XX  
 SO Sequence 11 AA;  
 Query Match 30.2%; Score 29; DB 8; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 4.9e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 6 HGVL 10  
 Db 7 HGVL 11

RESULT 61  
 ADP82514  
 ID ADP82514 standard; peptide; 11 AA.  
 XX  
 AC ADP82514;  
 XX  
 DT 26-AUG-2004 (first entry)  
 XX  
 DE DNA polymerase III delta' subunit peptide seqd 210.  
 XX  
 KW single-strand binding protein; SSB; DNA-protein complex;  
 KM DNA polymerase III-type enzyme complex; thermostable DNA polymerase III;  
 KW secondary structure element; replication; holB; DNA polymerase III;  
 KW delta' subunit.  
 XX  
 OS *Thermus thermophilus*.  
 XX  
 PN US2004110210-A1.  
 XX  
 PD 10-JUN-2004.  
 XX  
 PF 26-SEP-2003; 2003US-00673119.  
 XX  
 PR 08-APR-1997; 97US-0043202P.  
 PR 08-APR-1998; 98US-00057416.  
 PR 18-AUG-2000; 2000US-00642218.  
 PR 21-NOV-2000; 2000US-00716964.  
 XX  
 PA (ODON/) O'DONNELL M E.  
 PA (YUZH/) YUZHAKOV A.  
 PA (YURI/) YURIEVA O.  
 PA (JERU/) JERUZALMI D.  
 PA (BRUC/) BRUCK I.  
 PA (KURI/) KURIYAN J.  
 PI O'Donnell ME, Yuzhakov A, Yurleva O, Jeruzalmi D, Bruck I,  
 PI Kuriyan J;  
 DR WPI; 2004-440355/41.  
 XX  
 PT Novel isolated *Bacillus stearothermophilus* single-strand binding protein,  
 PT useful in removing secondary structure element from single-stranded DNA  
 PT during DNA replication.  
 XX  
 PS Example 14; SEQ ID NO 210; 245bp; English.  
 XX  
 CC The invention describes an isolated *Bacillus* sp. single-strand binding  
 CC protein (II), comprising a fully defined sequence (S1) of 164 amino acids  
 CC as given in specification or encoded by a nucleic acid molecule  
 CC hybridizing to the complement of a fully defined sequence (S2) of 492  
 CC base pairs as given in specification. Also described are: a DNA-protein  
 CC complex (II) comprising a DNA molecule containing a single-stranded  
 CC region and (I) that is bound to the single-stranded region of the DNA  
 CC molecule; a kit comprising a container that contains either a  
 CC deoxynucleoside triphosphate or a dideoxynucleoside triphosphate, and  
 CC container that contains a DNA polymerase III-type enzyme complex, and

CC container that contains (1); methods and products for identifying,  
 CC isolating and cloning DNA molecules encoding subunits encoded by genes of  
 CC DNA polymerase III-type enzyme; kits for amplification and sequencing of  
 CC DNA molecules; DNA polymerase III enzyme subunits; preparing DNA  
 CC polymerase III enzyme; DNA molecules obtained by amplifying and  
 CC sequencing using the DNA polymerase III enzymes; producing and isolating  
 CC a recombinant thermostable DNA polymerase III enzyme or its subunit from  
 CC thermophilic bacterium; DNA (III) encoding (I); an expression system  
 CC comprising an expression vector into which (III) is inserted; and a host  
 CC cell comprising a heterologous (III). (I) is useful in removing a  
 CC secondary structure element from single-stranded DNA (ssDNA),  
 CC particularly during replication. (I) binds to single stranded regions of  
 CC DNA strands during DNA replication and prevents the rewinding of the DNA  
 CC strands. This is the amino acid sequence of a DNA polymerase III delta  
 CC subunit peptide used to create a primer for the isolation of *Thermus*  
 CC thermophilus holB.

XX Sequence 11 AA;

Query Match 30.2%; Score 29; DB 8; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 4.9e+02; Mismatches 0; Indels 0; Gaps 0;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 HGYLE 10  
 |||||  
 Db 7 HGYLE 11

RESULT 62

AD515721  
 ID AD515721 standard; peptide; 11 AA.

XX AD515721;

DT 30-DEC-2004 (first entry)

XX Peptide for *T. thermophilus* DNA polymerase III delta PCR primer #2.

XX DNA polymerase III subunit; HolC; thermostable DNA polymerase;

KW thermophilic bacteria; gamma subunit; tau subunit; epsilon subunit;

KW alpha subunit; PolC; delta subunit; delta' subunit; beta subunit; SSB;

KW single stranded binding protein; long chain extension;

XX cognate sliding clamp; clamp loader; DNA stimulated ATPase.

XX Bacteria.

XX US2004197796-A1.

XX 07-OCT-2004.

XX 25-SEP-2003; 2003US-00671207.

XX 08-APR-1997; 97US-0043202P.

XX 08-APR-1998; 98US-00057416.

XX 18-AUG-2000; 2000US-00642218.

XX 21-NOV-2000; 2000US-00716964.

XX (ODON/) O'DONNELL M E.

XX (YUZH/) YUZHAKOV A.

XX (YURI/) YURIEVA O.

XX (JERU/) JERUZALMI D.

XX (BRUC/) BRUCK I.

XX (KURI/) KURIYAN J.

XX O'Donnell ME, Yuzhakov A, Yurieva O, Jeruzalmi D, Bruck I,  
 PI Kuriyan J;  
 PI Kuriyan J;  
 DR WPI; 2004-718457/70.  
 XX  
 XX  
 PT Novel isolated DNA molecule from *Bacillus* species encoding beta subunit  
 of DNA polymerase III-type enzyme, useful for producing recombinant  
 PT thermostable beta subunit of DNA polymerase III-type enzyme.  
 XX

PS Example 14; SEQ ID NO 210; 245bp; English.

XX The invention relates to an isolated DNA molecule from a *Bacillus* sp.  
 CC encoding a beta subunit of a DNA polymerase III-type enzyme (appearing as  
 CC AD515684 and encoding the protein appearing as AD515685), or hybridizing  
 CC to the complement of AD515684 under hybridization conditions comprising  
 CC at most about 0.9 M sodium citrate buffer at least 37C. Also included are  
 CC an expression system comprising an expression vector into which AD515684  
 CC is inserted and a host cell comprising AD515684. Also disclosed are  
 CC methods and products for identifying, isolating and cloning DNA molecules  
 CC which encode accessory subunits of a DNA polymerase III-type enzyme  
 CC (gamma, tau, epsilon, alpha, PolC, delta, delta', and beta as well as SSB  
 CC (single stranded binding protein)), methods for identifying polymerase  
 CC III-type enzymes, isolated and purified DNA polymerase III from *Thermus*  
 CC thermophilus and *B. stearothermophilus*, methods for preparing DNA  
 CC polymerase III-type enzyme and kits for amplification and sequencing of  
 CC DNA molecules that can achieve long chain extension of primed DNA. DNA  
 CC polymerase III beta DNA is useful for producing a recombinant  
 CC thermostable beta subunit of a DNA polymerase III-type enzyme from  
 CC *Bacillus* sp., which involves transforming a host cell with DNA polymerase  
 CC III beta DNA under conditions suitable for expression of the beta  
 CC subunit, and isolating the beta subunit. DNA polymerase III beta DNA  
 CC enables the investigator to obtain a thermostable polymerase III-type  
 CC enzyme from a thermophilic bacteria that exhibits the ability to extend a  
 CC primer over a long stretch (greater than 5 kb) of single-stranded (ss) DNA  
 CC at elevated temperature, the ability to be stimulated by a cognate  
 CC sliding clamp (e.g., beta) of the type that is assembled on DNA by  
 CC 'clamp' loader (e.g., gamma complex), and have a clamp loading subunit  
 CC that shows DNA stimulated ATPase activity at elevated temperatures and/or  
 CC ionic strength. The *Thermus thermophilus* HolC gene was isolated by  
 CC designing PCR primers from the peptide sequences of the genes immediately  
 CC 5' and 3' to it (nearest neighbours), relying on the presumption that the  
 CC gene arrangement would be preserved in closely related species. The  
 CC present sequence is a nearest neighbour peptide from a related species,  
 CC used to design primers for the amplification of *T. thermophilus* HolC  
 CC gene.  
 XX

XX Sequence 11 AA;

Query Match 30.2%; Score 29; DB 8; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 4.9e+02; Mismatches 0; Indels 0; Gaps 0;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 HGYLE 10  
 |||||  
 Db 7 HGYLE 11

RESULT 63

ADY55212  
 ID ADY55212 standard; peptide; 11 AA.

XX ADY55212;

XX 19-MAY-2005 (first entry)

XX *T. thermophilus* holB downstream peptide, SEQ ID 210.

XX DNA polymerase; DNA amplification; primer extension.

XX Synthetic.

XX US2005048510-A1.

XX 03-MAR-2005.

XX 26-SEP-2003; 2003US-0067120.

XX 08-APR-1997; 97US-0043202P.

XX 08-APR-1998; 98US-00057416.

XX 18-AUG-2000; 2000US-00642218.

XX 21-NOV-2000; 2000US-00716964.

PA (ODON/) O'DONNELL M E.  
 PA (YUZH/) YUZHAKOV A.  
 PA (YURI/) YURIEVA O.  
 PA (JERU/) JERUZALMI D.  
 PA (BRUC/) BRUCK I.  
 PA (KURI/) KURIYAN J.  
 XX  
 PI O'Donnell ME, Yuzhakov A, Yurieva O, Jeruzalmi D, Bruck I,  
 PI Kuriyan J,  
 DR WPI, 2005-202063/21.  
 DR N-PSDB; ADY55211.  
 XX  
 PT New isolated Aquifex delta prime subunit of DNA polymerase III-type  
 PT enzyme, useful for amplifying and sequencing DNA molecule.  
 XX  
 PS Disclosure; SEQ ID NO 210; 245bp; English.  
 XX  
 CC The invention relates to a novel isolated Aquifex delta prime subunit of  
 CC a DNA polymerase III-type enzyme. The subunit comprises a fully defined  
 CC 305 amino acid (ADY55128) sequence given in the specification, and  
 CC encoded by a nucleic acid molecule hybridizing to the complement of a  
 CC fully defined 1051 nucleotide (ADY55127) sequence given in the  
 CC specification. The invention further comprises: a clamp loader complex  
 CC comprising the Aquifex delta prime subunit; a DNA polymerase III-type  
 CC enzyme complex comprising the clamp loader complex; and a kit comprising  
 CC a container containing either a deoxynucleoside triphosphate or a  
 CC dideoxynucleoside triphosphate, and a container having a DNA polymerase  
 CC III-type enzyme complex. The Aquifex delta prime subunit is useful for  
 CC extending a primer over a long stretch of single-stranded DNA at an  
 CC elevated temperature. The Aquifex delta prime subunit or DNA polymerase  
 CC III-type enzyme complex is useful for amplifying and sequencing a DNA  
 CC molecule. This sequence represents a T. thermophilus holB downstream  
 CC peptide of the invention.  
 XX  
 SQ Sequence 11 AA;  
 XX  
 Query Match 30.2%; Score 29; DB 9; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 4.9e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 6 HGTYL 10  
 Db 7 HGTYL 11  
 XX  
 RESULT 64  
 ADZ76788  
 ID ADZ76788 standard; peptide; 11 AA.  
 XX  
 AC ADZ76788;  
 XX  
 DT 14-JUL-2005 (first entry)  
 XX  
 DE T. thermophilus holB gene primer derived peptide, SEQ ID 210.  
 XX  
 KW recombinant DNA; thermostable; PolC; DNA polymerase; PCR.  
 XX  
 OS Synthetic.  
 XX  
 PN US200510920-A1.  
 PD 12-MAY-2005.  
 XX  
 PP 25-SEP-2003; 2003US-00671412.  
 XX  
 PR 08-APR-1997; 97US-0043302P.  
 PR 08-APR-1998; 98US-00057416.  
 PR 18-AUG-2000; 2000US-00642218.  
 PR 21-NOV-2000; 2000US-00716964.  
 XX  
 PA (ODON/) O'DONNELL M E.  
 PA (YUZH/) YUZHAKOV A.

PA (YURI/) YURIEVA O.  
 PA (JERU/) JERUZALMI D.  
 PA (BRUC/) BRUCK I.  
 PA (KURI/) KURIYAN J.  
 XX  
 PI O'Donnell ME, Yuzhakov A, Yurieva O, Jeruzalmi D, Bruck I,  
 PI Kuriyan J,  
 DR WPI, 2005-354712/36.  
 DR N-PSDB; ADZ76787.  
 XX  
 PT New isolated DNA molecule from a Bacillus species encoding a PolC subunit  
 PT of a DNA polymerase III-type enzyme, useful in producing thermostable DNA  
 PT polymerases for use as chromosomal replicases.  
 XX  
 PS Example 14; SEQ ID NO 210; 245bp; English.  
 XX  
 CC The invention relates to a novel isolated DNA molecule from a Bacillus  
 CC species encoding a PolC subunit of a DNA polymerase III-type enzyme  
 CC comprising a sequence of 4301 base pairs (ADZ76761), encoding a sequence  
 CC of 1433 amino acids (ADZ76762), or hybridizing to the complement of  
 CC ADZ76761, where the sequences are given in the specification. The  
 CC invention further comprises: an expression system comprising an  
 CC expression vector into which is inserted the heterologous DNA molecule;  
 CC a host cell comprising the heterologous DNA molecule; a method for  
 CC producing a recombinant thermostable PolC subunit of a DNA polymerase III  
 CC -type enzyme from a Bacillus species; and an isolated DNA molecule from  
 CC Bacillus stearothermophilus encoding a PolC subunit of a DNA polymerase  
 CC III enzyme, where the PolC subunit can co-operate with a clamp loader to  
 CC form a DNA polymerase III-like particle. The methods and compositions of  
 CC the present invention are useful in producing thermostable DNA  
 CC polymerases for use as chromosomal replicases. The thermostable DNA  
 CC polymerases, for use as chromosomal replicases, provide a faster and  
 CC longer chain production in PCR, and a higher quality of DNA sequencing  
 CC ladders. This sequence represents a T. thermophilus holB gene primer  
 CC derived peptide of the invention.  
 XX  
 SQ Sequence 11 AA;  
 XX  
 Query Match 30.2%; Score 29; DB 9; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 4.9e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 6 HGTYL 10  
 Db 7 HGTYL 11  
 XX  
 RESULT 65  
 ABA24796  
 ID ABA24796 standard; peptide; 11 AA.  
 XX  
 AC ABA24796;  
 XX  
 DT 28-JUL-2005 (first entry)  
 XX  
 DE Thermus thermophilus HolB peptide for downstream PCR primer.  
 XX  
 KW cloning; DNA polymerase; thermostability; DNA replication.  
 XX  
 OS Thermus thermophilus.  
 XX  
 PN US2005112580-A1.  
 PD 26-MAY-2005.  
 XX  
 PP 26-SEP-2003; 2003US-00671859.  
 XX  
 PR 08-APR-1997; 97US-0043202P.  
 PR 08-APR-1998; 98US-00057416.  
 PR 18-AUG-2000; 2000US-00642218.  
 PR 21-NOV-2000; 2000US-00716964.  
 XX

PA (ODON/) O'DONNELL M E.  
PA (YUZH/) YUZHAKOV A.  
PA (YURI/) YURIEVA O.  
PA (JERU/) JERUZALMI D.  
PA (BRUC/) BRUCK I.  
PA (KURI/) KURIYAN J.  
XX  
XX  
PI Odonnell ME, Yuzhakov A, Yurieva O, Jeruzalmi D, Bruck I;  
PI Kuriyan J;  
XX  
XX WPI; 2005-371651/38.  
DR  
XX  
XX  
PT New isolated Bacillus delta or delta prime or tau subunit of DNA  
PT polymerase III-type enzymes, useful as thermostable DNA polymerases and  
PT chromosomal replicases, and in providing high-fidelity amplified copies  
PT of nucleic acid molecules.  
PS  
PS Example 14; SEQ ID NO 210; 245pp; English.  
XX  
XX  
CC The invention relates to an isolated Bacillus delta or delta prime or tau  
CC subunit of a DNA polymerase III-type enzyme, the isolated subunit  
CC comprising a fully defined sequence of 348, 252 or 559 amino acids  
CC (AEA24764, AEA24766 or AEA24768), or being encoded by a nucleic acid  
CC molecule hybridizing to the complement of a fully defined sequence of  
CC 1044, 757 or 1677 bp (AEA24763, AEA24765 or AEA24767) at 0.9 M sodium  
CC citrate buffer and at least 37 deg C. The methods and compositions of the  
CC present invention are useful in thermostable DNA polymerases,  
CC particularly to polymerases as chromosomal replicases derived from  
CC thermophilic bacteria, and for providing high-fidelity amplified copies  
CC of a nucleic acid molecule. This sequence represents a peptide from a DNA  
CC polymerase III subunit of the invention  
XX  
SQ Sequence 11 AA;

Query Match 30.2%; Score 29; DB 9; Length 11;  
Best Local Similarity 100.0%; Pred. No. 4.9e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 HGYLE 10  
| | | | |  
DB 7 HGYLE 11

RESULT 66  
AEA34219  
ID AEA34219 standard; peptide, 11 AA.  
XX  
XX AEA34219;  
AC  
XX  
XX

DT 28-JUL-2005 (first entry)

DE Thermus thermophilus HolB peptide for downstream PCR primer.

KW cloning; DNA polymerase; thermostability; DNA replication.

OS Thermus thermophilus.

XX US6897053-B1.  
XX  
XX

PD 24-MAY-2005.  
XX  
XX

PF 21-NOV-2000; 2000US-00716964.  
XX  
XX

PR 08-APR-1997; 97US-0043202P.  
XX  
XX

PR 08-APR-1998; 98US-00057416.  
XX  
XX

PR 18-AUG-2000; 2000US-00642218.  
XX  
XX

PA (UYRQ ) UNIV ROCKEFELLER.

XX Odonnell ME, Yurieva O,  
XX  
XX

DR WPI; 2005-370754/38.  
XX

PT New isolated DNA molecules encoding the delta subunit of DNA polymerase  
PT III-type enzymes that function as chromosomal replicase, useful for  
PT amplifying or sequencing DNA molecules.  
XX  
XX  
XX

PS Example 14; SEQ ID NO 210; 236pp; English.

CC The invention relates to an isolated Bacillus delta or delta prime or tau  
CC subunit of a DNA polymerase III-type enzyme, the isolated subunit  
CC comprising a fully defined sequence of 348, 252 or 559 amino acids  
CC (AEA34187, AEA34189 or AEA34191), or being encoded by a nucleic acid  
CC molecule hybridizing to the complement of a fully defined sequence of  
CC 1044, 757 or 1677 bp (AEA34186, AEA34188 or AEA34190) at 0.9 M sodium  
CC citrate buffer and at least 37 deg C. The methods and compositions of the  
CC present invention are useful in thermostable DNA polymerases,  
CC particularly to polymerases as chromosomal replicases derived from  
CC thermophilic bacteria, and for providing high-fidelity amplified copies  
CC of a nucleic acid molecule. This sequence represents a peptide from a DNA  
CC polymerase III subunit of the invention  
XX  
XX

SQ Sequence 11 AA;

Query Match 30.2%; Score 29; DB 9; Length 11;  
Best Local Similarity 100.0%; Pred. No. 4.9e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 HGYLE 10  
| | | | |  
DB 7 HGYLE 11

RESULT 67  
AEB51623  
ID AEB51623 standard; peptide, 11 AA.  
XX  
XX AEB51623;  
AC  
XX  
XX

DT 22-SEP-2005 (first entry)

DE DNA polymerase III-type enzyme holB peptide, SEQ ID 210.

XX DNA polymerase.  
XX  
XX

OS Thermus thermophilus.

XX US2005153299-A1.  
XX  
XX

PD 14-JUL-2005.  
XX  
XX

PF 25-SEP-2003; 2003US-00671106.  
XX  
XX

PR 08-APR-1997; 97US-0043202P.  
XX  
XX

PR 08-APR-1998; 98US-00057416.  
XX  
XX

PR 18-AUG-2000; 2000US-00642218.  
XX  
XX

PR 21-NOV-2000; 2000US-00716964.  
XX  
XX

PA (ODON/) O'DONNELL M E.

PA (YUZH/) YUZHAKOV A.

PA (YURI/) YURIEVA O.

PA (JERU/) JERUZALMI D.

PA (BRUC/) BRUCK I.  
XX  
XX

PA (KURI/) KURIYAN J.

XX

PI Odonnell ME, Yuzhakov A, Yurieva O, Jeruzalmi D, Bruck I;  
PI Kuriyan J;  
XX  
XX WPI; 2005-496822/50.  
XX  
XX

PT New isolated DNA molecule from Bacillus stearothermophilus encoding a  
PT delta prime subunit of a DNA polymerase III-type enzyme, useful producing  
PT recombinant thermostable delta prime subunit of a DNA polymerase III-type  
PT enzyme.  
XX  
XX

XX The present invention relates to a DNA polymerase III-type enzyme  
CC subunits and their coding sequences. The coding sequence for a Bacillus  
CC streptothermophilus delta prime subunit of DNA polymerase III-type enzyme  
CC is specifically claimed (AB51592). Also disclosed are: preparation  
CC methods for DNA Polymerase III-type enzymes; methods for amplifying and  
CC sequencing the DNA molecule; and DNA amplification kits. The present  
CC sequence was used to illustrate the invention.  
XX  
SQ Sequence 11 AA;  
DB 7 HGVL 11  
QY 6 HGVL 10  
Query Match 30.2%; Score 29; DB 9; Length 11;  
Best Local Similarity 100.0%; Pred. No. 4.9e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
DB 7 HGVL 11  
RESULT 68  
AAE26390  
ID AAE26390 standard; peptide; 12 AA.  
XX  
AC AAE26390;  
XX  
DT 13-DEC-2002 (first entry)  
XX  
DE Human wild-type GPR10 C-terminal peptide #1.  
XX  
KM Human; wakefulness; sleep disorder; prolactin releasing peptide receptor;  
KM P-RP; GPR10; therapy; epilepsy; narcolepsy; sleepiness; sleep apnoea;  
KM insomnia; idiopathic hypersomnia; psychogenic hypersomnia; seizure;  
KM anticonvulsant.  
XX  
OS Homo sapiens.  
XX  
PN US2002037533-A1.  
XX  
PD 28-MAR-2002.  
XX  
PF 17-AUG-2001; 2001US-00932161.  
XX  
PR 28-APR-2000; 2000US-00560915.  
XX  
PA (CIVE/) CIVELLI O.  
PA (LINS/) LIN S.  
PI Cive111 O, Lin S;  
PI  
DR WPI; 2002-403931/43.  
XX  
PT Screening for compounds useful for promoting wakefulness or sleep, and  
PT for treating sleeping disorders, e.g. insomnia, hypersomnia or sleep  
PT apnea, comprises administering a prolactin releasing peptide agonist or  
PT antagonist.  
XX  
PS Example 2; Page 22; 35pp; English.  
XX  
CC The present invention relates to a method of screening for compounds for  
CC promoting wakefulness or sleep in a mammal. The method involves  
CC administering a prolactin releasing peptide (PRP) receptor (GPR10)  
CC agonist or antagonist respectively and determining the ability of the  
CC compound to promote wakefulness or sleep. The compounds identified from  
CC the method are used in the therapy of epilepsy and other diseases  
CC associated with absence seizures and in promoting wakefulness and sleep  
CC in individuals having sleep disorders such as insomnia and narcolepsy.  
CC PRP receptor agonists may be used to treat common disorders which lead  
CC to sleepiness, e.g. sleep apnoea, narcolepsy, idiopathic hypersomnia and  
CC psychogenic hypersomnia. PRP receptor antagonists are useful for  
CC promoting sleep and for treating insomnia such as adjustment sleep  
CC disorder and psychophysiological insomnia. The present sequence is human  
CC wild-type GPR10 C-terminal peptide

XX  
SQ Sequence 12 AA;  
DB 1 PHGQNMIVSV 10  
QY 5 PHGVLITAAV 14  
Query Match 30.2%; Score 29; DB 5; Length 12;  
Best Local Similarity 50.0%; Pred. No. 5.5e+02;  
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
DB 1 PHGQNMIVSV 10  
RESULT 69  
AAE26398  
ID AAE26398 standard; peptide; 12 AA.  
XX  
AC AAE26398;  
XX  
DT 13-DEC-2002 (first entry)  
XX  
DE Human GPR10 mutant C-terminal peptide, I370A.  
XX  
KM Human; wakefulness; sleep disorder; prolactin releasing peptide receptor;  
KM P-RP; GPR10; therapy; epilepsy; narcolepsy; sleepiness; sleep apnoea;  
KM insomnia; idiopathic hypersomnia; psychogenic hypersomnia; seizure;  
KM anticonvulsant; mutant; mutein.  
XX  
OS Homo sapiens.  
OS Synthetic.  
FH Key Location/Qualifiers  
FT Misc-difference 12 /note= "wild-type Ile substituted with Ala; This position  
FT corresponds to position 370 of the wild-type protein"  
XX  
PN US2002037533-A1.  
XX  
PD 28-MAR-2002.  
XX  
PF 17-AUG-2001; 2001US-00932161.  
XX  
PR 28-APR-2000; 2000US-00560915.  
XX  
PA (CIVE/) CIVELLI O.  
PA (LINS/) LIN S.  
PI Cive111 O, Lin S;  
PI  
DR WPI; 2002-403931/43.  
XX  
PT Screening for compounds useful for promoting wakefulness or sleep, and  
PT for treating sleeping disorders, e.g. insomnia, hypersomnia or sleep  
PT apnea, comprises administering a prolactin releasing peptide agonist or  
PT antagonist.  
XX  
PS Example 2; Page 23; 35pp; English.  
XX  
CC The present invention relates to a method of screening for compounds for  
CC promoting wakefulness or sleep in a mammal. The method involves  
CC administering a prolactin releasing peptide (PRP) receptor (GPR10)  
CC agonist or antagonist respectively and determining the ability of the  
CC compound to promote wakefulness or sleep. The compounds identified from  
CC the method are used in the therapy of epilepsy and other diseases  
CC associated with absence seizures and in promoting wakefulness and sleep  
CC in individuals having sleep disorders such as insomnia and narcolepsy.  
CC PRP receptor agonists may be used to treat common disorders which lead  
CC to sleepiness, e.g. sleep apnoea, narcolepsy, idiopathic hypersomnia and  
CC psychogenic hypersomnia. PRP receptor antagonists are useful for  
CC promoting sleep and for treating insomnia such as adjustment sleep  
CC disorder and psychophysiological insomnia. The present sequence is human  
CC GPR10 mutant C-terminal peptide  
SQ Sequence 12 AA;

Query Match 30.2%; Score 29; DB 5; Length 12;  
 Best Local Similarity 50.0%; Pred. No. 5.5e+02;  
 Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 5 PHGYLTAAV 14  
 ||| : ||  
 DB 1 PHGQNMVSV 10

## RESULT 70

ID ADM35713 standard; peptide; 13 AA.

AC ADM35713;

DT 10-MAR-2005 (first entry)

DE HLA binding epitope #6463.

KM Virucide; cytostatic; gene therapy; vaccine; epitope; cytotoxic T cell;

KW MHC class I; CTL; HTL; A2-restricted cytotoxic lymphocyte; HLA;

OS Unidentified.

PN WO2003040165-A2.

PD 15-MAY-2003.

PF 18-OCT-2001; 2001WO-US051650.

PR 19-OCT-2000; 2000US-0242350P.

PT 20-APR-2001; 2001US-0285624P.

PA (EPIW-) EPIIMUNE INC.

PI Sette A, Sidney J, Southwood S;

DR WPI; 2003-441519/41.

PT New composition comprising at least one peptide having allele-specific binding motifs for HLA, useful for preventing, treating or diagnosing viral diseases and cancer.

PS Claim 1; Page 52-379; 382pp; English.

XX The invention relates to a composition comprising at least one peptide having an isolated, prepared epitope selected from any of the sequences from 30 lists given in the specification. Also disclosed is a method for inducing a cytotoxic T cell response against a pre-selected antigen in a patient expressing a specific MHC class I allele by contacting cytotoxic T cells from the patient with the composition cited above. The composition comprises an epitope that is joined by an amino acid linker. The epitope is admixed or joined to a CTL or HTL epitope. The epitope is bound to an HLA molecule on the antigen-presenting cell, where when an A2 binds to a complex of the HLA molecule and the epitope. Specifically claimed are peptides having allele-specific binding motifs for HLA. The compositions and methods are useful for preventing, treating or diagnosing viral diseases and cancer. The peptide epitopes are useful as diagnostic agents for evaluating immune responses, for making antibodies and for evaluating efficacy of a vaccine. Sequences given in ADM29251-ADM37745 represent epitopes of the invention as given in Tables 2-31.

XX Sequence 13 AA;

Query Match 30.2%; Score 29; DB 7; Length 13;

Best Local Similarity 41.7%; Pred. No. 6e+02;  
 Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 AFBPHGYLTAA 13  
 |:::| |

DB 1 AYZAYAYTLKAA 12

## RESULT 71

ID ADM34480

ADW34480 standard; peptide; 13 AA.

AC ADW34480;

DT 10-MAR-2005 (first entry)

DE HLA binding epitope #5230.

KM Virucide; cytostatic; gene therapy; vaccine; epitope; cytotoxic T cell;

KW MHC class I; CTL; HTL; A2-restricted cytotoxic lymphocyte; HLA;

OS Unidentified.

PN WO2003040165-A2.

PD 15-MAY-2003.

PF 18-OCT-2001; 2001WO-US051650.

PR 19-OCT-2000; 2000US-0242350P.

PT 20-APR-2001; 2001US-0285624P.

PA (EPIW-) EPIIMUNE INC.

PI Sette A, Sidney J, Southwood S;

DR WPI; 2003-441519/41.

PT New composition comprising at least one peptide having allele-specific binding motifs for HLA, useful for preventing, treating or diagnosing viral diseases and cancer.

PS Claim 1; Page 52-379; 382pp; English.

XX The invention relates to a composition comprising at least one peptide having an isolated, prepared epitope selected from any of the sequences from 30 lists given in the specification. Also disclosed is a method for inducing a cytotoxic T cell response against a pre-selected antigen in a patient expressing a specific MHC class I allele by contacting cytotoxic T cells from the patient with the composition cited above. The composition comprises an epitope that is joined by an amino acid linker. The epitope is admixed or joined to a CTL or HTL epitope. The epitope is bound to an HLA molecule on the antigen-presenting cell, where when an A2 binds to a complex of the HLA molecule and the epitope. Specifically claimed are peptides having allele-specific binding motifs for HLA. The compositions and methods are useful for preventing, treating or diagnosing viral diseases and cancer. The peptide epitopes are useful as diagnostic agents for evaluating immune responses, for making antibodies and for evaluating efficacy of a vaccine. Sequences given in ADM29251-ADM37745 represent epitopes of the invention as given in Tables 2-31.

XX Sequence 13 AA;

Query Match 30.2%; Score 29; DB 7; Length 13;

Best Local Similarity 41.7%; Pred. No. 6e+02;  
 Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 AFBPHGYLTAA 13  
 |:::| |

DB 1 AYZAYAYTLKAA 12

RESULT 72

ID ADM34479

ADW34479 standard; peptide; 13 AA.

XX

AC ADM344479,  
 XX 10-MAR-2005 (first entry)  
 XX HLA binding epitope #5229.  
 DE  
 XX  
 KM Virucide; cytostatic; gene therapy; vaccine; epitope; cytotoxic T cell;  
 KM MHC class I; CTL; HTL; A2-restricted cytotoxic lymphocyte; HLA;  
 KM viral disease; cancer.  
 XX  
 OS Unidentified.  
 XX  
 PN WO2003040165-A2.  
 XX  
 PD 15-MAY-2003.  
 XX  
 PF 18-OCT-2001; 2001WO-US051650.  
 XX  
 PR 19-OCT-2000; 2000US-0242350P.  
 PR 20-APR-2001; 2001US-0285624P.  
 XX  
 PA (EPIM-) EPIMMUNE INC.  
 XX  
 PI Sette A, Sidney J, Southwood S;  
 PI WPI; 2003-441519/41.  
 DR  
 XX  
 PT New composition comprising at least one peptide having allele-specific  
 PT binding motifs for HLA, useful for preventing, treating or diagnosing  
 PT viral diseases and cancer.  
 PS  
 XX  
 PS Claim 1; Page 52-379; 382pp; English.  
 CC The invention relates to a composition comprising at least one peptide  
 CC having an isolated, prepared epitope selected from any of the sequences  
 CC from 30 lists given in the specification. Also disclosed is a method for  
 CC inducing a cytotoxic T cell response against a pre-selected antigen in a  
 CC patient expressing a specific MHC class I allele by contacting cytotoxic  
 CC T cells from the patient with the composition cited above. The  
 CC composition comprises an epitope that is joined by an amino acid linker.  
 CC The epitope is admixed or joined to a CTL or HTL epitope. The epitope is  
 CC bound to an HLA molecule on the antigen-presenting cell, where when an A2  
 CC -restricted cytotoxic lymphocyte (CTL) is present, a receptor of the CTL  
 CC binds to a complex of the HLA molecule and the epitope. Specifically  
 CC claimed are peptides having allele-specific binding motifs for HLA. The  
 CC compositions and methods are useful for preventing, treating or  
 CC diagnosing viral diseases and cancer. The peptide epitopes are useful as  
 CC diagnostic agents for evaluating immune responses, for making antibodies  
 CC and for evaluating efficacy of a vaccine. Sequences given in ADM29251-  
 CC ADM37745 represent epitopes of the invention as given in Tables 2-31.  
 XX  
 SQ Sequence 13 AA;  
 XX  
 Query Match 30.2%; Score 29; DB 7; Length 13;  
 Best Local Similarity 41.7%; Pred. No. 6e+02;  
 Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
 QY 2 AFEPPHGYLTAA 13  
 DB 1 AYZAVAYTLKAA 12  
 XX  
 RESULT 73  
 ADM35712  
 ID ADM35712 standard; peptide; 13 AA.  
 XX  
 AC ADM35712;  
 XX  
 DT 10-MAR-2005 (first entry)  
 XX  
 DE HLA binding epitope #6462.  
 XX  
 KM Virucide; cytostatic; gene therapy; vaccine; epitope; cytotoxic T cell;

KM MHC class I; CTL; HTL; A2-restricted cytotoxic lymphocyte; HLA;  
 KM viral disease; cancer.  
 XX  
 OS Unidentified.  
 XX  
 PN WO2003040165-A2.  
 XX  
 PD 15-MAY-2003.  
 XX  
 PF 18-OCT-2001; 2001WO-US051650.  
 XX  
 PR 19-OCT-2000; 2000US-0242350P.  
 PR 20-APR-2001; 2001US-0285624P.  
 XX  
 PA (EPIM-) EPIMMUNE INC.  
 XX  
 PI Sette A, Sidney J, Southwood S;  
 PI WPI; 2003-441519/41.  
 DR  
 XX  
 PT New composition comprising at least one peptide having allele-specific  
 PT binding motifs for HLA, useful for preventing, treating or diagnosing  
 PT viral diseases and cancer.  
 PS  
 XX  
 PS Claim 1; Page 52-379; 382pp; English.  
 CC The invention relates to a composition comprising at least one peptide  
 CC having an isolated, prepared epitope selected from any of the sequences  
 CC from 30 lists given in the specification. Also disclosed is a method for  
 CC inducing a cytotoxic T cell response against a pre-selected antigen in a  
 CC patient expressing a specific MHC class I allele by contacting cytotoxic  
 CC T cells from the patient with the composition cited above. The  
 CC composition comprises an epitope that is joined by an amino acid linker.  
 CC The epitope is admixed or joined to a CTL or HTL epitope. The epitope is  
 CC bound to an HLA molecule on the antigen-presenting cell, where when an A2  
 CC -restricted cytotoxic lymphocyte (CTL) is present, a receptor of the CTL  
 CC binds to a complex of the HLA molecule and the epitope. Specifically  
 CC claimed are peptides having allele-specific binding motifs for HLA. The  
 CC compositions and methods are useful for preventing, treating or  
 CC diagnosing viral diseases and cancer. The peptide epitopes are useful as  
 CC diagnostic agents for evaluating immune responses, for making antibodies  
 CC and for evaluating efficacy of a vaccine. Sequences given in ADM29251-  
 CC ADM37745 represent epitopes of the invention as given in Tables 2-31.  
 XX  
 SQ Sequence 13 AA;  
 XX  
 Query Match 30.2%; Score 29; DB 7; Length 13;  
 Best Local Similarity 41.7%; Pred. No. 6e+02;  
 Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
 QY 2 AFEPPHGYLTAA 13  
 DB 1 AYZAVAYTLKAA 12  
 XX  
 RESULT 74  
 ADM30473  
 ID ADM30473 standard; peptide; 13 AA.  
 XX  
 AC ADM30473;  
 XX  
 DT 18-NOV-2004 (first entry)  
 XX  
 DE Kinase peptide K063D104.  
 XX  
 KM Cardiant; Vasotropic; Antiarteriosclerotic; Vulnery; Cytostatic;  
 KM Ophthalmological; Antidiabetic; Antirheumatic; Antiartritic;  
 KM Antipsoptic; Anorectic; Anti-HIV; Angiogenesis modulator; angiogenesis;  
 KM kinase; cardiovascular disease; cancer; rheumatoid arthritis; psoriasis;  
 KM obesity; haemangioma; AIDS; Kaposi sarcoma; arteriosclerosis; restenosis.  
 XX  
 OS Unidentified.  
 XX





XX 19-SEP-2002.  
PD  
XX  
PF 13-MAR-2002; 2002WO-US007855.  
XX  
PR 14-MAR-2001; 2001US-00809638.  
XX  
PA (AGEN-) AGENSYS INC.  
XX  
PI Farle M, Challita-Bid PM, Hubert RS, Afar DEH, Raitano AB, Ge W;  
PI Morrison RK, Morrison K, Jakobovits A;  
XX  
DR WPI; 2002-713510/77.  
XX  
PT New composition comprising a substance that modulates the status of  
PT 125P5C8 gene or a molecule that is modulated by 125P5C8, useful for  
PT treating or preventing cancer that expresses or over expresses 125P5C8.  
XX  
PS Disclosure; Page 206; 274pp; English.  
XX  
CC The present invention relates to compositions comprising a substance that  
CC modulates the status of 125P5C8 or a molecule that is modulated by  
CC 125P5C8. The status of a cell that expresses 125P5C8 is modulated. The  
CC composition is useful for treating cancer, particularly prostate,  
CC bladder, kidney, colon, ovary or breast cancer. The 125P5C8 protein  
CC and/or a nucleotide sequence encoding the protein is useful for  
CC immunising a mammal against cancer. The present sequence is a 125P5C8  
CC epitope shown in the exemplification of the invention  
XX  
SQ Sequence 15 AA;  
XX  
Query Match 30.2%; Score 29; DB 5; Length 15;  
Best Local Similarity 36.4%; Pred. No. 7.2e+02;  
Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;  
OY 7 GYLLTAVSPG 17  
DB 5 GHILNGTNP 15  
XX  
RESULT 77  
ABJ14367  
ID ABJ14367 standard; peptide; 15 AA.  
XX  
AC ABJ14367;  
XX  
DT 10-DEC-2002 (first entry)  
XX  
DE Human 125P5C8 epitope #2993.  
XX  
KW Human; 125P5C8; cancer; cytostatic; breast cancer; prostate cancer;  
KW bladder cancer; kidney cancer; colon cancer; ovarian cancer; epitope.  
XX  
OS Homo sapiens.  
XX  
PN WO200272785-A2.  
XX  
PD 19-SBP-2002.  
XX  
PF 13-MAR-2002; 2002WO-US007855.  
XX  
PR 14-MAR-2001; 2001US-00809638.  
XX  
PA (AGEN-) AGENSYS INC.  
XX  
PI Farle M, Challita-Bid PM, Hubert RS, Afar DEH, Raitano AB, Ge W;  
PI Morrison RK, Morrison K, Jakobovits A;  
XX  
DR WPI; 2002-713510/77.  
XX  
PT New composition comprising a substance that modulates the status of  
PT 125P5C8 gene or a molecule that is modulated by 125P5C8, useful for  
PT treating or preventing cancer that expresses or over expresses 125P5C8.

XX Disclosure; Page 200; 274pp; English.  
PS  
XX  
CC The present invention relates to compositions comprising a substance that  
CC modulates the status of 125P5C8 or a molecule that is modulated by  
CC 125P5C8. The status of a cell that expresses 125P5C8 is modulated. The  
CC composition is useful for treating cancer, particularly prostate,  
CC bladder, kidney, colon, ovary or breast cancer. The 125P5C8 protein  
CC and/or a nucleotide sequence encoding the protein is useful for  
CC immunising a mammal against cancer. The present sequence is a 125P5C8  
CC epitope shown in the exemplification of the invention  
XX  
SQ Sequence 15 AA;  
XX  
Query Match 30.2%; Score 29; DB 5; Length 15;  
Best Local Similarity 36.4%; Pred. No. 7.2e+02;  
Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;  
OY 7 GYLLTAVSPG 17  
DB 5 GHILNGTNP 15  
XX  
RESULT 78  
ABJ14669  
ID ABJ14669 standard; peptide; 15 AA.  
XX  
AC ABJ14669;  
XX  
DT 10-DEC-2002 (first entry)  
XX  
DE Human 125P5C8 epitope #3295.  
XX  
KW Human; 125P5C8; cancer; cytostatic; breast cancer; prostate cancer;  
KW bladder cancer; kidney cancer; colon cancer; ovarian cancer; epitope.  
XX  
OS Homo sapiens.  
XX  
PN WO200272785-A2.  
XX  
PD 19-SBP-2002.  
XX  
PF 13-MAR-2002; 2002WO-US007855.  
XX  
PR 14-MAR-2001; 2001US-00809638.  
XX  
PA (AGEN-) AGENSYS INC.  
XX  
PI Farle M, Challita-Bid PM, Hubert RS, Afar DEH, Raitano AB, Ge W;  
PI Morrison RK, Morrison K, Jakobovits A;  
XX  
DR WPI; 2002-713510/77.  
XX  
PT New composition comprising a substance that modulates the status of  
PT 125P5C8 gene or a molecule that is modulated by 125P5C8, useful for  
PT treating or preventing cancer that expresses or over expresses 125P5C8.  
XX  
PS Disclosure; Page 207; 274pp; English.  
XX  
CC The present invention relates to compositions comprising a substance that  
CC modulates the status of 125P5C8 or a molecule that is modulated by  
CC 125P5C8. The status of a cell that expresses 125P5C8 is modulated. The  
CC composition is useful for treating cancer, particularly prostate,  
CC bladder, kidney, colon, ovary or breast cancer. The 125P5C8 protein  
CC and/or a nucleotide sequence encoding the protein is useful for  
CC immunising a mammal against cancer. The present sequence is a 125P5C8  
CC epitope shown in the exemplification of the invention  
XX  
SQ Sequence 15 AA;  
XX  
Query Match 30.2%; Score 29; DB 5; Length 15;  
Best Local Similarity 36.4%; Pred. No. 7.2e+02;  
Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;



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XX 20-MAY-2004 (first entry)
DT
XX 125P5C8 protein-related peptide #3154.
DE
XX 125P5C8; cancer-associated gene; cancer-associated protein; cancer.
XX
XX Unidentified.
OS
XX US2003219444-A1.
XX
XX 27-NOV-2003.
PD
XX 13-MAR-2002; 2002US-00099460.
PF
XX 14-MAR-2001; 2001US-00809638.
PR
XX (PARI/) PARIS M.
XX (CHAL/) CHALLITA-BID P M.
XX (HUBE/) HUBERT R S.
XX (AFAR/) AFAR D E H.
XX (RAIT/) RAITANO A B.
XX (GEMW/) GE W.
XX (MORR/) MORRISON R K.
XX (MORR/) MORRISON K J M.
XX (JAKO/) JAKOBOVITS A.
XX
XX Farib M, Challita-Bid PM, Hubert RS, Afar DEH, Raitano AB, Ge W;
PI Morrison RK, Morrison KJM, Jakobovits A;
XX
XX WPI; 2004-021932/02.
XX
XX New composition comprising a substance that modulates the status of
PT 125P5C8 gene or a molecule that is modulated by 125P5C8, useful for
PT diagnosing or treating cancer.
XX
XX Example 51; Page 127; 183pp; English.
XX
XX The invention comprises a composition which contains a substance that can
CC modulate the status of 125P5C8 (125P5C8 is a novel cancer-associated
CC gene/protein), or a molecule that is modulated by 125P5C8. The
CC composition of the invention is useful for diagnosing or treating cancer.
CC The present amino acid sequence represents a 125P5C8-related peptide
CC which was used in an example of the invention.
XX
XX Sequence 15 AA;
SQ
Query Match 30.2%; Score 29; DB 8; Length 15;
Best Local Similarity 36.4%; Pred. No. 7.2e+02;
Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
QY 7 GYLLTAAVSPG 17
|:|:|:|
Db 5 GHILSGTNGP 15
RESULT 82
ADL21870
ID ADL21870 standard; peptide; 15 AA.
XX
XX ADL21870;
AC
XX 20-MAY-2004 (first entry)
DT
XX 125P5C8 protein-related peptide #3118.
DE
XX
XX 125P5C8; cancer-associated gene; cancer-associated protein; cancer.
XX Unidentified.
OS
XX US2003219444-A1.
XX
XX 27-NOV-2003.
PD

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```

XX 13-MAR-2002; 2002US-00099460.
PF
XX 14-MAR-2001; 2001US-00809638.
PR
XX (PARI/) PARIS M.
XX (CHAL/) CHALLITA-BID P M.
XX (HUBE/) HUBERT R S.
XX (AFAR/) AFAR D E H.
XX (RAIT/) RAITANO A B.
XX (GEMW/) GE W.
XX (MORR/) MORRISON R K.
XX (MORR/) MORRISON K J M.
XX (JAKO/) JAKOBOVITS A.
XX
XX Farib M, Challita-Bid PM, Hubert RS, Afar DEH, Raitano AB, Ge W;
PI Morrison RK, Morrison KJM, Jakobovits A;
XX
XX WPI; 2004-021932/02.
XX
XX New composition comprising a substance that modulates the status of
PT 125P5C8 gene or a molecule that is modulated by 125P5C8, useful for
PT diagnosing or treating cancer.
XX
XX Example 51; Page 126; 183pp; English.
XX
XX The invention comprises a composition which contains a substance that can
CC modulate the status of 125P5C8 (125P5C8 is a novel cancer-associated
CC gene/protein), or a molecule that is modulated by 125P5C8. The
CC composition of the invention is useful for diagnosing or treating cancer.
CC The present amino acid sequence represents a 125P5C8-related peptide
CC which was used in an example of the invention.
XX
XX Sequence 15 AA;
SQ
Query Match 30.2%; Score 29; DB 8; Length 15;
Best Local Similarity 36.4%; Pred. No. 7.2e+02;
Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
QY 7 GYLLTAAVSPG 17
|:|:|:|
Db 5 GHILSGTNGP 15
RESULT 83
ADL21604
ID ADL21604 standard; peptide; 15 AA.
XX
XX ADL21604;
AC
XX 20-MAY-2004 (first entry)
DT
XX 125P5C8 protein-related peptide #2852.
DE
XX
XX 125P5C8; cancer-associated gene; cancer-associated protein; cancer.
XX Unidentified.
OS
XX US2003219444-A1.
XX
XX 27-NOV-2003.
PD
XX 13-MAR-2002; 2002US-00099460.
PF
XX 14-MAR-2001; 2001US-00809638.
PR
XX (PARI/) PARIS M.
XX (CHAL/) CHALLITA-BID P M.
XX (HUBE/) HUBERT R S.
XX (AFAR/) AFAR D E H.
XX (RAIT/) RAITANO A B.
XX (GEMW/) GE W.
XX (MORR/) MORRISON R K.

```

PA (MORR/) MORRISON K J M.  
PA (JAKO/) JAKOBOVITS A.  
XX  
PI Paris M, Challita-Eid PM, Hubert RS, Afar DEH, Raitano AB, Ge W,  
PI Morrison RK, Morrison KDM, Jakobovits A;  
XX  
DR MPI; 2004-021932/02.  
XX  
PT New composition comprising a substance that modulates the status of  
PT 125P5C8 gene or a molecule that is modulated by 125P5C8, useful for  
PT diagnosing or treating cancer.  
XX  
XX Example 51; Page 124; 183pp; English.  
XX  
XX The invention comprises a composition which contains a substance that can  
CC modulate the status of 125P5C8 (125P5C8 is a novel cancer-associated  
CC gene/protein), or a molecule that is modulated by 125P5C8. The  
CC composition of the invention is useful for diagnosing or treating cancer.  
CC The present amino acid sequence represents a 125P5C8-related peptide  
CC which was used in an example of the invention.  
XX  
XX Sequence 15 AA;  
SQ  
Query Match 30.2%; Score 29; DB 8; Length 15;  
Best Local Similarity 36.4%; Pred. No. 7.2e+02;  
Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;  
QY 7 GYLLTAAVSRG 17  
Db 5 GHLLNGSTNPG 15  
RESULT 84  
ID ABB14772 standard; protein; 17 AA.  
XX  
AC ABB14772;  
XX  
DT 23-JAN-2002 (first entry)  
XX  
DE Human nervous system related polypeptide SEQ ID NO 3429.  
XX  
XX Human; nootropic; neuroprotective; cytosolic; dermatological; virucide;  
KW immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnereary;  
KW antiparasitism; antisticking; antiamebic; antiaerobic; cancer;  
KW antipneumatic; hepatotropic; cerebroprotective; antiinflammatory;  
KW antiallergic; antidiabetic; antitumor; anticonvulsant; antifungal;  
KW antiparasitic; cardiac; immune disorder; cardiovascular disorder;  
KW neurological disease; infection; nephrotropic; gene therapy; vaccine.  
XX  
OS Homo sapiens.  
XX  
XX WO200159063-A2.  
PN  
PD 16-AUG-2001.  
XX  
XX 17-JAN-2001; 2001WO-US001334.  
PF  
XX  
PR 31-JAN-2000; 2000US-0179065P.  
PR 04-FEB-2000; 2000US-0180628P.  
PR 24-FEB-2000; 2000US-0184664P.  
PR 02-MAR-2000; 2000US-0186350P.  
PR 16-MAR-2000; 2000US-0189874P.  
PR 17-MAR-2000; 2000US-0190076P.  
PR 18-APR-2000; 2000US-0198123P.  
PR 19-MAY-2000; 2000US-0205515P.  
PR 07-JUN-2000; 2000US-0209467P.  
PR 28-JUN-2000; 2000US-0214886P.  
PR 30-JUN-2000; 2000US-0215135P.  
PR 07-JUL-2000; 2000US-0216647P.  
PR 07-JUL-2000; 2000US-0216880P.  
PR 11-JUL-2000; 2000US-0217487P.  
PR 11-JUL-2000; 2000US-0217496P.

PR 14-JUL-2000; 2000US-0218290P.  
PR 26-JUL-2000; 2000US-0220963P.  
PR 26-JUL-2000; 2000US-0220964P.  
PR 14-AUG-2000; 2000US-0224518P.  
PR 14-AUG-2000; 2000US-0224519P.  
PR 14-AUG-2000; 2000US-0225213P.  
PR 14-AUG-2000; 2000US-0225214P.  
PR 14-AUG-2000; 2000US-0225267P.  
PR 14-AUG-2000; 2000US-0225268P.  
PR 14-AUG-2000; 2000US-0225270P.  
PR 14-AUG-2000; 2000US-0225447P.  
PR 14-AUG-2000; 2000US-0225477P.  
PR 14-AUG-2000; 2000US-0225577P.  
PR 14-AUG-2000; 2000US-0225758P.  
PR 14-AUG-2000; 2000US-0225759P.  
PR 18-AUG-2000; 2000US-0226779P.  
PR 22-AUG-2000; 2000US-0226681P.  
PR 22-AUG-2000; 2000US-0226688P.  
PR 22-AUG-2000; 2000US-0227182P.  
PR 23-AUG-2000; 2000US-0227009P.  
PR 30-AUG-2000; 2000US-0228924P.  
PR 01-SEP-2000; 2000US-0229287P.  
PR 01-SEP-2000; 2000US-0229343P.  
PR 01-SEP-2000; 2000US-0229344P.  
PR 01-SEP-2000; 2000US-0229345P.  
PR 05-SEP-2000; 2000US-0229509P.  
PR 05-SEP-2000; 2000US-0229513P.  
PR 06-SEP-2000; 2000US-0230437P.  
PR 06-SEP-2000; 2000US-0230438P.  
PR 08-SEP-2000; 2000US-0231242P.  
PR 08-SEP-2000; 2000US-0231243P.  
PR 08-SEP-2000; 2000US-0231244P.  
PR 08-SEP-2000; 2000US-0231413P.  
PR 08-SEP-2000; 2000US-0231414P.  
PR 08-SEP-2000; 2000US-0232080P.  
PR 08-SEP-2000; 2000US-0232081P.  
PR 12-SEP-2000; 2000US-0231968P.  
PR 14-SEP-2000; 2000US-0232397P.  
PR 14-SEP-2000; 2000US-0232398P.  
PR 14-SEP-2000; 2000US-0232399P.  
PR 14-SEP-2000; 2000US-0232400P.  
PR 14-SEP-2000; 2000US-0232401P.  
PR 14-SEP-2000; 2000US-0233063P.  
PR 14-SEP-2000; 2000US-0233064P.  
PR 14-SEP-2000; 2000US-0233065P.  
PR 21-SEP-2000; 2000US-0234223P.  
PR 21-SEP-2000; 2000US-0234274P.  
PR 25-SEP-2000; 2000US-0234997P.  
PR 25-SEP-2000; 2000US-0234998P.  
PR 26-SEP-2000; 2000US-0235484P.  
PR 27-SEP-2000; 2000US-0235834P.  
PR 27-SEP-2000; 2000US-0235836P.  
PR 29-SEP-2000; 2000US-0236327P.  
PR 29-SEP-2000; 2000US-0236376P.  
PR 29-SEP-2000; 2000US-0236386P.  
PR 29-SEP-2000; 2000US-0236397P.  
PR 29-SEP-2000; 2000US-0236398P.  
PR 02-OCT-2000; 2000US-0236802P.  
PR 02-OCT-2000; 2000US-0237037P.  
PR 02-OCT-2000; 2000US-0237038P.  
PR 02-OCT-2000; 2000US-0237039P.  
PR 02-OCT-2000; 2000US-0237040P.  
PR 13-OCT-2000; 2000US-0239352P.  
PR 13-OCT-2000; 2000US-0239377P.  
PR 20-OCT-2000; 2000US-0240960P.  
PR 20-OCT-2000; 2000US-0241785P.  
PR 20-OCT-2000; 2000US-0241786P.  
PR 20-OCT-2000; 2000US-0241787P.  
PR 20-OCT-2000; 2000US-0241808P.  
PR 20-OCT-2000; 2000US-0241809P.  
PR 20-OCT-2000; 2000US-0241826P.  
PR 20-OCT-2000; 2000US-0242221P.  
PR 01-NOV-2000; 2000US-0244617P.

PR 08-NOV-2000; 2000US-0246474P.  
 PR 08-NOV-2000; 2000US-0246475P.  
 PR 08-NOV-2000; 2000US-0246476P.  
 PR 08-NOV-2000; 2000US-0246477P.  
 PR 08-NOV-2000; 2000US-0246478P.  
 PR 08-NOV-2000; 2000US-0246523P.  
 PR 08-NOV-2000; 2000US-0246524P.  
 PR 08-NOV-2000; 2000US-0246525P.  
 PR 08-NOV-2000; 2000US-0246526P.  
 PR 08-NOV-2000; 2000US-0246527P.  
 PR 08-NOV-2000; 2000US-0246528P.  
 PR 08-NOV-2000; 2000US-0246532P.  
 PR 08-NOV-2000; 2000US-0246609P.  
 PR 08-NOV-2000; 2000US-0246610P.  
 PR 08-NOV-2000; 2000US-0246611P.  
 PR 08-NOV-2000; 2000US-0246613P.  
 PR 17-NOV-2000; 2000US-0249207P.  
 PR 17-NOV-2000; 2000US-0249208P.  
 PR 17-NOV-2000; 2000US-0249209P.  
 PR 17-NOV-2000; 2000US-0249210P.  
 PR 17-NOV-2000; 2000US-0249211P.  
 PR 17-NOV-2000; 2000US-0249212P.  
 PR 17-NOV-2000; 2000US-0249213P.  
 PR 17-NOV-2000; 2000US-0249215P.  
 PR 17-NOV-2000; 2000US-0249216P.  
 PR 17-NOV-2000; 2000US-0249217P.  
 PR 17-NOV-2000; 2000US-0249218P.  
 PR 17-NOV-2000; 2000US-0249244P.  
 PR 17-NOV-2000; 2000US-0249245P.  
 PR 17-NOV-2000; 2000US-0249264P.  
 PR 17-NOV-2000; 2000US-0249265P.  
 PR 17-NOV-2000; 2000US-0249267P.  
 PR 17-NOV-2000; 2000US-0249299P.  
 PR 17-NOV-2000; 2000US-0249300P.  
 PR 01-DEC-2000; 2000US-0250391P.  
 PR 01-DEC-2000; 2000US-0251160P.  
 PR 05-DEC-2000; 2000US-0251030P.  
 PR 05-DEC-2000; 2000US-0251988P.  
 PR 06-DEC-2000; 2000US-0251719P.  
 PR 08-DEC-2000; 2000US-0251479P.  
 PR 08-DEC-2000; 2000US-0251856P.  
 PR 08-DEC-2000; 2000US-0251868P.  
 PR 08-DEC-2000; 2000US-0251869P.  
 PR 08-DEC-2000; 2000US-0251989P.  
 PR 11-DEC-2000; 2000US-0251990P.  
 PR 05-JAN-2001; 2001US-0259678P.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PT Rosen CA, Barash SC, Ruben SM;  
 PT  
 DR WPI, 2001-541565/60.  
 DR N-PSDB; ABA11098.  
 XX  
 PT Nucleic acids encoding 3224 human nervous system antigen polypeptides,  
 PT useful for preventing, diagnosing and/or treating nervous system cancers  
 PT and metastases.  
 XX  
 XX  
 XX Claim 11; SEQ ID NO 3429; 1701pp + Sequence listing; English.  
 XX  
 CC The invention relates to novel genes (ABA11004-ABA21534) and proteins  
 CC (AB14678-AB18001) useful for preventing, treating or ameliorating  
 CC medical conditions e.g. by protein or gene therapy. The genes are  
 CC isolated from a range of human tissues disclosed in the specification.  
 CC The nucleic acids, proteins, antibodies and (ant)agonists are useful in  
 CC the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and  
 CC ovarian cancer and other cancers of the adrenal gland, bone, bone marrow,  
 CC breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune  
 CC disorders e.g. Addison's disease, allergies, autoimmune haemolytic  
 CC anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,  
 CC multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c)

CC cardiovascular disorders such as myocardial ischaemias; (d) wound healing  
 CC ; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f)  
 CC infectious diseases such as viral, bacterial, fungal and parasitic  
 CC infections. Note: The sequence data for this patent did not form part of  
 CC the printed specification, but was obtained in electronic format directly  
 CC from WIPO at [http://wipo.int/pub/published\\_pct\\_sequences](http://wipo.int/pub/published_pct_sequences)  
 XX  
 XX Sequence 17 AA;  
 SQ  
 Query Match 30.2%; Score 29; DB 4; Length 17;  
 Best Local Similarity 54.5%; Pred. No. 8.4e+02;  
 Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
 QY 3 PEPHYLTNA 13  
 Db 1 WDPGLSVTAA 11  
 RESULT 85  
 ID AEB11968 standard; peptide; 17 AA.  
 XX  
 AC AEB11968;  
 XX  
 DT 25-AUG-2005 (first entry)  
 XX  
 DE Salmonella flagellin tryptic peptide.  
 XX  
 KM Flagellin; cytostatic; antidote; cancer; neoplasm; stress; tranquilizer.  
 XX  
 OS Salmonella typhimurium.  
 XX  
 PN WO2005056042-A2.  
 XX  
 PD 23-JUN-2005.  
 XX  
 PF 02-DEC-2004; 2004WO-US040753.  
 XX  
 PR 02-DEC-2003; 2003US-0526460P.  
 PR 02-DEC-2003; 2003US-0526461P.  
 PR 02-DEC-2003; 2003US-0526496P.  
 PR 02-DEC-2003; 2003US-0526666P.  
 XX  
 PA (CLEV-) CLEVELAND CLINIC FOUND.  
 XX  
 PI Gudkov AV;  
 XX  
 DR WPI, 2005-458516/46.  
 XX  
 PT Protecting patient from effects of radiation treatment or treatment or  
 PT condition that triggers apoptosis comprises administering flagellin.  
 PT  
 XX  
 PS Example 3; Fig 3; 67pp; English.  
 XX  
 CC The invention provides a method of protecting a mammal from the effects  
 CC of radiation by administering a composition comprising flagellin. The  
 CC composition may be administered in combination with a radioprotectant,  
 CC such as an antioxidant selected from amifostine and vitamin B, or a  
 CC cytokine such as stem cell factor. The method may also be used to protect  
 CC a patient from one or more treatments or conditions that trigger  
 CC apoptosis, such as cancer treatment by chemotherapy or radiotherapy, or a  
 CC stress resulting from radiation, wounding, poisoning, infection or  
 CC temperature shock. Preferably the flagellin is derived from a *Salmonella*  
 CC species. The present sequence is that of a tryptic peptide of a  
 CC *Salmonella* flagellin, isolated in an example from the invention which  
 CC showed that flagellin activates nuclear factor-kappa B.  
 XX  
 SQ Sequence 17 AA;  
 Query Match 30.2%; Score 29; DB 9; Length 17;  
 Best Local Similarity 50.0%; Pred. No. 8.4e+02;  
 Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 7 GYLTTAAVSPGK 18  
| : : | : : |  
DB 6 GAVVTDVAVPDK 17

RESULT 86  
ID AEB11815 standard; peptide; 17 AA.  
XX AEB11815;  
AC

XX 25-AUG-2005 (first entry)  
DT  
XX

DE Salmonella typhimurium flagellin tryptic peptide.

XX Nuclear factor kappa B inducer; flagellin; cytoskeletal; flagellin; cancer;  
KM neoplasm; stress; tranquilizer.

OS Salmonella typhimurium.

PN MO2005056054-A2.

PD 23-JUN-2005.

XX 02-DEC-2004; 2004MO-US040749.

PR 02-DEC-2003; 2003US-0526461P.

PR 02-DEC-2003; 2003US-0526496P.

PR 02-DEC-2004; 2004US-0526460P.

XX (CLEV-) CLEVELAND CLINIC FOUND.

PI Gudkov AV, Stark G, Lu T, Burdelya L;  
XX WPI; 2005-458520/45.

PT Protection of a patient from at least one treatment e.g. cancer treatment  
PT that trigger apoptosis involves administering a composition comprising an  
PT agent, which induces NF-KB.

PS Example 3; Fig 3; 68pp; English.

XX The present invention relates to a method of protecting a patient from  
CC one or more treatments that trigger apoptosis by administering a  
CC composition comprising an agent that induces nuclear factor kappa B (NF-  
CC KB). The agent may be flagellin or transforming growth factor-beta. The  
CC treatment may be administered prior to, together with, or after a  
CC treatment for the cancer. The invention also provides methods of using  
CC the NF-KB inducer agent to: treat a mammal suffering from a  
CC constitutively active NF-KB cancer; treat a mammal suffering from damage  
CC to normal tissue attributable to treatment of a cancer or to stress; and  
CC to modulate cell aging in a mammal. Also provided is a method of  
CC screening for an inducer of NF-KB. The cancer treatment includes  
CC treatment for breast, colon, lung, kidney, liver cancer etc. The stress  
CC includes wounding, poisoning, infection and temperature shock. The  
CC treatment modulates cell aging and avoids side effects. In an example  
CC from the invention, the NF-KB activating factor in a Salmonella culture  
CC broth was identified as flagellin by mass spectrometry. The present  
CC sequence is that of an isolated flagellin tryptic peptide.

XX Sequence 17 AA;

Query Match 30.2%; Score 29; DB 9; Length 17;  
Best Local Similarity 50.0%; Pred. No. 8.4e+02;  
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 7 GYLTTAAVSPGK 18  
| : : | : : |  
DB 6 GAVVTDVAVPDK 17

RESULT 87  
ID AEA52660  
XX AEA52660 standard; peptide; 17 AA.  
XX

AC AEA52660;

XX 25-AUG-2005 (first entry)  
DT  
XX

DE Peptide from Salmonella flagellin, peptide #11.

XX Apoptosis modulation; flagellin; drug screening; p53 modulator;  
KM cytoskeletal; antiemetic; tranquilizer; antimicrobial; antidote;  
KM antipruritic; cancer; stress; radiation sickness; poison intoxication;  
XX infection; temperature disorder.

OS Salmonella.

PN MO2005057218-A2.

PD 23-JUN-2005.

XX 02-DEC-2004; 2004MO-US040579.

PR 02-DEC-2003; 2003US-0526460P.

PR 02-DEC-2003; 2003US-0526461P.

PR 02-DEC-2003; 2003US-0526496P.

XX (CLEV-) CLEVELAND CLINIC FOUND.

PI Gudkov AV;

XX WPI; 2005-445220/45.

PT Screening for apoptosis modulator, involves adding suspected modulator to  
PT cell-based apoptosis system, separately adding control to cell-based  
PT apoptosis system, and comparing level of apoptosis of suspected modulator  
PT and control.

PS Disclosure; Fig 3; 68pp; English.

XX The present invention relates to a method of protecting a patient from  
CC treatments that trigger apoptosis by administering an agent that induces  
CC nuclear factor-kappaB. The agent may be flagellin or TGFbeta. Claimed is  
CC a method of screening (M1) for a modulator of apoptosis (I), by adding a  
CC suspected modulator to a cell-based apoptosis system; separately adding a  
CC control to a cell-based apoptosis system; and comparing the level of  
CC apoptosis in steps (a) and (b). The suspected modulator is derived from a  
CC mammalian parasite, such as Salmonella, Mycoplasma and Chlamydia. (M1)  
CC preferably involves screening for a modulator of NF-kappaB, of  
CC transforming growth factor beta (TGFbeta), or modulator of p53.  
CC Cytostatic; Antiemetic; Tranquillizer; Vulnerary; Antimicrobial; Antidote;  
CC Vasotrophic. Apoptosis modulator; NF-kappa B modulator; TGFbeta; modulator  
CC; p53 pathway modulator. (M1) is useful for screening a modulator of  
CC apoptosis, preferably modulator of NF-kappaB, TGFbeta or p53. The  
CC modulator is useful for treating cancer, which involves administering (I)  
CC to a subject in need of treatment, where (I) enhances apoptosis. The  
CC treatment is a cancer treatment such as chemotherapy or radiation  
CC therapy. (I) is useful for treating a mammal suffering from damage to  
CC normal tissue attributable to treatment of a cancer, modulating cell  
CC aging in a mammal, and for protecting a patient from conditions that  
CC trigger apoptosis, where the condition is stress, radiation, wounding,  
CC poisoning, infection and temperature shock. The present sequence is a  
CC peptide from flagellin, peptide #11.

XX Sequence 17 AA;

Query Match 30.2%; Score 29; DB 9; Length 17;  
Best Local Similarity 50.0%; Pred. No. 8.4e+02;  
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 7 GYLTTAAVSPGK 18  
| : : | : : |

Db 6 GAVVTDVADPK 17

RESULT 88

ABE53031

ID ABE53031 standard; peptide; 17 AA.

XX

XX ABE53031;

AC

XX

DT 22-SEP-2005 (first entry)

XX

DE Salmomella flagellin peptide #11.

XX

XX vulnerability; antimicrobial; cyostatic; tranquilizer; apoptosis inhibition;

KM therapeutic; chemotherapy; radiotherapy; infection; poison intoxication;

KM anticancer; toxicity and intoxication; wound healing; injury; stress;

XX psychiatric disorder; cancer neoplasm; flagellin.

XX

OS Salmomella.

XX

PN W02005056055-A2.

XX

PD 23-JUN-2005.

XX

PF 02-DEC-2004; 2004WO-US040750.

XX

PR 02-DEC-2003; 2003US-0526460P.

PR 02-DEC-2003; 2003US-0526461P.

PR 02-DEC-2003; 2003US-0526466P.

PR 02-DEC-2003; 2003US-0526666P.

XX

PA (CLEV-) CLEVEBLAND CLINIC FOUND.

XX

PI Gudkov AV;

XX

DR WPI; 2005-458521/46.

XX

PT Use of a composition (A) comprising an agent which induces necrosis

PT factor (NF)-kappa B for protection of mammal from the effects of

PT radiation and for the treatment or condition that trigger apoptosis.

XX

PS Example 3; Fig 3; 67pp; English.

XX

XX The invention describes a method of protecting a mammal from the effects

CC of radiation comprising administration of a composition (A) comprising an

CC agent which induces necrosis factor (NF)-kappa B. (1) is useful for the

CC treatment (such as cancer treatment, chemotherapy, radiation therapy or

CC stress e.g. radiation, wounding, poisoning, infection or temperature

CC shock) or conditions that trigger apoptosis. (1) is useful for the

CC protection of a mammal from the effects of radiation. This is the amino

CC acid sequence of a salmonella flagellin peptide identified from a cell

CC culture extract identifying flagellin as inducing NF-kB DNA binding

CC activity.

XX

XX

SO Sequence 17 AA;

Query Match 30.2%; Score 29; DB 9; Length 17;

Best Local Similarity 50.0%; Pred. No. 8.4e+02;

Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 7 GYLTAAVSPBK 18

DB 6 GAVVTDVADPK 17

RESULT 89

ABU09114

ID ABU09114 standard; peptide; 18 AA.

XX

XX ABU09114;

AC

XX

DT 16-JUN-2003 (first entry)

XX

DE C. elegans Mad peptide containing a SID domain.

XX

XX Mad; SID; msin3 interacting domain; bHLHZip; gene expression;

KM basic region-helix-loop-helix-leucine zipper protein;

KM transcriptional repressor; transcriptional regulator.

XX

OS Caenorhabditis elegans.

XX

XX US6528620-B1.

PN

XX

PD 04-MAR-2003.

XX

PF 08-NOV-2000; 2000US-00708906.

XX

PR 08-NOV-1999; 99US-0163960P.

XX

PA (UTAH) UNIV UTAH RES FOUND.

XX

PI Ayer DE, Billin AN;

XX

DR WPI; 2003-370637/35.

XX

PT New chimeric transcriptional regulator useful for regulating

PT transcription of a selected gene in a cell and for gene therapy

PT applications, comprises DNA-binding domain and a msin3A interaction

PT domain.

XX

PS Example 2; Fig 2A; 25pp; English.

XX

XX The invention relates to a chimeric transcriptional regulator comprising

CC a DNA-binding domain and a msin3A interaction domain (SID) capable of

CC binding msin3A. The SID consists of amino acids 8-20 of the human basic

CC region-helix-loop-helix-leucine zipper (bHLHZip) protein, Mad1. The SID

CC appears as ABU09103). Also included are a fusion comprising a SID capable

CC of binding msin3A, where the SID is linked to a DNA-binding molecule and

CC creating a transcriptional regulator, by synthesizing an msin3A-binding

CC molecule and linking the msin3A-binding molecule to a heterologous DNA-

CC binding molecule. The chimeric regulator and fusion protein are useful

CC for repressing transcription of a selected gene in a cell and in the

CC field of functional genomics as analytical tools to modulate the

CC transcription of any gene being studied in either cell or tissue cultures

CC or in whole living organisms. The chimeric regulator, preferably a

CC chimeric repressor, is useful in gene therapy applications. The present

CC sequence is a SID domain containing peptide derived from a basic region-

CC helix-loop-helix-leucine zipper (bHLHZip) protein, used to determine a

CC minimal SID domain peptide sequence

XX

SO Sequence 18 AA;

Query Match 30.2%; Score 29; DB 6; Length 18;

Best Local Similarity 85.7%; Pred. No. 9e+02;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 GYLTAA 13

DB 3 GHULTAA 9

RESULT 90

ADE37053

ID ADE37053 standard; peptide; 19 AA.

XX

XX ADE37053;

AC

XX

DT 29-JAN-2004 (first entry)

XX

DE Nylon suture binding peptide SEQ ID NO:114.

XX

XX interfacial biomaterial; binding agent; biological substrate; cyostatic;

KM T1e2 receptor antagonist; cell culture; biological array;

KM transplanted cell; transplanted tissue; T1e2 receptor modulation;

KM tumour angiogenesis.

XX

OS Synthetic.  
XX  
PN WO2003072542-A2.  
XX  
PD 04-SEP-2003.  
XX  
PF 20-NOV-2002; 2002WO-US037414.  
XX  
PR 20-NOV-2001; 2001US-0331843P.  
XX  
PA (UYDU-) UNIV DUKE.  
XX  
PI Grinstaff MW, Kenan DJ, Walsh EB, Middleton C;  
XX  
DR WPI; 2003-833266/77.  
XX  
PT New interfacial biomaterial having binding agents that binds a non-  
PT biological and biological substrate, useful in cell culture, in the  
PT preparation of biological arrays, and for diagnostic and therapeutic  
PT interface.  
XX  
XX Example 6; SEQ ID NO 114; 150pp; English.  
XX  
CC The present invention describes an interfacial biomaterial (I) comprising  
CC binding agents, each having a first ligand that specifically binds a  
CC target non-biological substrate and a second ligand that specifically  
CC binds a target biological substrate. The binding agents define an  
CC interface between the target non-biological substrate and the target  
CC biological substrate, or a non-binding domain substantially lacks binding  
CC to a target biological substrate. (I) has cytostatic activity, and can be  
CC used as a T1e2 receptor antagonist. The methods and compositions of the  
CC present invention can be used in cell culture of fibroblasts, endothelial  
CC cells, stem cells, embryonic and newborn tissue cells and osteoblasts, in  
CC the preparation of biological arrays, in the enhancement of an  
CC interaction between biological materials, for coating implants for in  
CC vivo use, for coating donor transplant cells or tissues, for diagnostic  
CC and therapeutic interface, and for modulating T1e2 receptors in tumour  
CC angiogenesis. The present sequence is used in the exemplification of the  
CC present invention.  
XX  
SQ Sequence 19 AA;  
XX  
Query Match 30.2%; Score 29; DB 7; Length 19;  
Best Local Similarity 62.5%; Pred. No. 9.6e+02;  
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 DAFEPHGY 8  
DB 3 DFFNRHGY 10  
XX  
RESULT 91  
AAW21835  
ID AAW21835 standard; peptide; 20 AA.  
XX  
AC AAW21835;  
XX  
DT 26-OCT-1997 (first entry)  
XX  
DE KHLN-containing peptide.  
XX  
KM Immunosuppression; major histocompatibility complex class II; MHC;  
KM mixed lymphocyte reaction; allorecognition; cytotoxic T cell;  
KM alloimmunity; autoimmune disease; organ transplant; multiple sclerosis;  
KM rheumatoid arthritis.  
XX  
OS Synthetic.  
XX  
PN WO9710711-A1.  
XX  
PD 27-MAR-1997.  
XX  
PF 23-SEP-1996; 96WO-US015662.

XX  
PR 21-SEP-1995; 95US-0004117P.  
XX  
PA (AUTO-) AUTOIMMUNE INC.  
XX  
PI Sayegh MH, Murphy BT, Carpenter CB;  
XX  
DR WPI; 1997-202534/18.  
XX  
PT Suppression of immune responses with major histocompatibility complex  
PT class II peptide(s) - useful in allo:immunity, e.g. organ  
PT transplantation, and auto:immunity, e.g. in multiple sclerosis or  
PT rheumatoid arthritis.  
XX  
PS Disclosure; Page 13; 55pp; English.  
XX  
CC KHLN-containing peptides (AAW21835-37) derived from the alpha chain of  
CC the class II MHC can be administered to an individual as a means of  
CC suppressing an immune response. The peptides can suppress at least one  
CC (preferably all) of the following: a mixed lymphocyte reaction or other T  
CC -cell allorecognition reaction; generation of cytotoxic T-cells  
CC recognising an alloantigen; lymphocyte proliferation against tissue  
CC antigen; and stimulatory cytokine production by lymphocytes. Immune  
CC responses that can be abated or suppressed include alloimmunity (e.g. in  
CC organ transplantation) and autoimmunity (e.g. in multiple sclerosis or  
CC rheumatoid arthritis). Immune responses can be down-regulated  
CC specifically without the adverse effects of conventional treatments  
XX  
SQ Sequence 20 AA;  
XX  
Query Match 30.2%; Score 29; DB 2; Length 20;  
Best Local Similarity 46.2%; Pred. No. 1e+03;  
Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;  
QY 3 FEPHGYLTLAAVS 15  
DB 1 FDPQGLRMAYVA 13  
XX  
RESULT 92  
ADX83646  
ID ADX83646 standard; peptide; 16 AA.  
XX  
AC ADX83646;  
XX  
DT 05-MAY-2005 (first entry)  
XX  
DE Rat insulin receptor substrate -1 (449-664) phosphopeptide, seqid:15.  
XX  
KM Insulin receptor substrate protein kinase inhibitor; insulin receptor;  
KM agonist; pharmaceutical; protein kinase C zeta inhibitor;  
KM protein kinase C inhibitor; non-insulin dependent diabetes;  
KM endocrine disease; gastrointestinal disease; metabolic disorder;  
KM antidiabetic; phosphorylation.  
XX  
OS Ratus sp.  
XX  
PN EP1508806-A1.  
XX  
PD 23-FEB-2005.  
XX  
PF 16-AUG-2003; 2003EP-00018517.  
XX  
PR 16-AUG-2003; 2003EP-00018517.  
XX  
PA (AVER ) AVENTIS PHARMA DEUT GMBH.  
XX  
PI Temagels N, Eckel J, Metzger S, Sommerfeld M;  
XX  
DR WPI; 2005-174505/19.  
XX  
PT Identifying insulin receptor substrate (IRS) protein kinase inhibitor, by  
PT contacting protein kinase C (PKC)-zeta with IRS peptide having PKC-zeta-



PT Ser-phosphorylation site and putative inhibitor, and measuring  
 PT phosphorylation.  
 XX  
 PS Example 5, SEQ ID NO 15, 50pp; English.  
 CC The present invention relates to a method for the identification of  
 CC insulin receptor substrate (IRS) protein kinase inhibitors or agonists  
 CC which involves contacting protein kinase C (PKC)-zeta with at least one  
 CC IRS peptide comprising at least one PKC-zeta-Ser-phosphorylation site in  
 CC the presence of at least one putative inhibitor and measuring the  
 CC phosphorylation of the PKC-zeta-Ser-phosphorylation site. The IRS-1  
 CC peptides of the invention are useful for producing antibodies against a  
 CC PKC-zeta-Ser-phosphorylation site and for preparing a pharmaceutical  
 CC composition for the treatment of diabetes type II. The invention also  
 CC provides an automated and miniaturized method for screening IRS kinase  
 CC protein inhibitors or agonists. The present sequence is rat insulin  
 CC receptor substrate (IRS)-1 (449-664) phosphopeptide. This peptide is used  
 CC in the identification and functional analysis of IRS-1 serine  
 CC phosphorylation sites targeted by PKC.  
 XX  
 SQ Sequence 16 AA;  
 Query Match 29.7%; Score 28.5; DB 9; Length 16;  
 Best Local Similarity 40.0%; Pred. No. 9.Se+02;  
 Matches 6; Conservative 5; Mismatches 1; Indels 3; Gaps 1;  
 QY 4 EPHGYL--TAAVS 15  
 :|:|:|:|:|:|  
 Db 2 DPNGYMMSPSMAAS 16  
 RESULT 93  
 ADO37172  
 ID ADO37172 standard; peptide; 6 AA.  
 XX  
 AC ADO37172;  
 XX  
 DT 29-JUL-2004 (first entry)  
 XX  
 DE Binding partner polypeptide of the invention SEQ ID NO:232.  
 XX  
 KM polypeptide-tagged collection; capture system; tagged polypeptide;  
 KM pharmaceutical; diagnostic.  
 XX  
 OS Synthetic.  
 XX  
 PN WO2004039962-A2.  
 XX  
 PD 13-MAY-2004.  
 XX  
 PF 30-OCT-2003; 2003WO-US034821.  
 XX  
 PR 30-OCT-2002; 2002US-0422923P.  
 PR 30-OCT-2002; 2002US-0423018P.  
 XX  
 PA (POIN-) POINTILLISTE INC.  
 XX  
 PI Ault-Riche D, Atkinson B, Geysen MH;  
 XX  
 DR WPI; 2004-376185/35.  
 XX  
 PT Evenly distributing tags among members of a starting library, useful in  
 PT developing pharmaceuticals and diagnostics, comprises dividing the  
 PT starting library into sub libraries and attaching a tag to members of  
 PT each sub library.  
 XX  
 PS Claim 141; SEQ ID NO 232; 510pp; English.  
 XX  
 CC The invention relates to novel methods for producing polypeptide-tagged  
 CC collections and capture systems containing the tagged polypeptides. The  
 CC method is useful for evenly distributing tags among members of a starting  
 CC library. The system, collection, kits and methods are useful in  
 CC developing pharmaceuticals and diagnostics. The present sequence is used

CC in the exemplification of the invention.  
 XX  
 SQ Sequence 6 AA;  
 Query Match 29.2%; Score 28; DB 8; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 5 PHGY 8  
 :|:|:|:|  
 Db 1 PHGY 4  
 RESULT 94  
 ADO37180  
 ID ADO37180 standard; peptide; 6 AA.  
 XX  
 AC ADO37180;  
 XX  
 DT 29-JUL-2004 (first entry)  
 XX  
 DE Binding partner polypeptide of the invention SEQ ID NO:240.  
 XX  
 KM polypeptide-tagged collection; capture system; tagged polypeptide;  
 KM pharmaceutical; diagnostic.  
 XX  
 OS Synthetic.  
 XX  
 PN WO2004039962-A2.  
 XX  
 PD 13-MAY-2004.  
 XX  
 PF 30-OCT-2003; 2003WO-US034821.  
 XX  
 PR 30-OCT-2002; 2002US-0422923P.  
 PR 30-OCT-2002; 2002US-0423018P.  
 XX  
 PA (POIN-) POINTILLISTE INC.  
 XX  
 PI Ault-Riche D, Atkinson B, Geysen MH;  
 XX  
 DR WPI; 2004-376185/35.  
 XX  
 PT Evenly distributing tags among members of a starting library, useful in  
 PT developing pharmaceuticals and diagnostics, comprises dividing the  
 PT starting library into sub libraries and attaching a tag to members of  
 PT each sub library.  
 XX  
 PS Claim 141; SEQ ID NO 240; 510pp; English.  
 XX  
 CC The invention relates to novel methods for producing polypeptide-tagged  
 CC collections and capture systems containing the tagged polypeptides. The  
 CC method is useful for evenly distributing tags among members of a starting  
 CC library. The system, collection, kits and methods are useful in  
 CC developing pharmaceuticals and diagnostics. The present sequence is used  
 CC in the exemplification of the invention.  
 XX  
 SQ Sequence 6 AA;  
 Query Match 29.2%; Score 28; DB 8; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 5 PHGY 8  
 :|:|:|:|  
 Db 1 PHGY 4  
 RESULT 95  
 ADO27694  
 ID ADO27694 standard; peptide; 6 AA.  
 XX  
 AC ADO27694;

XX 12-AUG-2004 (first entry)  
DT Capture system related peptide, SEQ ID 232.  
XX  
DE Capture system.  
XX  
KW Synthetic.  
OS  
XX MO2004042019-A2.  
XX  
XX 21-MAY-2004.  
XX  
XX 30-OCT-2003; 2003MO-US034693.  
PF  
XX 30-OCT-2002; 2002US-0422923P.  
PR 30-OCT-2002; 2002US-0423018P.  
XX  
XX (POIN-) POINTILLISTE INC.  
PA  
XX Ault-Riche D, Atkinson B, Jeseatis L, Kumble KD, Sperinde G;  
PI WPI; 2004-431543/40.  
XX  
XX  
XX Capturing biological particles, by contacting biological particles with  
PT capture system comprising addressed loci, addressed collection of  
PT polypeptide tagged molecules, capture agents, and polypeptide tag to  
PT which capture agent binds.  
XX  
XX Disclosure; SEQ ID NO 232; 505pp; English.  
XX  
XX The present invention relates to a method for the capture and analysis of  
CC biological particle using a capture system. The method is useful for  
CC capturing biological particles such as cells, portions of cells, cell  
CC membranes, viruses, viral capsids, viral particles, bacterial cells,  
CC subcellular compartments, organelles and micelles, prokaryotic cells,  
CC eukaryotic cells, intracellular particles, nuclei, cell membranes, cell  
CC membrane fragments, nuclear membranes, nuclear membranes fragments, viral  
CC vectors or viral capsids with or without packaged nucleic acid, phage,  
CC phage vectors, phage capsids with or without encapsulated nucleotide  
CC acid, liposomes and other micellar agents. The biological particles are  
CC cells chosen from immune cells, neurons, cancer cells, bacterial cells  
CC and infected cells, subcellular compartment, organelles, viral particles  
CC or pathogens. The cells are dendritic cells, T cells, or B cells. The  
CC method is also useful for identifying molecules that interact with  
CC infectious agents, for profiling the surface of a biological particles,  
CC for identifying a modulator of an interaction among proteins in the  
CC biological particle, for identifying molecules that modulates the  
CC trafficking, activity or functional or structural property in the  
CC biological particle, and for mapping epitopes of molecules displayed on  
CC the surface of a biological particles. The method is also useful for  
CC sorting biological particles, for identifying a receptor on the surface  
CC of biological particle that transduces a signal from a polypeptide, and  
CC for identifying the molecule that interacts with an apically-localized  
CC molecule on a biological particle. The present sequence was used to  
CC illustrate the invention.  
XX  
XX Sequence 6 AA;  
SQ  
Query Match 29.2%; Score 28; DB 8; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 5 PHGY 8  
DB 1 PHGY 4  
RESULT 96  
ID ADO27702 standard; peptide; 6 AA.  
XX  
XX ADO27702;  
AC

XX 12-AUG-2004 (first entry)  
DT Capture system related peptide, SEQ ID 240.  
XX  
DE Capture system.  
XX  
KW Synthetic.  
OS  
XX MO2004042019-A2.  
XX  
XX 21-MAY-2004.  
XX  
XX 30-OCT-2003; 2003MO-US034693.  
PF  
XX 30-OCT-2002; 2002US-0422923P.  
PR 30-OCT-2002; 2002US-0423018P.  
XX  
XX (POIN-) POINTILLISTE INC.  
PA  
XX Ault-Riche D, Atkinson B, Jeseatis L, Kumble KD, Sperinde G;  
PI WPI; 2004-431543/40.  
XX  
XX  
XX Capturing biological particles, by contacting biological particles with  
PT capture system comprising addressed loci, addressed collection of  
PT polypeptide tagged molecules, capture agents, and polypeptide tag to  
PT which capture agent binds.  
XX  
XX Disclosure; SEQ ID NO 240; 505pp; English.  
XX  
XX The present invention relates to a method for the capture and analysis of  
CC biological particle using a capture system. The method is useful for  
CC capturing biological particles such as cells, portions of cells, cell  
CC membranes, viruses, viral capsids, viral particles, bacterial cells,  
CC subcellular compartments, organelles and micelles, prokaryotic cells,  
CC eukaryotic cells, intracellular particles, nuclei, cell membranes, cell  
CC membrane fragments, nuclear membranes, nuclear membranes fragments, viral  
CC vectors or viral capsids with or without packaged nucleic acid, phage,  
CC phage vectors, phage capsids with or without encapsulated nucleotide  
CC acid, liposomes and other micellar agents. The biological particles are  
CC cells chosen from immune cells, neurons, cancer cells, bacterial cells  
CC and infected cells, subcellular compartment, organelles, viral particles  
CC or pathogens. The cells are dendritic cells, T cells, or B cells. The  
CC method is also useful for identifying molecules that interact with  
CC infectious agents, for profiling the surface of a biological particles,  
CC for identifying a modulator of an interaction among proteins in the  
CC biological particle, for identifying molecules that modulates the  
CC trafficking, activity or functional or structural property in the  
CC biological particle, and for mapping epitopes of molecules displayed on  
CC the surface of a biological particles. The method is also useful for  
CC sorting biological particles, for identifying a receptor on the surface  
CC of biological particle that transduces a signal from a polypeptide, and  
CC for identifying the molecule that interacts with an apically-localized  
CC molecule on a biological particle. The present sequence was used to  
CC illustrate the invention.  
XX  
XX Sequence 6 AA;  
SQ  
Query Match 29.2%; Score 28; DB 8; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 5 PHGY 8  
DB 1 PHGY 4  
RESULT 97  
ID ADR49879 standard; peptide; 6 AA.  
XX  
XX ADR49879;  
AC

XX 18-NOV-2004 (first entry)  
XX 6-mer peptide epitope works as a highly specific capture agent Seq 240.  
XX self-assembly array; capture agent; epitope; binding partner.  
XX Synthetic.  
XX WO2004071641-A2.  
XX 26-AUG-2004.  
XX 30-OCT-2003; 2003WO-US034747.  
XX 10-FEB-2003; 2003US-0446687P.  
XX (POIN-) POINTILLISTE INC.  
XX (AULT/) AULT-RICHE D.  
XX (KUMB/) KUMBLE K D.  
XX (SCHU/) SCHULZ R.  
XX (SCHU/) SCHULZ K.  
XX Ault-Riche D, Kumble KD, Schulz R, Schulz K;  
XX WPI; 2004-635071/61.  
XX Self-assembled array for monitoring interaction of molecules, comprising  
XX addressable array of capture agents having predetermined binding partners  
XX and conjugates comprising biological particle and/or molecule linked to  
XX binding partners.  
XX Disclosure; SEQ ID NO 240; 443pp; English.  
XX  
XX This invention relates to novel self-assembly arrays that each comprises  
XX an addressable collection of capture agents that have predetermined  
XX binding partners, as well as reagents for the covalent conjugation of the  
XX binding partners to molecules for display in the array. Specifically, it  
XX refers to the production of a flexible experimental surface, which can be  
XX adapted for use with almost any analytical system. The present invention  
XX describes apparatus useful for monitoring an interaction of an exogenous  
XX molecule with a capture agent of the array both in the presence and  
XX absence of candidate compounds, identifying molecules that modulate  
XX trafficking in biological particles or modulate activity, functional or  
XX structural properties of the biological particle. As such, it can be used  
XX for elucidating biological pathways and their reactions that occur either  
XX simultaneously or sequentially, disease processes, inhibitors and  
XX enhancers of a molecular system or for understanding receptor-signal  
XX recognition. In particular, it enables assaying one or more biological  
XX samples having one or more targets per sample on a single array, such  
XX that it is cost effective and specific. This peptide sequence is an  
XX exemplary 6-mer peptide epitope that provides a highly specific capture  
XX agent of the invention.  
XX  
XX Sequence 6 AA;  
XX  
XX Query Match 29.2%; Score 28; DB 8; Length 6;  
XX Best Local Similarity 100.0%; Pred. No. 2e+06;  
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
XX QY 5 PHGY 8  
XX ||||  
XX 1 PHGY 4  
XX  
XX Db  
XX  
XX RESULT 98  
XX ADR49871  
XX ID ADR49871 standard; peptide; 6 AA.  
XX AC ADR49871;  
XX XX  
XX DT 18-NOV-2004 (first entry)  
XX XX

DE 6-mer peptide epitope works as a highly specific capture agent Seq 232.  
XX self-assembly array; capture agent; epitope; binding partner.  
XX Synthetic.  
XX WO2004071641-A2.  
XX 26-AUG-2004.  
XX 30-OCT-2003; 2003WO-US034747.  
XX 10-FEB-2003; 2003US-0446687P.  
XX (POIN-) POINTILLISTE INC.  
XX (AULT/) AULT-RICHE D.  
XX (KUMB/) KUMBLE K D.  
XX (SCHU/) SCHULZ R.  
XX (SCHU/) SCHULZ K.  
XX Ault-Riche D, Kumble KD, Schulz R, Schulz K;  
XX WPI; 2004-635071/61.  
XX Self-assembled array for monitoring interaction of molecules, comprising  
XX addressable array of capture agents having predetermined binding partners  
XX and conjugates comprising biological particle and/or molecule linked to  
XX binding partners.  
XX Disclosure; SEQ ID NO 232; 443pp; English.  
XX  
XX This invention relates to novel self-assembly arrays that each comprises  
XX an addressable collection of capture agents that have predetermined  
XX binding partners, as well as reagents for the covalent conjugation of the  
XX binding partners to molecules for display in the array. Specifically, it  
XX refers to the production of a flexible experimental surface, which can be  
XX adapted for use with almost any analytical system. The present invention  
XX describes apparatus useful for monitoring an interaction of an exogenous  
XX molecule with a capture agent of the array both in the presence and  
XX absence of candidate compounds, identifying molecules that modulate  
XX trafficking in biological particles or modulate activity, functional or  
XX structural properties of the biological particle. As such, it can be used  
XX for elucidating biological pathways and their reactions that occur either  
XX simultaneously or sequentially, disease processes, inhibitors and  
XX enhancers of a molecular system or for understanding receptor-signal  
XX recognition. In particular, it enables assaying one or more biological  
XX samples having one or more targets per sample on a single array, such  
XX that it is cost effective and specific. This peptide sequence is an  
XX exemplary 6-mer peptide epitope that provides a highly specific capture  
XX agent of the invention.  
XX  
XX Sequence 6 AA;  
XX  
XX Query Match 29.2%; Score 28; DB 8; Length 6;  
XX Best Local Similarity 100.0%; Pred. No. 2e+06;  
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
XX QY 5 PHGY 8  
XX ||||  
XX 1 PHGY 4  
XX  
XX Db  
XX  
XX RESULT 99  
XX ADS95517  
XX ID ADS95517 standard; peptide; 6 AA.  
XX AC ADS95517;  
XX XX  
XX DT 13-JAN-2005 (first entry)  
XX XX  
XX DB Tagged polypeptide-associated peptide #46.  
XX XX  
XX KM Peptide tag; epitope; antibody; single-chain antibody fragment; ScFv.

XX Synthetic.  
 OS  
 XX  
 PN US2004209282-A1.  
 PD  
 XX 21-OCT-2004.  
 PF 30-OCT-2003; 2003US-00699088.  
 PR 30-OCT-2002; 2002US-0422923P.  
 PR 30-OCT-2002; 2002US-0423018P.  
 XX  
 PA (AULT/) AULT-RICHE D.  
 PA (ATKI/) ATKINSON B.  
 PI Ault-Riche D, Atkinson B;  
 DR WPI; 2004-756825/74.  
 XX  
 PT Evenly distributing tags among members of starting library by dividing  
 PT starting library into sublibraries, attaching tag to members of  
 PT sublibrary, mixing tagged sublibraries and splitting mixed library into  
 PT array libraries.  
 PS  
 XX Disclosure; SEQ ID NO 232; 293pp; English.  
 XX  
 CC The invention relates to evenly distributing tags (e.g. epitopes) or  
 CC nucleic acid molecules encoding polypeptide tags among members of a  
 CC starting library, involving optionally adjusting the diversity of a  
 CC starting library so that the diversity is within an order of magnitude of  
 CC the number of molecules in the library, dividing the starting library  
 CC into n sublibraries designated 1-n, where n is equal to or less than the  
 CC number of unique tags (where each unique tag specifically binds to a  
 CC different capture agent), attaching a tag to several members of each  
 CC sublibrary to produce n tagged sublibraries containing tagged members  
 CC (where each member has the same tag, and the tag is unique to each  
 CC sublibrary), mixing some or all of the tagged sublibraries to produce a  
 CC mixed library (where the number of tagged molecules added from each  
 CC sublibrary is the same), and splitting the mixed library into q array  
 CC libraries, where q is from 1 up to a predetermined number of arrays. Also  
 CC included are a collection of tagged molecules produced by the method, a  
 CC capture system comprising the tagged polypeptides and an addressable  
 CC collection of capture agent (where each locus in the collection contains  
 CC capture agents that specifically bind to the same tag, and the tagged  
 CC molecules are specifically bound to capture agents), capturing molecules  
 CC (involving contacting a capture system with molecules under conditions,  
 CC where molecules bind to the capture system, and the capture system  
 CC comprises several of addressed loci with an addressed collection of  
 CC polypeptide-tagged molecules bound to addressed capture agents at each  
 CC locus, the capture agents at each locus bind to the same polypeptide tag,  
 CC the polypeptide tag to which the capture agent binds is different among  
 CC the loci, each locus in capture system contains a several of different  
 CC molecules, each with the same tag bound to the capture agent, and the  
 CC polypeptide tags are evenly distributed among the tagged molecules such  
 CC that the diversity of tagged molecules at each locus in the capture  
 CC system is within one order of magnitude), sorting molecules or reducing  
 CC their diversity, and reducing the diversity of a collection of molecules.  
 CC The starting library encodes antibodies (or their fragments or single-  
 CC chain antibody fragments (ScrVs)) or is comprised of antibodies (or their  
 CC fragment), where the antibodies or their fragments specifically bind to  
 CC antigens. The methods are useful for evenly distributing tags among  
 CC members of starting library, for identifying modulators of interactions  
 CC between capture systems and molecules (which involves adding/exposing a  
 CC test compound to the capture system to a condition before, during or  
 CC after contacting the capture system with molecules or before, during or  
 CC after contacting the capture agents with the tagged molecules, and  
 CC identifying a change in an interaction of the molecules with the capture  
 CC system or tagged molecules with the capture agents to identify a test  
 CC compound that modulates the interaction between the molecules and the  
 CC capture system or between tagged molecules and capture agents. The change  
 CC is assessed by detecting a change in binding pattern or a physical or  
 CC chemical change in the bound molecules or a conformational change in the  
 CC bound molecules and/or tagged molecules). The present sequence is a

CC peptide included in the sequence listing but not mentioned anywhere else  
 CC in the specification.  
 CC  
 XX  
 SQ Sequence 6 AA;  
 Query Match 29.2%; Score 28; DB 8; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 5 PHGY 8  
 |||||  
 DB 1 PHGY 4  
 RESULT 100  
 ADS95525  
 ID ADS95525 standard; peptide; 6 AA.  
 XX  
 AC ADS95525;  
 XX  
 DT 13-JAN-2005 (first entry)  
 XX  
 DE Tagged polypeptide-associated peptide #54.  
 XX  
 KM Peptide tag; epitope; antibody; single-chain antibody fragment; ScFv.  
 XX  
 OS Synthetic.  
 XX  
 PN US2004209282-A1.  
 PD  
 XX 21-OCT-2004.  
 PF 30-OCT-2003; 2003US-00699088.  
 PR 30-OCT-2002; 2002US-0422923P.  
 PR 30-OCT-2002; 2002US-0423018P.  
 XX  
 PA (AULT/) AULT-RICHE D.  
 PA (ATKI/) ATKINSON B.  
 PI Ault-Riche D, Atkinson B;  
 DR WPI; 2004-756825/74.  
 XX  
 PT Evenly distributing tags among members of starting library by dividing  
 PT starting library into sublibraries, attaching tag to members of  
 PT sublibrary, mixing tagged sublibraries and splitting mixed library into  
 PT array libraries.  
 PS  
 XX Disclosure; SEQ ID NO 240; 293pp; English.  
 XX  
 CC The invention relates to evenly distributing tags (e.g. epitopes) or  
 CC nucleic acid molecules encoding polypeptide tags among members of a  
 CC starting library, involving optionally adjusting the diversity of a  
 CC starting library so that the diversity is within an order of magnitude of  
 CC the number of molecules in the library, dividing the starting library  
 CC into n sublibraries designated 1-n, where n is equal to or less than the  
 CC number of unique tags (where each unique tag specifically binds to a  
 CC different capture agent), attaching a tag to several members of each  
 CC sublibrary to produce n tagged sublibraries containing tagged members  
 CC (where each member has the same tag, and the tag is unique to each  
 CC sublibrary), mixing some or all of the tagged sublibraries to produce a  
 CC mixed library (where the number of tagged molecules added from each  
 CC sublibrary is the same), and splitting the mixed library into q array  
 CC libraries, where q is from 1 up to a predetermined number of arrays. Also  
 CC included are a collection of tagged molecules produced by the method, a  
 CC capture system comprising the tagged polypeptides and an addressable  
 CC collection of capture agent (where each locus in the collection contains  
 CC capture agents that specifically bind to the same tag, and the tagged  
 CC molecules are specifically bound to capture agents), capturing molecules  
 CC (involving contacting a capture system with molecules under conditions,  
 CC where molecules bind to the capture system, and the capture system  
 CC comprises several of addressed loci with an addressed collection of

CC polypeptide-tagged molecules bound to addressed capture agents at each  
 CC locus, the capture agents at each locus bind to the same polypeptide tag,  
 CC the polypeptide tag to which the capture agent binds is different among  
 CC the loci, each locus in capture system contains a several of different  
 CC molecules, each with the same tag bound to the capture agents, and the  
 CC polypeptide tags are evenly distributed among the tagged molecules such  
 CC that the diversity of tagged molecules at each locus in the capture  
 CC system is within one order of magnitude, sorting molecules or reducing  
 CC their diversity, and reducing the diversity of a collection of molecules.  
 CC The starting library encodes antibodies (or their fragments or single-  
 CC chain antibody fragments (ScFvs)) or is comprised of antibodies (or their  
 CC fragments), where the antibodies or their fragments specifically bind to  
 CC antigens. The methods are useful for evenly distributing tags among  
 CC members of starting library, for identifying modulators of interactions  
 CC between capture systems and molecules (which involves adding/exposing a  
 CC test compound to the capture system to a condition before, during or  
 CC after contacting the capture system with molecules or before, during or  
 CC identifying a change in an interaction of the molecules with the capture  
 CC system or tagged molecules with the capture agents to identify a test  
 CC compound that modulates the interaction between the molecules and the  
 CC capture system or between tagged molecules and capture agents. The change  
 CC is assessed by detecting a change in binding pattern or a physical or  
 CC chemical change in the bound molecules or a conformational change in the  
 CC bound molecules and/or tagged molecules). The present sequence is a  
 CC peptide included in the sequence listing but not mentioned anywhere else  
 CC in the specification.

XX  
 SQ Sequence 6 AA;

Query Match 29.2%; Score 28; DB 8; Length 6;

Best Local Similarity 100.0%; Pred. No. 2e+06;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PHGY 8  
 ||||  
 Db 1 PHGY 4

Search completed: January 20, 2006, 19:05:24  
 Job time : 72.0192 secs

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OM protein - protein search, using sw model

Run on: January 20, 2006, 18:58:05 ; Search time 18.8654 Seconds  
(without alignments)  
78.883 Million cell updates/sec

Title: US-09-662-293-6

Perfect score: 96  
Sequence: 1 DAFPHGYLTAAVSPK 18

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 223517

Minimum DB seq length: 0  
Maximum DB seq length: 20

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 100 summaries

Database :

Issued Patents AA: \*  
1: /cgn2\_6/ptodata/1/1aa/5 COMB.pep: \*  
2: /cgn2\_6/ptodata/1/1aa/6 COMB.pep: \*  
3: /cgn2\_6/ptodata/1/1aa/H COMB.pep: \*  
4: /cgn2\_6/ptodata/1/1aa/PTUS COMB.pep: \*  
5: /cgn2\_6/ptodata/1/1aa/RB COMB.pep: \*  
6: /cgn2\_6/ptodata/1/1aa/backfile1.pep: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	96	100.0	18	2	US-09-292-225-6
2	33	34.4	12	2	US-09-560-915-8
3	33	34.4	12	2	US-09-932-161-8
4	33	34.4	18	2	US-09-171-646-4
5	32	33.3	12	2	US-09-560-915-9
6	32	33.3	12	2	US-09-932-161-9
7	32	33.3	16	2	US-09-171-705-26
8	32	33.3	16	2	US-09-657-757-26
9	31	32.3	9	2	US-09-870-0898-13
10	31	32.3	19	2	US-08-885-707-17
11	31	32.3	19	2	US-09-383-062-63
12	31	32.3	19	2	US-09-839-884-63
13	30	31.2	10	2	US-08-822-586-11
14	30	31.2	11	2	US-08-766-596A-66
15	30	31.2	12	2	US-09-560-915-11
16	30	31.2	12	2	US-09-932-161-11
17	29	30.2	11	2	US-09-716-964B-210
18	29	30.2	12	2	US-09-560-915-4
19	29	30.2	12	2	US-09-560-915-12
20	29	30.2	12	2	US-09-932-161-4
21	29	30.2	16	2	US-09-932-161-12
22	29	30.2	16	2	US-09-747-287A-205
23	29	30.2	18	2	US-09-708-906-12
24	29	30.2	20	6	5258287-19
25	29	30.2	20	6	5258287-22
26	28	29.2	11	2	US-08-875-309-13
27	28	29.2	11	4	PCT-US96-00310-13

28	28	29.2	13	2	US-08-875-309-14	Sequence 14, App1
29	28	29.2	13	4	PCT-US96-00310-14	Sequence 14, App1
30	28	29.2	15	1	US-08-190-802A-17	Sequence 17, App1
31	28	29.2	15	2	US-08-875-309-17	Sequence 17, App1
32	28	29.2	15	2	US-08-477-346-17	Sequence 17, App1
33	28	29.2	15	2	US-08-473-089-17	Sequence 17, App1
34	28	29.2	15	2	US-09-009-953-176	Sequence 176, App
35	28	29.2	15	2	US-09-009-953-183	Sequence 183, App
36	28	29.2	15	2	US-08-487-072A-17	Sequence 17, App1
37	28	29.2	18	2	US-08-469-318-188	Sequence 188, App
38	28	29.2	18	2	US-08-469-318-189	Sequence 189, App
39	28	29.2	18	2	US-08-468-609A-188	Sequence 188, App
40	28	29.2	18	2	US-08-468-609A-189	Sequence 189, App
41	28	29.2	18	2	US-08-468-609A-189	Sequence 189, App
42	28	29.2	18	2	US-08-468-609A-189	Sequence 189, App
43	28	29.2	18	2	US-08-468-609A-189	Sequence 189, App
44	28	29.2	18	2	US-08-762-227A-188	Sequence 188, App
45	28	29.2	18	4	PCT-US95-01185-188	Sequence 189, App
46	28	29.2	18	4	PCT-US95-01185-189	Sequence 189, App
47	28	29.2	20	1	US-08-416-950-7	Sequence 7, App1
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49	28	29.2	20	1	US-08-468-279-35	Sequence 35, App1
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51	28	29.2	20	2	US-08-463-486-18	Sequence 18, App1
52	28	29.2	20	2	US-08-464-496-11	Sequence 11, App1
53	28	29.2	20	2	US-08-197-484-101	Sequence 101, App
54	28	29.2	20	2	US-08-591-502B-7	Sequence 7, App1
55	28	29.2	20	2	US-09-790-497A-446	Sequence 446, App
56	28	29.2	20	2	US-09-576-824A-446	Sequence 446, App
57	28	29.2	20	2	US-09-325-917A-4	Sequence 4, App1
58	28	29.2	20	2	US-09-863-054-18	Sequence 18, App1
59	28	29.2	20	4	PCT-US92-07218-11	Sequence 11, App1
60	28	29.2	20	4	PCT-US94-02195-11	Sequence 11, App1
61	28	29.2	20	4	PCT-US95-02121-101	Sequence 101, App
62	27.5	28.6	11	2	US-08-652-871-52	Sequence 52, App1
63	27.5	28.6	11	2	US-08-476-515A-52	Sequence 52, App1
64	27.5	28.6	17	4	US-08-408-604A-27	Sequence 27, App1
65	27.5	28.6	17	4	PCT-US93-09626-27	Sequence 27, App1
66	27.5	28.6	20	2	US-08-256-747C-15	Sequence 15, App1
67	27.5	28.6	20	2	US-08-834-130A-15	Sequence 15, App1
68	27.5	28.6	20	6	5164481-6	Patent No. 5164481
69	27	28.1	10	2	US-08-822-586-19	Sequence 19, App1
70	27	28.1	10	2	US-08-822-586-23	Sequence 23, App1
71	27	28.1	10	2	US-08-822-586-27	Sequence 27, App1
72	27	28.1	11	2	US-08-802-981-161	Sequence 161, App
73	27	28.1	11	2	US-09-747-287A-215	Sequence 215, App
74	27	28.1	11	2	US-09-394-019C-169	Sequence 169, App
75	27	28.1	12	2	US-08-802-981-162	Sequence 162, App
76	27	28.1	12	2	US-09-929-266-13	Sequence 13, App
77	27	28.1	12	2	US-09-747-287A-216	Sequence 216, App
78	27	28.1	13	2	US-09-394-019C-170	Sequence 170, App
79	27	28.1	13	2	US-08-802-981-42	Sequence 42, App1
80	27	28.1	13	2	US-08-802-981-43	Sequence 43, App1
81	27	28.1	13	2	US-08-802-981-46	Sequence 46, App1
82	27	28.1	13	2	US-08-802-981-51	Sequence 51, App1
83	27	28.1	13	2	US-08-802-981-170	Sequence 170, App
84	27	28.1	13	2	US-08-802-981-171	Sequence 171, App
85	27	28.1	13	2	US-08-802-981-175	Sequence 175, App
86	27	28.1	13	2	US-08-802-981-176	Sequence 176, App
87	27	28.1	13	2	US-09-747-287A-40	Sequence 40, App1
88	27	28.1	13	2	US-09-747-287A-41	Sequence 41, App1
89	27	28.1	13	2	US-09-747-287A-44	Sequence 44, App1
90	27	28.1	13	2	US-09-747-287A-50	Sequence 50, App1
91	27	28.1	13	2	US-09-747-287A-224	Sequence 224, App1
92	27	28.1	13	2	US-09-747-287A-225	Sequence 225, App
93	27	28.1	13	2	US-09-747-287A-229	Sequence 229, App
94	27	28.1	13	2	US-09-747-287A-230	Sequence 230, App
95	27	28.1	13	2	US-09-394-019C-5	Sequence 5, App1
96	27	28.1	13	2	US-09-394-019C-6	Sequence 6, App1
97	27	28.1	13	2	US-09-394-019C-9	Sequence 9, App1
98	27	28.1	13	2	US-09-394-019C-15	Sequence 15, App1
99	27	28.1	13	2	US-09-394-019C-178	Sequence 178, App
100	27	28.1	13	2	US-09-394-019C-179	Sequence 179, App

## ALIGNMENTS

## RESULT 1

US-09-292-225-6  
Sequence 6, Application US/09292225  
Patent No. 6455686  
GENERAL INFORMATION:  
APPLICANT: McCall, Catherine A.  
APPLICANT: Hunter, Shirley Wu  
APPLICANT: Weber, Eric R.  
TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS  
FILE REFERENCE: AL-2-C3  
CURRENT APPLICATION NUMBER: US/09/292,225  
CURRENT FILING DATE: 1999-04-15  
EARLIER APPLICATION NUMBER: 60/098,909  
EARLIER FILING DATE: 1998-09-02  
EARLIER APPLICATION NUMBER: 60/085,295  
EARLIER FILING DATE: 1998-05-13  
EARLIER APPLICATION NUMBER: 60/098,565  
EARLIER FILING DATE: 1998-04-17  
EARLIER APPLICATION NUMBER: 09/062,013  
EARLIER FILING DATE: 1998-04-17  
NUMBER OF SEQ ID NOS: 49  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 6  
LENGTH: 18  
TYPE: PRT  
ORGANISM: Dermatophagoides farinae  
US-09-292-225-6

Query Match 100.0%; Score 96; DB 2; Length 18;  
Best Local Similarity 100.0%; Pred. No. 5.2e-10;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEPPHGYLTAAVSPGK 18  
DB 1 DAEPPHGYLTAAVSPGK 18

## RESULT 2

US-09-560-915-8  
Sequence 8, Application US/09560915  
Patent No. 6383764  
GENERAL INFORMATION:  
APPLICANT: Clivell, Olivier  
APPLICANT: Lin, Steven  
TITLE OF INVENTION: Therapeutic Compositions and Methods  
FILE REFERENCE: Relating To Prolactin Releasing Peptide (P-RP)  
FILE REFERENCE: F-UC 3534  
CURRENT APPLICATION NUMBER: US/09/560,915  
CURRENT FILING DATE: 2000-04-28  
NUMBER OF SEQ ID NOS: 24  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 8  
LENGTH: 12  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: human GPR10 variant  
US-09-560-915-8

Query Match 34.4%; Score 33; DB 2; Length 12;  
Best Local Similarity 60.0%; Pred. No. 28;

Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 PHGYLTAAV 14  
DB 1 PHGYLTAAV 10

## RESULT 3

US-09-932-161-8  
Sequence 8, Application US/09932161  
Patent No. 6884596  
GENERAL INFORMATION:  
APPLICANT: Clivell, Olivier  
APPLICANT: Lin, Steven  
TITLE OF INVENTION: Screening and Therapeutic Methods For  
TITLE OF INVENTION: Promoting Wakefulness and Sleep  
FILE REFERENCE: P-UC 4679  
CURRENT APPLICATION NUMBER: US/09/932,161  
CURRENT FILING DATE: 2001-08-17  
PRIOR APPLICATION NUMBER: US 09/560,915  
PRIOR FILING DATE: 2000-04-28  
NUMBER OF SEQ ID NOS: 24  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 8  
LENGTH: 12  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: human GPR10 variant  
US-09-932-161-8

Query Match 34.4%; Score 33; DB 2; Length 12;  
Best Local Similarity 60.0%; Pred. No. 28;

Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 PHGYLTAAV 14  
DB 1 PHGYLTAAV 10

## RESULT 4

US-09-171-646-4  
Sequence 4, Application US/09171646A  
Patent No. 6235516  
GENERAL INFORMATION:  
APPLICANT: Ghisalba, Oreste  
APPLICANT: Kitzelmann, Matthias  
APPLICANT: Laumen, Kurt  
APPLICANT: Walser-Volken, Paula  
TITLE OF INVENTION: Biocatalysts With Amine Acylase Activity  
FILE REFERENCE: 4-20825/A/PCT  
CURRENT APPLICATION NUMBER: US/09/171,646A  
CURRENT FILING DATE: 1998-11-12  
EARLIER APPLICATION NUMBER: 96810266.5  
EARLIER FILING DATE: 1996-04-25  
NUMBER OF SEQ ID NOS: 4  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 4  
LENGTH: 18  
TYPE: PRT  
ORGANISM: Arthrobacter aureus  
FEATURE:  
NAME/KEY: UNSURE  
OTHER INFORMATION: amino acid is uncertain  
LOCATION: (4...)  
NAME/KEY: UNSURE  
OTHER INFORMATION: amino acid is uncertain  
LOCATION: (6...)  
FEATURE:  
OTHER INFORMATION: amino acid is uncertain  
NAME/KEY: UNSURE  
LOCATION: (9...)  
OTHER INFORMATION: amino acid is unknown  
US-09-171-646-4

Query Match 34.4%; Score 33; DB 2; Length 18;  
Best Local Similarity 41.2%; Pred. No. 46;

Matches 7; Conservative 3; Mismatches 7; Indels 0; Gaps 0;



```

Oy      2 APEPHGYLLTAAVSPGK 18
         | || | :|:|:
Db      2 AIRIRGYXDTPSVAPGE 18

```

```

RESULT 5
US-09-560-915-9
; Sequence 9, Application US/09560915
; Patent No. 6183764
; GENERAL INFORMATION:
; APPLICANT: Civeili, Oliver
; TITLE OF INVENTION: Therapeutic Compositions and Methods
; FILE REFERENCE: P-UC 354
; CURRENT APPLICATION NUMBER: US/09/560,915
; CURRENT FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: human GPR10 variant
US-09-560-915-9

```

Query Match	33.3%	Score 32	DB 2	Length 12
Best Local Similarity	60.0%	Pred. No. 42		
Matches 6	Conservative	1	Mismatches 3	Indels 0
			Gaps	0

```

QY      5 PHGYLLTAAY 14
          ||| : |||
DB      1 PHGQNTVAAY 10

```

```

RESULT 6
US-09-932-161-9
/ Sequence 9, Application US/09932161
/ Patent No. 6884596
/ GENERAL INFORMATION:
/ APPLICANT: Civeilly, Olivier
/ APPLICANT: Ian, Steven
/ TITLE OF INVENTION: Screening and Therapeutic Methods For
/ TITLE OF INVENTION: Promoting Wakefulness and Sleep
/ FILE REFERENCE: P-UC 4679
/ CURRENT APPLICATION NUMBER: US/09/932,161
/ CURRENT FILING DATE: 2001-08-17
/ PRIOR APPLICATION NUMBER: US 09/560,915
/ PRIOR FILING DATE: 2000-04-28
/ NUMBER OF SEQ ID NOS: 24
/ SOFTWARE: Pharseq for Windows Version 4.0
/ SEQ ID NO 9
/ LENGTH: 12
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURES:
/ OTHER INFORMATION: human GPR10 variant
US-09-932-161-9

```

Query Match	33.3%	Score 32;	DB 2;	Length 12;
Best Local Similarity	60.0%	Pred. No. 42;		
Matches	6;	Conservative	1;	Mismatches 3; Indels 0; Gaps 0;

Qy 5 PHGYLLTAAY 14  
||| : |||  
Db 1 PHGQNTVAY 10

RESULT 7  
US-09-171-705-26  
; Sequence 26, Application US/09171705  
; Patent No. 6184204

```

GENERAL INFORMATION:
APPLICANT: BOOTS, ANNA M.H.
APPLICANT: VERHEIDEN, GILBERTUS F.M.
TITLE OF INVENTION: NOVEL PEPTIDES SUITABLE FOR USE IN ANTIGEN SPECIFIC
TITLE OF INVENTION: IMMUNOSUPPRESSIVE THERAPY
FILE REFERENCE: O/96198 US
CURRENT APPLICATION NUMBER: US/09/171,705
CURRENT FILING DATE: 1999-02-09
NUMBER OF SEQ ID NOS: 78
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 26
LENGTH: 16
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURES:
OTHER INFORMATION: Description of Artificial Sequence: DERIVED FROM
OTHER INFORMATION: SEQUENCE OF HUMAN CARTILAGE (HC) -39 PROTEIN
US-09-171-705-26

```

Query Match	33.3%	Score 32;	DB 2;	Length 16;
Best Local Similarity	70.0%	Pred. No. 59;		
Matches	7;	Conservative	2;	Mismatches 1;
				Indels 0;
				Gaps 0;

```
QY      9 LTTAAVSPGK 16
          ||:||:|
Db      2 LLSAALSAGK 11
```

RESULT 8  
 US-09-657-757-26  
 Sequence 26, Application US/09657757  
 Patent No. 6881824  
 GENERAL INFORMATION:  
 APPLICANT: BOOTS, ANNA M.H.  
 APPLICANT: VERHEIJENDEN, GILBERTUS F.M.  
 TITLE OF INVENTION: NOVEL PEPTIDES SUITABLE FOR USE IN ANTIGEN SPECIFIC  
 TITLE OF INVENTION: IMMUNOSUPPRESSIVE THERAPY  
 PTL REFERENCE: C/96198 US  
 CURRENT APPLICATION NUMBER: US/09/657,757  
 CURRENT FILING DATE: 2000-09-08  
 PRIOR APPLICATION NUMBER: US/09/171,705  
 PRIOR FILING DATE: 1998-10-23  
 NUMBER OF SEQ ID NOS: 78  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO 26  
 LENGTH: 16  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURES:  
 OTHER INFORMATION: Description of Artificial Sequence: DERIVED FROM  
 OTHER INFORMATION: SEQUENCE OF ANTIEN CANTILAGE (HC) -39 PROTEIN  
 US-09-657-757-26

Query Match	33.3%	Score 32	DB 2	Length 16
Best Local Similarity	70.0%	Pred. No	59	
Matches 7, Conservative	2	Mismatches	1	Gaps 0

```
QY      9 LTTAVSPGK 18
          ||:||:|
Db      2 LLSAALSAGK 11
```

RESULT 9  
US-09-870-0895-13  
Sequence 13. Application US/09670089B  
Patent No. 6737062  
GENERAL INFORMATION:  
APPLICANT: Charles A. Nicolette  
TITLE OF INVENTION: THERAPEUTIC  
PILLS REFERENCE: 6812681209900  
CURRENT APPLICATION NUMBER: US/09/870,089B  
CURRENT FILING DATE: 2001-05-30  
NUMBER OF SEQ ID NOS: 14



Best Local Similarity 54.5%; Pred. No. 1.1e+02;  
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DAFPHGYLT 11  
Db 7 DAEQPHQFVT 17

## RESULT 13

US-08-822-586-11  
Sequence 11, Application US/08822586  
Patent No. 6015890  
GENERAL INFORMATION:  
APPLICANT: WILLIAM R. JACOBS, JR., JAMES M. MUSSER AND  
APPLICANT: AMALIO TELENTE  
TITLE OF INVENTION: AN ENCBAB OPERON OF MYCOBACTERIA AND  
NUMBER OF SEQUENCES: 57  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: AMSTER, ROTHSTEIN & EBENSTEIN  
STREET: 90 PARK AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: U.S.A.  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 INCH 1.44 MB STORAGE  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/822,586  
FILING DATE: MARCH 20, 1997  
ATTORNEY/AGENT INFORMATION:  
NAME: ELIZABETH A. BOGOSIAN  
REGISTRATION NUMBER: 39,911  
REFERENCE/DOCKET NUMBER: 96700/437  
TELEPHONE: (212) 697-5995  
TELEFAX: (212) 286-0854 or 286-0082  
TELEX: TWX 710-581-4766  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULAR TYPE: peptide  
DESCRIPTION: NO  
HYPOTHETICAL: NO  
FRAGMENT TYPE: Internal fragment  
US-08-822-586-11

Query Match 31.2%; Score 30; DB 2; Length 10;  
Best Local Similarity 85.7%; Pred. No. 75;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GYLTTAA 13  
Db 4 GYLTTVA 10

## RESULT 14

US-08-766-596A-66  
Sequence 66, Application US/08766596A  
Patent No. 6462171  
GENERAL INFORMATION:  
APPLICANT: SOTO-JARA, Claudio  
APPLICANT: BAUMANN, Marc  
APPLICANT: FAUDONN, Blas  
TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL  
TITLE OF INVENTION: COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES

TITLE OF INVENTION: ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE  
TITLE OF INVENTION: DEPOSITS  
NUMBER OF SEQUENCES: 69  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROWDY AND NEIMARK  
STREET: 419 Seventh Street, N.W., Suite 400  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Releasee #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/766,596A  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/630,645  
FILING DATE: 10-APR-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/478,326  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: YUN, Allen C.  
REGISTRATION NUMBER: 37,971  
REFERENCE/DOCKET NUMBER: SOTO-JARA-1A  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
INFORMATION FOR SEQ ID NO: 66:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULAR TYPE: peptide  
US-08-766-596A-66

Query Match 31.2%; Score 30; DB 2; Length 11;  
Best Local Similarity 63.6%; Pred. No. 84;  
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 7 GYLTTAAVSFG 17  
Db 1 GYLTTVAAVFRG 11

## RESULT 15

US-09-560-915-11  
Sequence 11, Application US/09560915  
Patent No. 638764  
GENERAL INFORMATION:  
APPLICANT: CIVELLI, Olivier  
APPLICANT: Lhn, Steven  
TITLE OF INVENTION: Therapeutic Compositions and Methods  
TITLE OF INVENTION: Relating To Protraction Releasing Peptide (P-RP)  
FILE REFERENCE: P-UC 3534  
CURRENT APPLICATION NUMBER: US/09/560,915  
CURRENT FILING DATE: 2000-04-28  
NUMBER OF SEQ ID NOS: 24  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 11  
LENGTH: 12  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: human GPR10 variant  
US-09-560-915-11

Query Match 31.2%; Score 30; DB 2; Length 12;

Best Local Similarity 45.5%; Pred. No. 93;  
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 5 PHGYLTAAVS 15  
||| : : :  
Db 1 PHQNMNTVSVA 11

## RESULT 15

US-09-932-161-11  
; Sequence 11, Application US/09932161  
; Patent No. 6884596  
; GENERAL INFORMATION:  
; APPLICANT: Civeilli, Olivier  
; APPLICANT: Lin, Steven  
; TITLE OF INVENTION: Screening and Therapeutic Methods For  
; FILE REFERENCE: P-UC 4679  
; CURRENT APPLICATION NUMBER: US/09/932,161  
; PRIOR FILING DATE: 2001-08-17  
; PRIOR APPLICATION NUMBER: US 09/560,915  
; PRIOR FILING DATE: 2000-04-28  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 11  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: human GPR10 variant  
US-09-932-161-11

Query Match 31.2%; Score 30; DB 2; Length 12;  
Best Local Similarity 45.5%; Pred. No. 93;  
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 5 PHGYLTAAVS 15  
||| : : :  
Db 1 PHQNMNTVSVA 11

## RESULT 17

US-09-716-964B-210  
; Sequence 210, Application US/09716964B  
; Patent No. 6897053  
; GENERAL INFORMATION:  
; APPLICANT: O'Donnell, Michael E.  
; APPLICANT: Yuzhakov, Alexander  
; APPLICANT: Yurleva, Olga  
; APPLICANT: Jernuzalmi, David  
; APPLICANT: Bruck, Irina  
; APPLICANT: Kiriyan, John  
; TITLE OF INVENTION: ENZYMES DERIVED FROM THERMOPHILIC ORGANISMS THAT  
; TITLE OF INVENTION: FUNCTION AS A CHROMOSOMAL REPLICASE, PREPARATION AND  
; FILE REFERENCE: 22221/1030  
; CURRENT APPLICATION NUMBER: US/09/716,964B  
; PRIOR FILING DATE: 2000-11-21  
; PRIOR APPLICATION NUMBER: 60/143,202  
; PRIOR FILING DATE: 1997-04-08  
; PRIOR APPLICATION NUMBER: 08/823,407  
; PRIOR FILING DATE: 1997-04-08  
; PRIOR APPLICATION NUMBER: 09/057,416  
; PRIOR FILING DATE: 1998-04-08  
; NUMBER OF SEQ ID NOS: 212  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 210  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: polypeptide  
US-09-716-964B-210

Query Match 30.2%; Score 29; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 HGYYL 10  
|||||  
Db 7 HGYYL 11

## RESULT 18

US-09-560-915-4  
; Sequence 4, Application US/09560915  
; Patent No. 6183764  
; GENERAL INFORMATION:  
; APPLICANT: Civeilli, Olivier  
; APPLICANT: Lin, Steven  
; TITLE OF INVENTION: Therapeutic Compositions and Methods  
; TITLE OF INVENTION: Relating To Prolactin Releasing Peptide (PRRP)  
; FILE REFERENCE: P-UC 3534  
; CURRENT APPLICATION NUMBER: US/09/560,915  
; PRIOR FILING DATE: 2000-04-28  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-09-560-915-4

Query Match 30.2%; Score 29; DB 2; Length 12;  
Best Local Similarity 50.0%; Pred. No. 1.4e+02;  
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 5 PHGYLTAAV 14  
||| : : :  
Db 1 PHQNMNTVSV 10

## RESULT 19

US-09-560-915-12  
; Sequence 12, Application US/09560915  
; Patent No. 6183764  
; GENERAL INFORMATION:  
; APPLICANT: Civeilli, Olivier  
; APPLICANT: Lin, Steven  
; TITLE OF INVENTION: Therapeutic Compositions and Methods  
; TITLE OF INVENTION: Relating To Prolactin Releasing Peptide (PRRP)  
; FILE REFERENCE: P-UC 3534  
; CURRENT APPLICATION NUMBER: US/09/560,915  
; PRIOR FILING DATE: 2000-04-28  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 12  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: human GPR10 variant  
US-09-560-915-12

Query Match 30.2%; Score 29; DB 2; Length 12;  
Best Local Similarity 50.0%; Pred. No. 1.4e+02;  
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 5 PHGYLTAAV 14  
||| : : :  
Db 1 PHQNMNTVSV 10

## RESULT 20

US-09-932-161-4  
; Sequence 4, Application US/09932161

```
/ Patent No. 6884596
/ GENERAL INFORMATION:
/ APPLICANT: Civeilli, Olivier
/ APPLICANT: Lin, Steven
/ TITLE OF INVENTION: Screening and Therapeutic Methods For
/ TITLE OF INVENTION: Promoting Wakefulness and Sleep
/ FILE REFERENCE: P-UC 4679
/ CURRENT APPLICATION NUMBER: US/09/932,161
/ CURRENT FILING DATE: 2001-08-17
/ PRIOR APPLICATION NUMBER: US 09/560,915
/ PRIOR FILING DATE: 2000-04-28
/ NUMBER OF SEQ ID NOS: 24
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 4
/ LENGTH: 12
/ TYPE: PRT
/ ORGANISM: Homo Sapien
US-09-932-161-4
```

```
Query Match          30.2%; Score 29; DB 2; Length 12;
Best Local Similarity 50.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      5 PHGYLTAAY 14
      |||:|:|
DB      1 PHGQNMVSV 10
```

```
RESULT 21
US-09-932-161-12
/ Sequence 12, Application US/09932161
/ Patent No. 6884596
/ GENERAL INFORMATION:
/ APPLICANT: Civeilli, Olivier
/ APPLICANT: Lin, Steven
/ TITLE OF INVENTION: Screening and Therapeutic Methods For
/ TITLE OF INVENTION: Promoting Wakefulness and Sleep
/ FILE REFERENCE: P-UC 4679
/ CURRENT APPLICATION NUMBER: US/09/932,161
/ CURRENT FILING DATE: 2001-08-17
/ PRIOR APPLICATION NUMBER: US 09/560,915
/ PRIOR FILING DATE: 2000-04-28
/ NUMBER OF SEQ ID NOS: 24
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 12
/ LENGTH: 12
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: human GPR10 variant
US-09-932-161-12
```

```
Query Match          30.2%; Score 29; DB 2; Length 12;
Best Local Similarity 50.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      5 PHGYLTAAY 14
      |||:|:|
DB      1 PHGQNMVSV 10
```

```
RESULT 22
US-09-747-287A-205
/ Sequence 205, Application US/09747287A
/ Patent No. 6893868
/ GENERAL INFORMATION:
/ APPLICANT: KOMORIYA, AKIRA
/ APPLICANT: PACKARD, BEVERLY S.
/ TITLE OF INVENTION: HOMO-DOUBLY LABELED COMPOSITIONS FOR THE DETECTION OF ENZYME
/ TITLE OF INVENTION: ACTIVITY IN BIOLOGICAL SAMPLES
/ FILE REFERENCE: 300-948600US
/ CURRENT APPLICATION NUMBER: US/09/747,287A
/ CURRENT FILING DATE: 2000-12-22
```

```
/ PRIOR APPLICATION NUMBER: US 09/349,019
/ PRIOR FILING DATE: 1999-09-10
/ PRIOR APPLICATION NUMBER: US08/802,981
/ PRIOR FILING DATE: 1997-02-20
/ PRIOR APPLICATION NUMBER: PCT/US00/24882
/ PRIOR FILING DATE: 2000-09-11
/ NUMBER OF SEQ ID NOS: 246
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 205
/ LENGTH: 16
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: Synthetic peptide.
/ NAME/KEY: misc_feature
/ LOCATION: (4)..(4)
/ OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-09-747-287A-205
```

```
Query Match          30.2%; Score 29; DB 2; Length 16;
Best Local Similarity 42.9%; Pred. No. 2e+02;
Matches 6; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
```

```
QY      4 EPHGYLTAAYSPG 17
      :||:|:|
DB      2 DFXGVHDAFVPRKG 15
```

```
RESULT 23
US-09-708-906-12
/ Sequence 12, Application US/09708906
/ Patent No. 6528620
/ GENERAL INFORMATION:
/ APPLICANT: Ayer, Donald E.
/ APPLICANT: Billin, Andrew N.
/ TITLE OF INVENTION: STD-POLYAMIDE FUSIONS: A POTENT METHOD OF REGULATING
/ TITLE OF INVENTION: GENE EXPRESSION
/ FILE REFERENCE: 1321.2.37
/ CURRENT APPLICATION NUMBER: US/09/708,906
/ CURRENT FILING DATE: 2000-11-08
/ PRIOR APPLICATION NUMBER: 60/163,960
/ PRIOR FILING DATE: 1999-11-08
/ NUMBER OF SEQ ID NOS: 27
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 12
/ LENGTH: 18
/ TYPE: PRT
/ ORGANISM: Caenorhabditis elegans
US-09-708-906-12
```

```
Query Match          30.2%; Score 29; DB 2; Length 18;
Best Local Similarity 85.7%; Pred. No. 2.3e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      7 GYLLTA 13
      |:|:|:|
DB      3 GHLLTA 9
```

```
RESULT 24
5258287-19
/ Patent No. 5258287
/ APPLICANT: BAXTER, ROBERT C.; WOOD, WILLIAM I.
/ TITLE OF INVENTION: DNA ENCODING AND METHODS OF PRODUCTION
/ OF INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN BP53
/ NUMBER OF SEQUENCES: 58
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/07/171,623
/ FILING DATE: 22-MAR-1988
/ SEQ ID NO:19;
/ LENGTH: 20
5258287-19
```

Query Match 30.2%; Score 29; DB 6; Length 20;  
Best Local Similarity 60.0%; Pred. No. 2.6e+02;  
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 8 YLTTAAVSPG 17  
||| |  
2 YLLPAPPAPG 11

Db

RESULT 25  
5258287-22  
; Patent No. 5258287  
; APPLICANT: BAXTER, ROBERT C.; WOOD, WILLIAM I.  
; TITLE OF INVENTION: DNA ENCODING AND METHODS OF PRODUCTION  
; OF INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN BP53  
; NUMBER OF SEQUENCES: 58  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/171,623  
; FILING DATE: 22-MAR-1988  
; SEQ ID NO:22:  
; LENGTH: 20  
5258287-22

Query Match 30.2%; Score 29; DB 6; Length 20;  
Best Local Similarity 60.0%; Pred. No. 2.6e+02;  
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 8 YLTTAAVSPG 17  
||| |  
2 YLLPAPPAPG 11

Db

RESULT 26  
US-08-875-309-13  
; Sequence 13, Application US/08875309  
; Patent No. 6180600  
; GENERAL INFORMATION:  
; APPLICANT: Jameson, Bradford A.  
; APPLICANT: Choksel, Swati  
; APPLICANT: Korngold, Robert  
; APPLICANT: Huang, Ziwel  
; TITLE OF INVENTION: CD8 Antagonists  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6180600R18  
; STREET: One Liberty Place, 46th Floor  
; CITY: Philadelphia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19103  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Wordperfect  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/875,309  
; FILING DATE: 26-NOV-1997  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US96/00310  
; FILING DATE: 17-JAN-1996  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/372,952  
; FILING DATE: 17-JAN-1995  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Deluca, Mark  
; REGISTRATION NUMBER: 33,229  
; REFERENCE/DOCKET NUMBER: TJU-1772  
; TELECOMMUNICATION INFORMATION:

TELEPHONE: 215-568-3100  
; TELEFAX: 215-568-3439  
; INFORMATION FOR SEQ ID NO: 13:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-875-309-13

Query Match 29.2%; Score 28; DB 2; Length 11;  
Best Local Similarity 50.0%; Pred. No. 1.9e+02;  
Matches 7; Conservative 1; Mismatches 2; Indels 4; Gaps 1;

QY 3 FEPHGYLTTAAVSP 16  
|:| |  
1 FQPRG---AAASP 10

Db

RESULT 27  
PCT-US96-00310-13  
; Sequence 13, Application PC/TUS9600310  
; GENERAL INFORMATION:  
; APPLICANT: Jameson, Bradford A.  
; APPLICANT: Choksel, Swati  
; APPLICANT: Korngold, Robert  
; APPLICANT: Huang, Ziwel  
; TITLE OF INVENTION: CD8 Antagonists  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & Norris  
; STREET: One Liberty Place, 46th Floor  
; CITY: Philadelphia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19103  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Wordperfect  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US96/00310  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/372,952  
; FILING DATE: 17-JAN-1995  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Deluca, Mark  
; REGISTRATION NUMBER: 33,229  
; REFERENCE/DOCKET NUMBER: TJU-1752  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 215-568-3100  
; TELEFAX: 215-568-3439  
; INFORMATION FOR SEQ ID NO: 13:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
PCT-US96-00310-13

Query Match 29.2%; Score 28; DB 4; Length 11;  
Best Local Similarity 50.0%; Pred. No. 1.9e+02;  
Matches 7; Conservative 1; Mismatches 2; Indels 4; Gaps 1;

QY 3 FEPHGYLTTAAVSP 16  
|:| |  
1 FQPRG---AAASP 10

Db

RESULT 28  
US-08-875-309-14  
Sequence 14, Application US/08875309  
Patent No. 6180600  
GENERAL INFORMATION:  
APPLICANT: Jameson, Bradford A.  
APPLICANT: Choksi, Swati  
APPLICANT: Korgold, Robert  
APPLICANT: Huang, Zimei  
TITLE OF INVENTION: CD8 Antagonists  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Woodcock Washburn Kurtz Mackiewicz & No. 6180600r1s  
STREET: One Liberty Place, 46th Floor  
CITY: Philadelphia  
STATE: PA  
COUNTRY: USA  
ZIP: 19103  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Wordperfect  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/875,309  
FILING DATE: 26-NOV-1997  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US96/00310  
FILING DATE: 17-JAN-1996  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/372,952  
FILING DATE: 17-JAN-1995  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Deluca, Mark  
REGISTRATION NUMBER: 33,229  
REFERENCE/DOCKET NUMBER: T0U-1772  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215-568-3100  
TELEFAX: 215-568-3439  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 13 amino acids  
TYPE: amino acid  
TOPOLOGY: circular  
MOLECULE TYPE: protein  
US-08-875-309-14

Query Match 29.2% Score 28; DB 2; Length 13;  
Best Local Similarity 50.0%; Pred. No. 2.3e+02;  
Matches 7; Conservative 1; Mismatches 2; Indels 4; Gaps 1;

QY 3 FEHGYLTTAAVSP 16  
DB 2 FQPRG---AAASP 11

RESULT 29  
PCT-US96-00310-14  
Sequence 14, Application PC/TUS9600310  
GENERAL INFORMATION:  
APPLICANT: Jameson, Bradford A.  
APPLICANT: Choksi, Swati  
APPLICANT: Korgold, Robert  
APPLICANT: Huang, Zimei  
TITLE OF INVENTION: CD8 Antagonists  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Woodcock Washburn Kurtz Mackiewicz & Norris  
STREET: One Liberty Place, 46th Floor  
CITY: Philadelphia

STATE: PA  
COUNTRY: USA  
ZIP: 19103  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Wordperfect  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US96/00310  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/372,952  
FILING DATE: 17-JAN-1995  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Deluca, Mark  
REGISTRATION NUMBER: 33,229  
REFERENCE/DOCKET NUMBER: T0U-1752  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215-568-3100  
TELEFAX: 215-568-3439  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 13 amino acids  
TYPE: amino acid  
TOPOLOGY: circular  
MOLECULE TYPE: protein  
PCT-US96-00310-14

Query Match 29.2% Score 28; DB 4; Length 13;  
Best Local Similarity 50.0%; Pred. No. 2.3e+02;  
Matches 7; Conservative 1; Mismatches 2; Indels 4; Gaps 1;

QY 3 FEHGYLTTAAVSP 16  
DB 2 FQPRG---AAASP 11

RESULT 30  
US-08-190-802A-17  
Sequence 17, Application US/08190802A  
Patent No. 5519003  
GENERAL INFORMATION:  
APPLICANT: Mochly-Rosen, Daria  
APPLICANT: Ron, Dorit  
TITLE OF INVENTION: WD-40 - Derived Peptides and Uses  
NUMBER OF SEQUENCES: 265  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Dehlinger & Associates  
STREET: P.O. Box 60850  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94306-0850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/190,802A  
FILING DATE: 01-FEB-1994  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Fabian, Gary R.  
REGISTRATION NUMBER: 33,875  
REFERENCE/DOCKET NUMBER: 8600-0139  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 324-0880  
TELEFAX: (415) 324-0960

INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: GBH Peptide rV, Fig. 24  
US-08-190-802A-17

Query Match 29.2%; Score 28; DB 1; Length 15;  
Best Local Similarity 66.7%; Pred. No. 2.7e+02;  
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 8 YLTAAVSP 16  
|||  
1 YLNTVTVP 9

RESULT 31  
US-08-875-309-17  
Sequence 17, Application US/08875309  
Patent No. 6180600  
GENERAL INFORMATION:  
APPLICANT: Jameson, Bradford A.  
APPLICANT: Chokel, Swati  
APPLICANT: Koringold, Robert  
APPLICANT: Huang, Ziwel  
TITLE OF INVENTION: CD8 Antagonists  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESSES:  
ADDRESSER: Woodcock Washburn Kurtz Mackiewicz & No. 61806000ris  
STREET: One Liberty Place, 46th Floor  
CITY: Philadelphia  
STATE: PA  
COUNTRY: USA  
ZIP: 19103  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Wordperfect  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/875,309  
FILING DATE: 26-NOV-1997  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US96/00310  
FILING DATE: 17-JAN-1996  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/372,952  
FILING DATE: 17-JAN-1995  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Deluca, Mark  
REGISTRATION NUMBER: 33,229  
REFERENCE/DOCKET NUMBER: TJU-1772  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215-568-3100  
TELEFAX: 215-568-3439  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-875-309-17  
Query Match 29.2%; Score 28; DB 2; Length 15;  
Best Local Similarity 50.0%; Pred. No. 2.7e+02;

Matches 7; Conservative 1; Mismatches 2; Indels 4; Gaps 1;  
QY 3 FEPHGYLTAAVSP 16  
|||  
5 FQPRG---AAASP 14

RESULT 32  
US-08-477-346-17  
Sequence 17, Application US/08477346  
Patent No. 6262023  
GENERAL INFORMATION:  
APPLICANT: Mochly-Rosen, Daria  
APPLICANT: Ron, Dorit  
TITLE OF INVENTION: WD-40 - Derived Peptides and Uses  
TITLE OF INVENTION: Thereof  
NUMBER OF SEQUENCES: 265  
CORRESPONDENCE ADDRESSES:  
ADDRESSER: Morrison & Foerster  
STREET: 2000 Pennsylvania Avenue, NW  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20006-1812  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/477,346  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/487,072  
FILING DATE: 07-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: MURASHIGER, KATE H.  
REGISTRATION NUMBER: 29,959  
REFERENCE/DOCKET NUMBER: 2550-0025.20  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 887-1500  
TELEFAX: (202) 887-0763  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: GBH Peptide rV, Fig. 24  
US-08-477-346-17

Query Match 29.2%; Score 28; DB 2; Length 15;  
Best Local Similarity 66.7%; Pred. No. 2.7e+02;  
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 8 YLTAAVSP 16  
|||  
1 YLNTVTVP 9

RESULT 33  
US-08-473-089-17  
Sequence 17, Application US/08473089  
Patent No. 6342368  
GENERAL INFORMATION:  
APPLICANT: Mochly-Rosen, Daria  
APPLICANT: Ron, Dorit  
TITLE OF INVENTION: WD-40 - Derived Peptides and Uses  
TITLE OF INVENTION: Thereof



NUMBER OF SEQUENCES: 265  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Morrison & Roester  
STREET: 2000 Pennsylvania Avenue, NW  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20006-1812  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/473,089  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: MURASHIGE, KATE H.  
REGISTRATION NUMBER: 29,959  
REFERENCE/DOCKET NUMBER: 2550-0025.22  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 887-0763  
TELEFAX: (202) 887-1500  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: GBH Peptide IV, Fig. 24  
US-08-473-089-17

Query Match 29.2%; Score 28; DB 2; Length 15;  
Best Local Similarity 66.7%; Pred. No. 2.7e+02;  
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 8 YLTAAVSP 16  
|||  
1 YLNTVTVP 9

Db

RESULT 34  
US-09-009-953-176  
Sequence 176, Application US/09009953  
Patent No. 6413517  
GENERAL INFORMATION:  
APPLICANT: Sette, Alessandro  
TITLE OF INVENTION: Identification of Broadly  
Reactive DR Restricted Epitopes  
NUMBER OF SEQUENCES: 274  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/009,953  
FILING DATE: 21-Jan-1998  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/036,713  
FILING DATE: 23-JAN-1997

APPLICATION NUMBER: US 60/037,432  
FILING DATE: 07-FEB-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Weber, Ellen Lauver  
REGISTRATION NUMBER: 32,762  
REFERENCE/DOCKET NUMBER: 018623-011520US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-576-0200  
TELEFAX: 415-576-0300  
TELEX: <Unknown>  
INFORMATION FOR SEQ ID NO: 176:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 176:  
US-09-009-953-176

Query Match 29.2%; Score 28; DB 2; Length 15;  
Best Local Similarity 66.7%; Pred. No. 2.7e+02;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 LPTAAVSPG 17  
|||  
6 LPTAIIISPG 14

Db

RESULT 35  
US-09-009-953-183  
Sequence 183, Application US/09009953  
Patent No. 6413517  
GENERAL INFORMATION:  
APPLICANT: Sette, Alessandro  
TITLE OF INVENTION: Identification of Broadly  
Reactive DR Restricted Epitopes  
NUMBER OF SEQUENCES: 274  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/009,953  
FILING DATE: 21-Jan-1998  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/036,713  
FILING DATE: 23-JAN-1997  
APPLICATION NUMBER: US 60/037,432  
FILING DATE: 07-FEB-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Weber, Ellen Lauver  
REGISTRATION NUMBER: 32,762  
REFERENCE/DOCKET NUMBER: 018623-011520US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-576-0200  
TELEFAX: 415-576-0300  
TELEX: <Unknown>  
INFORMATION FOR SEQ ID NO: 183:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear

MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 183;  
US-09-009-953-183

Query Match 29.2%; Score 28; DB 2; Length 15;  
Best Local Similarity 66.7%; Pred. No. 2.7e+02;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 YLTAAVSPG 17  
DB 3 LRPAILSPG 11

## RESULT 36

US-08-487-072A-17  
Sequence 17, Application US/08487072A  
Patent No. 6423684  
GENERAL INFORMATION:  
APPLICANT: Mochly-Rosen, Daria  
TITLE OF INVENTION: MD-40 - Derived Peptides and Uses  
TITLE OF INVENTION: Thereof  
NUMBER OF SEQUENCES: 265  
CORRESPONDENCE ADDRESSES:  
ADDRESSER: Morrison & Foerster  
STREET: 2000 Pennsylvania Avenue, NW  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20006-1812  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/487,072A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: MORASHIGE, KATE H.  
REGISTRATION NUMBER: 29,959  
REFERENCE/DOCKET NUMBER: 2550-0025.20  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 887-1500  
TELEFAX: (202) 887-0763  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: GRH Peptide rv, Fig. 24  
US-08-487-072A-17

Query Match 29.2%; Score 28; DB 2; Length 15;  
Best Local Similarity 66.7%; Pred. No. 2.7e+02;  
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 8 YLTAAVSP 16  
DB 1 YLNTVTVP 9

RESULT 37  
US-08-469-318-188  
Sequence 188, Application US/08469318  
Patent No. 6022535  
GENERAL INFORMATION:  
APPLICANT:

TITLE OF INVENTION: Multivariant IL-3 Hematopoiesis Fusion  
TITLE OF INVENTION: Protein  
NUMBER OF SEQUENCES: 196  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/469,318  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/446,872  
FILING DATE:  
INFORMATION FOR SEQ ID NO: 188:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-469-318-188

Query Match 29.2%; Score 28; DB 2; Length 18;  
Best Local Similarity 40.0%; Pred. No. 3.4e+02;  
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 8 YLTAAVSPG 17  
DB 1 YVIEGRISPG 10

RESULT 38  
US-08-469-318-189  
Sequence 189, Application US/08469318  
Patent No. 6022535  
GENERAL INFORMATION:  
APPLICANT:  
TITLE OF INVENTION: Multivariant IL-3 Hematopoiesis Fusion  
TITLE OF INVENTION: Protein  
NUMBER OF SEQUENCES: 196  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/469,318  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/446,872  
FILING DATE:  
INFORMATION FOR SEQ ID NO: 189:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-469-318-189

Query Match 29.2%; Score 28; DB 2; Length 18;  
Best Local Similarity 40.0%; Pred. No. 3.4e+02;  
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 8 YLTAAVSPG 17  
DB 1 YVIEGRISPG 10

## RESULT 39

```

US-08-468-609A-188
; Sequence 188, Application US/08468609A
; Patent No. 6030812
; GENERAL INFORMATION:
; APPLICANT: Abrams, Mark A.
; APPLICANT: Bauer, S. C.
; APPLICANT: Bradford-Goldberg, Sarah R.
; APPLICANT: Caparon, Maïre H.
; APPLICANT: Easton, Alan M.
; APPLICANT: Klein, Barbara K.
; APPLICANT: McKearn, John P.
; APPLICANT: Oline, Peter O.
; APPLICANT: Paik, Kuman
; APPLICANT: Thomas, John W.
; TITLE OF INVENTION: Fusion Proteins Comprising Multiply Mutated Interleukin-3 (IL-
; NUMBER OF SEQUENCES: 197
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dennis A. Bennett, G.D. Searle & Co.,
; ADDRESSEE: Corporate Patent Dept.
; STREET: P. O. Box 5110
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60680
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,609A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/192,325
; FILING DATE: 14-FEB-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Bennett, Dennis A.
; REGISTRATION NUMBER: 34,547
; REFERENCE/DOCKET NUMBER: C-2790/3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314)737-6986
; TELEFAX: (314)737-6972
; INFORMATION FOR SEQ ID NO: 188:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-468-609A-188

Query Match      29.2%; Score 28; DB 2; Length 18;
Best Local Similarity 40.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY      8 YLLTAAVSPG 17
      |:::|
      1 YVIEGRISPG 10

RESULT 40
US-08-468-609A-189
; Sequence 189, Application US/08468609A
; Patent No. 6030812
; GENERAL INFORMATION:
; APPLICANT: Abrams, Mark A.
; APPLICANT: Bauer, S. C.
; APPLICANT: Bradford-Goldberg, Sarah R.
; APPLICANT: Caparon, Maïre H.
; APPLICANT: Easton, Alan M.
; APPLICANT: Klein, Barbara K.
; APPLICANT: McKearn, John P.
; APPLICANT: Oline, Peter O.
; APPLICANT: Paik, Kuman
; APPLICANT: Thomas, John W.
; TITLE OF INVENTION: Multivariant IL-3 Hematopoiesis
; NUMBER OF SEQUENCES: 197
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dennis A. Bennett, G.D. Searle & Co.,
; ADDRESSEE: Corporate Patent Dept.
; STREET: P. O. Box 5110
; CITY: Chicago

```

```

; APPLICANT: Oline, Peter O.
; APPLICANT: Paik, Kuman
; APPLICANT: Thomas, John W.
; TITLE OF INVENTION: Fusion Proteins Comprising Multiply Mutated Interleukin-3 (IL-
; NUMBER OF SEQUENCES: 197
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dennis A. Bennett, G.D. Searle & Co.,
; ADDRESSEE: Corporate Patent Dept.
; STREET: P. O. Box 5110
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60680
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,609A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/192,325
; FILING DATE: 14-FEB-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Bennett, Dennis A.
; REGISTRATION NUMBER: 34,547
; REFERENCE/DOCKET NUMBER: C-2790/3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314)737-6986
; TELEFAX: (314)737-6972
; INFORMATION FOR SEQ ID NO: 189:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-468-609A-189

Query Match      29.2%; Score 28; DB 2; Length 18;
Best Local Similarity 40.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY      8 YLLTAAVSPG 17
      |:::|
      1 YVIEGRISPG 10

RESULT 41
US-08-468-609A-188
; Sequence 188, Application US/08468609A
; Patent No. 6030812
; GENERAL INFORMATION:
; APPLICANT: Abrams, Mark A.
; APPLICANT: Bauer, S. C.
; APPLICANT: Bradford-Goldberg, Sarah R.
; APPLICANT: Caparon, Maïre H.
; APPLICANT: Easton, Alan M.
; APPLICANT: Klein, Barbara K.
; APPLICANT: McKearn, John P.
; APPLICANT: Oline, Peter O.
; APPLICANT: Paik, Kuman
; APPLICANT: Thomas, John W.
; TITLE OF INVENTION: Multivariant IL-3 Hematopoiesis
; NUMBER OF SEQUENCES: 197
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dennis A. Bennett, G.D. Searle & Co.,
; ADDRESSEE: Corporate Patent Dept.
; STREET: P. O. Box 5110
; CITY: Chicago

```

STATE: Illinois  
COUNTRY: USA  
ZIP: 60680  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Releasee #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/446,872A  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/192,325  
FILING DATE: 14-FEB-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Bennett, Dennis A.  
REGISTRATION NUMBER: 34,547  
REFERENCE/DOCKET NUMBER: C-2790/1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (314)737-6986  
TELEFAX: (314)737-6972  
INFORMATION FOR SEQ ID NO: 188:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-446-872A-188

Query Match 29.2%; Score 28; DB 2; Length 18;  
Best Local Similarity 40.0%; Pred. No. 3.4e+02;  
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 8 YLITAAVSPG 17  
|:::|  
DB 1 YVIEGRISPG 10

RESULT 42  
US-08-446-872A-189  
Sequence 189, Application US/08446872A  
Patent No. 6361977  
GENERAL INFORMATION:  
APPLICANT: Abrams, Mark A.  
APPLICANT: Bauer, S. C.  
APPLICANT: Braford-Goldberg, Sarah R.  
APPLICANT: Caparon, Maïre H.  
APPLICANT: Easton, Alan M.  
APPLICANT: Klein, Barbara K.  
APPLICANT: McKearn, John P.  
APPLICANT: Olin, Peter O.  
APPLICANT: Paik, Kuman  
APPLICANT: Thomas, John W.  
TITLE OF INVENTION: Multivariant IL-3 Hematopoiesis  
TITLE OF INVENTION: Fusion Protein  
NUMBER OF SEQUENCES: 197  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dennis A. Bennett, G.D. Searle & Co.,  
ADDRESSEE: Corporate Patent Dept.,  
STREET: P. O. Box 5110  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60680  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Releasee #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/446,872A

FILING DATE: 06-JUN-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/192,325  
FILING DATE: 14-FEB-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Bennett, Dennis A.  
REGISTRATION NUMBER: 34,547  
REFERENCE/DOCKET NUMBER: C-2790/1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (314)737-6986  
TELEFAX: (314)737-6972  
INFORMATION FOR SEQ ID NO: 189:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-446-872A-189

Query Match 29.2%; Score 28; DB 2; Length 18;  
Best Local Similarity 40.0%; Pred. No. 3.4e+02;  
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 8 YLITAAVSPG 17  
|:::|  
DB 1 YVIEGRISPG 10

RESULT 43  
US-08-762-227A-188  
Sequence 188, Application US/08762227A  
Patent No. 6436387  
GENERAL INFORMATION:  
APPLICANT: Abrams, Mark A.  
APPLICANT: Bauer, S. C.  
APPLICANT: Braford-Goldberg, Sarah R.  
APPLICANT: Caparon, Maïre H.  
APPLICANT: Easton, Alan M.  
APPLICANT: Klein, Barbara K.  
APPLICANT: McKearn, John P.  
APPLICANT: Olin, Peter O.  
APPLICANT: Paik, Kuman  
APPLICANT: Thomas, John W.  
TITLE OF INVENTION: Multivariant IL-3 Hematopoiesis  
TITLE OF INVENTION: Fusion Protein  
NUMBER OF SEQUENCES: 197  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dennis A. Bennett, G.D. Searle & Co.,  
ADDRESSEE: Corporate Patent Dept.,  
STREET: P. O. Box 5110  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60680  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Releasee #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/762,227A  
FILING DATE: 09-Dec-1996  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/192,325  
FILING DATE: 14-FEB-1994  
APPLICATION NUMBER: US 08/446,872  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Bennett, Dennis A.  
REGISTRATION NUMBER: 34,547

REFERENCE/DOCKET NUMBER: C-2790/5  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (708)470-6501  
TELEFAX: (708)470-6881  
INFORMATION FOR SEQ ID NO: 188:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
MOLECULE TYPE: peptide  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 188:  
US-08-762-227A-188

Query Match 29.2%; Score 28; DB 2; Length 18;  
Best Local Similarity 40.0%; Pred. No. 3.4e+02;  
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 8 YLTTAAVSPG 17  
|:::|  
Db 1 YVIEGRISPG 10

RESULT 44  
US-08-762-227A-189  
Sequence 189, Application US/08762227A  
Patent No. 6436387  
GENERAL INFORMATION:  
APPLICANT: Abrams, Mark A.  
Bauer, S. C.  
Bartford-Goldberg, Sarah R.  
Caparon, Alan M.  
Easton, Alan M.  
Klein, Barbara K.  
McKearn, John P.  
Olins, Peter O.  
Palk, Kuman  
Thomas, John W.  
TITLE OF INVENTION: Multivariant IL-3 Hematopoiesis  
Fusion Protein  
NUMBER OF SEQUENCES: 197  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dennis A. Bennett, G.D. Searle & Co.,  
STREET: P. O. Box 5110  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60680  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/762,227A  
FILING DATE: 09-Dec-1996  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/192,325  
FILING DATE: 14-FEB-1994  
APPLICATION NUMBER: US 08/446,872  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Bennett, Dennis A.  
REGISTRATION NUMBER: 34,547  
REFERENCE/DOCKET NUMBER: C-2790/5  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (708)470-6501  
TELEFAX: (708)470-6881  
INFORMATION FOR SEQ ID NO: 189:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids

TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 189:  
US-08-762-227A-189

Query Match 29.2%; Score 28; DB 2; Length 18;  
Best Local Similarity 40.0%; Pred. No. 3.4e+02;  
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 8 YLTTAAVSPG 17  
|:::|  
Db 1 YVIEGRISPG 10

RESULT 45  
PCT-US95-01185-188  
Sequence 188, Application PC/TUS9501185  
GENERAL INFORMATION:  
APPLICANT:  
TITLE OF INVENTION: Multivariant IL-3 Hematopoiesis Fusion  
Fusion Protein  
NUMBER OF SEQUENCES: 196  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30 (BPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/01185  
FILING DATE: 02-FEB-1995  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/192325

;; FILING DATE: 14-FEB-1994  
;; INFORMATION FOR SEQ ID NO: 189:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 18 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS:  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
PCT-US95-01185-189

Query Match 29.2%; Score 28; DB 4; Length 18;  
Best Local Similarity 40.0%; Pred. No. 3.4e+02;  
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 8 YLTLTAVSPG 17  
|:::|  
Db 1 YVIEGRISPG 10

RESULT 47  
US-08-416-950-7  
Sequence 7, Application US/08416950  
Patent No. 5780036

GENERAL INFORMATION:  
APPLICANT: CHISARI, Francis V.  
TITLE OF INVENTION: PEPTIDES FOR INDUCING CYTOTOXIC T  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend Hourie and Crew  
STREET: One Market Plaza, Stewart Street Tower  
CITY: San Francisco  
STATE: CA  
COUNTRY: U.S.A.  
ZIP: 94105-1492

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/416,950  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US

FILING DATE:  
APPLICATION NUMBER: US 07/935,898  
FILING DATE: 26-AUG-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/749,540  
FILING DATE: 26-AUG-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Parmelee, Steven W.  
REGISTRATION NUMBER: 31,990  
REFERENCE/DOCKET NUMBER: 14740-2-2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 467-9600  
TELEFAX: (415) 543-5043  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-416-950-7

Query Match 29.2%; Score 28; DB 1; Length 20;  
Best Local Similarity 50.0%; Pred. No. 3.9e+02;  
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 5 PHGYLTAIV 14

Db 1 PHHYALRQAI 10  
||| | | |

RESULT 48  
US-08-464-235-18  
Sequence 18, Application US/08464235  
Patent No. 5788969

GENERAL INFORMATION:  
APPLICANT: CHISARI, Francis V.  
TITLE OF INVENTION: PEPTIDES FOR INDUCING CYTOTOXIC T  
NUMBER OF SEQUENCES: 27  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend  
STREET: One Market Plaza, Stewart Street Tower  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94105

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/464,235  
FILING DATE: 05-JUN-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/024,120  
FILING DATE: 26-FEB-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Parmelee, Steven W.  
REGISTRATION NUMBER: 31,990  
REFERENCE/DOCKET NUMBER: 14740-4  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-467-9600  
TELEFAX: 415-543-5043

INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-464-235-18

Query Match 29.2%; Score 28; DB 1; Length 20;  
Best Local Similarity 50.0%; Pred. No. 3.9e+02;  
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 5 PHGYLTAIV 14  
||| | | |  
Db 1 PHHYALRQAI 10

RESULT 49  
US-08-468-279-35  
Sequence 35, Application US/08468279  
Patent No. 5840303

GENERAL INFORMATION:  
APPLICANT: CHISARI, Francis V.  
APPLICANT: FERRARI, Carlo  
APPLICANT: PENNA, Amalia  
APPLICANT: MISSALE, Gabriele  
TITLE OF INVENTION: T-LYMPHOCYTE RESPONSES TO HEPATITIS B VIRUS  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend  
STREET: One Market Plaza, Stewart Street Tower  
CITY: San Francisco

STATE: CA  
COUNTRY: USA  
ZIP: 94105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/468,279  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/935,898  
FILING DATE: 26-AUG-1992  
APPLICATION NUMBER: US 07/749,540  
FILING DATE: 26-AUG-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Parmelee, Steven W.  
REGISTRATION NUMBER: 31,990  
REFERENCE/DOCKET NUMBER: 14740-2-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-467-9600  
TELEFAX: 415-543-5043  
INFORMATION FOR SEQ ID NO: 35:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-468-279-35

Query Match 29.2%; Score 28; DB 1; Length 20;  
Best Local Similarity 50.0%; Pred. No. 3.9e+02;  
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 5 PHGYLTAAY 14  
DB 1 PHRYALRQAI 10

RESULT 50  
US-08-469-830-7  
Sequence 7, Application US/08469830  
Patent No. 593224  
GENERAL INFORMATION:  
APPLICANT: CHISARI, Francis V.  
TITLE OF INVENTION: PEPTIDES FOR INDUCING CYTOTOXIC T  
TITLE OF INVENTION: LYMPHOCYTE RESPONSES TO HEPATITIS B VIRUS  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Townsend and Townsend Kourile and Crew  
STREET: One Market Plaza, Stewart Street Tower  
CITY: San Francisco  
STATE: CA  
COUNTRY: U.S.A.  
ZIP: 94105-1492  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/469,830  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/100,870  
FILING DATE: 02-AUG-1993  
APPLICATION NUMBER: US 07/935,898  
FILING DATE: 26-AUG-1992  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/749,540  
FILING DATE: 26-AUG-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Parmelee, Steven W.  
REGISTRATION NUMBER: 31,990  
REFERENCE/DOCKET NUMBER: 14740-2-2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 467-9600  
TELEFAX: (415) 543-5043  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-469-830-7

Query Match 29.2%; Score 28; DB 1; Length 20;  
Best Local Similarity 50.0%; Pred. No. 3.9e+02;  
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 5 PHGYLTAAY 14  
DB 1 PHRYALRQAI 10

RESULT 51  
US-08-463-486-18  
Sequence 18, Application US/08463486  
Patent No. 6235288  
GENERAL INFORMATION:  
APPLICANT: CHISARI, Francis V.  
TITLE OF INVENTION: PEPTIDES FOR INDUCING CYTOTOXIC T  
TITLE OF INVENTION: LYMPHOCYTE RESPONSES TO HEPATITIS B VIRUS  
NUMBER OF SEQUENCES: 27  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Townsend and Townsend  
STREET: One Market Plaza, Stewart Street Tower  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/463,486  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/024,120  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Parmelee, Steven W.  
REGISTRATION NUMBER: 31,990  
REFERENCE/DOCKET NUMBER: 14740-4  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-467-9600  
TELEFAX: 415-543-5043  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-463-486-18

Query Match 29.2%; Score 28; DB 2; Length 20;  
Best Local Similarity 50.0%; Pred. No. 3.9e+02;

Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
QY 5 PHGYLITAAV 14  
DB 1 PHRYALROAI 10

RESULT 52  
US-08-464-496-11  
Sequence 11, Application US/08464496  
Patent No. 6322789  
GENERAL INFORMATION:  
APPLICANT: Epimmune, Inc.  
APPLICANT: Viciello, Maria  
APPLICANT: Chesnut, Robert  
TITLE OF INVENTION: HLA-RESTRICTED HEPATITIS B VIRUS CTL  
TITLE OF INVENTION: EPITOPES  
FILE REFERENCE: 39963-20001.13  
CURRENT APPLICATION NUMBER: US/08/464,496  
CURRENT FILING DATE: 1995-06-05  
PRIOR APPLICATION NUMBER: 07/935,811  
PRIOR FILING DATE: 1992-08-26  
PRIOR APPLICATION NUMBER: 07/874,491  
PRIOR FILING DATE: 1992-04-27  
PRIOR APPLICATION NUMBER: 07/827,682  
PRIOR FILING DATE: 1992-01-29  
PRIOR APPLICATION NUMBER: 07/749,568  
PRIOR FILING DATE: 1991-08-26  
NUMBER OF SEQ ID NOS: 75  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 11  
LENGTH: 20  
TYPE: PRT  
ORGANISM: HBV HBC 50-69  
US-08-464-496-11

Query Match 29.2%; Score 28; DB 2; Length 20;  
Best Local Similarity 50.0%; Pred. No. 3.9e+02;  
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 5 PHGYLITAAV 14  
DB 1 PHRYALROAI 10

RESULT 53  
US-08-197-484-101  
Sequence 101, Application US/08197484  
Patent No. 6419931  
GENERAL INFORMATION:  
APPLICANT: VITIELLO, Maria A.  
APPLICANT: CHESTNUT, Robert W.  
APPLICANT: SETTE, Alessandro D.  
APPLICANT: GRAY, Howard  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING  
TITLE OF INVENTION: CTL IMMUNITY  
NUMBER OF SEQUENCES: 153  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend Kourile and Crew  
STREET: Steuart Street Tower, One Market Plaza  
CITY: San Francisco  
STATE: California  
COUNTRY: US  
ZIP: 94105-1493  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Releasee #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/197,484  
FILING DATE: 16-FEB-1994

CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/935,811  
FILING DATE: 26-AUG-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/874,491  
FILING DATE: 27-APR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/827,682  
FILING DATE: 29-JAN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/749,568  
FILING DATE: 26-AUG-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Parmelee, Steven W.  
REGISTRATION NUMBER: 31,990  
REFERENCE/DOCKET NUMBER: 14137-26-4  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 467-9600  
TELEFAX: (206) 623-6793  
INFORMATION FOR SEQ ID NO: 101:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1..20  
OTHER INFORMATION:  
OTHER INFORMATION: /note= "HTL-inducing peptide  
US-08-197-484-101  
specific for HBV, HBC50-69"

Query Match 29.2%; Score 28; DB 2; Length 20;  
Best Local Similarity 50.0%; Pred. No. 3.9e+02;  
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 5 PHGYLITAAV 14  
DB 1 PHRYALROAI 10

RESULT 54  
US-08-591-502B-7  
Sequence 7, Application US/08591502B  
Patent No. 6607727  
GENERAL INFORMATION:  
APPLICANT: Chisari, Francis V.  
TITLE OF INVENTION: Peptides for Inducing Cytotoxic T  
NUMBER OF SEQUENCES: 99  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Releasee #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/591,502B  
FILING DATE: 20-May-1996  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/749,540  
FILING DATE: 26-AUG-1991  
APPLICATION NUMBER: US 07/935,898  
FILING DATE: 26-AUG-1992



APPLICATION NUMBER: US 08/100,870  
FILING DATE: 02-AUG-1993  
APPLICATION NUMBER: WO PCT/US94/08685  
FILING DATE: 01-AUG-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Weber, Ellen Lauver  
REGISTRATION NUMBER: 32,762  
REFERENCE/DOCKET NUMBER: 014740-000230US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 7:  
US-08-591-502B-7

Query Match 29.2%; Score 28; DB 2; Length 20;  
Best Local Similarity 50.0%; Pred. No. 3.9e+02;  
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 5 PHGYLTAAY 14  
DB 1 PHHYALRKAI 10

RESULT 55  
US-09-790-497A-446  
Sequence 446, Application US/09790497A  
Patent No. 6649735  
GENERAL INFORMATION:  
APPLICANT: De Levy, Robert  
TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES CORRESPONDING  
TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THEIR USE IN  
TITLE OF INVENTION: A PROCESS FOR DETERMINATION OF ANTIBODIES OF  
TITLE OF INVENTION: BIOTINYLATED PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT  
TITLE OF INVENTION: EPITOPES, A PROCESS FOR PREPARING THEM AND COMPOSITIONS  
FILE REFERENCE: 2752-16  
CURRENT APPLICATION NUMBER: US/09/790,497A  
CURRENT FILING DATE: 2001-02-23  
PRIOR APPLICATION NUMBER: 09/576,824  
PRIOR FILING DATE: 2000-05-23  
PRIOR APPLICATION NUMBER: 08/723,425  
PRIOR FILING DATE: 1996-09-30  
PRIOR APPLICATION NUMBER: 09/146,028  
PRIOR FILING DATE: 1993-11-22  
PRIOR APPLICATION NUMBER: PCT/EP93/00517  
PRIOR FILING DATE: 1993-03-08  
PRIOR APPLICATION NUMBER: EP 92400598.6  
PRIOR FILING DATE: 1992-03-06  
NUMBER OF SEQ ID NOS: 600  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 446  
LENGTH: 20  
TYPE: PRT  
ORGANISM: Hepatitis C virus  
US-09-790-497A-446

Query Match 29.2%; Score 28; DB 2; Length 20;  
Best Local Similarity 66.7%; Pred. No. 3.9e+02;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 LTRAVSPG 17  
DB 10 LTRAVSPG 18

RESULT 56

US-09-576-824A-446  
Sequence 446, Application US/09576824A  
Patent No. 667387  
GENERAL INFORMATION:  
APPLICANT: De Levy, Robert  
TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES CORRESPONDING  
TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THEIR USE IN  
TITLE OF INVENTION: A PROCESS FOR DETERMINATION OF ANTIBODIES OF  
TITLE OF INVENTION: BIOTINYLATED PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT  
TITLE OF INVENTION: EPITOPES, A PROCESS FOR PREPARING THEM AND COMPOSITIONS  
FILE REFERENCE: 2752-11  
CURRENT APPLICATION NUMBER: US/09/576,824A  
CURRENT FILING DATE: 2000-05-23  
PRIOR APPLICATION NUMBER: 08/723,425  
PRIOR FILING DATE: 1996-09-30  
PRIOR APPLICATION NUMBER: 09/146,028  
PRIOR FILING DATE: 1993-11-22  
PRIOR APPLICATION NUMBER: PCT/EP93/00517  
PRIOR FILING DATE: 1993-03-08  
PRIOR APPLICATION NUMBER: EP 92400598.6  
PRIOR FILING DATE: 1992-03-06  
NUMBER OF SEQ ID NOS: 600  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 446  
LENGTH: 20  
TYPE: PRT  
ORGANISM: Hepatitis C virus  
US-09-576-824A-446

Query Match 29.2%; Score 28; DB 2; Length 20;  
Best Local Similarity 66.7%; Pred. No. 3.9e+02;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 LTRAVSPG 17  
DB 10 LTRAVSPG 18

RESULT 57  
US-09-325-917A-4  
Sequence 47A, Application US/09325917A  
Patent No. 6911316  
GENERAL INFORMATION:  
APPLICANT: Higazi, Abd Al-Roof  
TITLE OF INVENTION: Medical Uses of scdPA/suPAR Complex  
FILE REFERENCE: 2741,1001-000  
CURRENT APPLICATION NUMBER: US/09/325,917A  
CURRENT FILING DATE: 1999-06-04  
PRIOR APPLICATION NUMBER: PCT/IL97/00402  
PRIOR FILING DATE: 1999-12-09  
PRIOR APPLICATION NUMBER: 60/032,676  
PRIOR FILING DATE: 1996-12-09  
NUMBER OF SEQ ID NOS: 5  
SOFTWARE: PasteSeq for Windows Version 4.0  
SEQ ID NO 4  
LENGTH: 20  
TYPE: PRT  
ORGANISM: unknown  
FEATURE:  
OTHER INFORMATION: homo sapien  
US-09-325-917A-4

Query Match 29.2%; Score 28; DB 2; Length 20;  
Best Local Similarity 55.6%; Pred. No. 3.9e+02;  
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 10 LTRAVSPG 18  
DB 9 VTLVSPGR 17

RESULT 58

US-09-863-054-18  
; Sequence 18, Application US/09863054  
; Patent No. 6919203  
; GENERAL INFORMATION:  
; APPLICANT: Chisari, Francis V.  
; TITLE OF INVENTION: Peptides for inducing cytotoxic T  
; Lymphocyte Responses to Hepatitis B Virus  
; NUMBER OF SEQUENCES: 57  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSER: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/863,054  
; FILING DATE: 21-May-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/935,898  
; FILING DATE: 26-AUG-1992  
; APPLICATION NUMBER: US 08/024,120  
; FILING DATE: 26-FEB-1993  
; APPLICATION NUMBER: US 08/396,283  
; FILING DATE: 27-FEB-1995  
; APPLICATION NUMBER: US 08/463,486  
; FILING DATE: 05-JUN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lockyer, Jean M.  
; REGISTRATION NUMBER: 44,879  
; REFERENCE/DOCKET NUMBER: 014740-000421US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 18:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 20 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: <Unknown>  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; SEQUENCE DESCRIPTION: SEQ ID NO: 18:  
US-09-863-054-18  
  
Query Match 29.2%; Score 28; DB 2; Length 20;  
Best Local Similarity 50.0%; Pred. No. 3.9e+02;  
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
  
QY 5 PHGYLTAAY 14  
DB 1 PHHYALRQAI 10  
  
RESULT 59  
PCT-US92-07218-11  
; Sequence 11, Application PC/TUS9207218  
; GENERAL INFORMATION:  
; APPLICANT: Vitello, Maria A.  
; APPLICANT: Chesnut, Robert W.  
; TITLE OF INVENTION: HLA-RESTRICTED HEPATITIS B VIRUS CTL  
; TITLE OF INVENTION: EPITOPES  
; NUMBER OF SEQUENCES: 35  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSER: Townsend and Townsend  
; STREET: One Market Plaza, Stewart Street Tower  
; CITY: San Francisco  
; STATE: California

COUNTRY: USA  
ZIP: 94105  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US92/07218  
; FILING DATE: 19920826  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/749,568  
; FILING DATE: 26-AUG-1991  
; APPLICATION NUMBER: US 07/827,682  
; FILING DATE: 29-JAN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/874,491  
; FILING DATE: 27-APR-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, William M.  
; REGISTRATION NUMBER: 30,223  
; REFERENCE/DOCKET NUMBER: 14137-26-3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-326-2400  
; TELEFAX: 415-543-5043  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 20 amino acids  
; TYPE: AMINO ACID  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
PCT-US92-07218-11  
  
Query Match 29.2%; Score 28; DB 4; Length 20;  
Best Local Similarity 50.0%; Pred. No. 3.9e+02;  
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
  
QY 5 PHGYLTAAY 14  
DB 1 PHHYALRQAI 10  
  
RESULT 60  
PCT-US94-02195-18  
; Sequence 18, Application PC/TUS9402195  
; GENERAL INFORMATION:  
; APPLICANT: Chisari, Francis V.  
; TITLE OF INVENTION: PEPTIDES FOR INDUCING CYTOTOXIC T  
; Lymphocyte Responses to Hepatitis B Virus  
; NUMBER OF SEQUENCES: 27  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSER: Townsend and Townsend  
; STREET: One Market Plaza, Stewart Street Tower  
; CITY: San Francisco  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94105  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US94/02195  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Parmelee, Steven W.  
; REGISTRATION NUMBER: 31,990  
; REFERENCE/DOCKET NUMBER: 14740-4

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-467-9600  
TELEFAX: 415-543-5043  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
PCT-US94-02195-18

Query Match 29.2%; Score 28; DB 4; Length 20;  
Best Local Similarity 50.0%; Pred. No. 3.9e+02;  
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 5 PHGYLTAHV 14  
Db 1 PHHYALRQAI 10

RESULT 61  
PCT-US95-02121-101  
Sequence 101, Application PC/TUS9502121  
GENERAL INFORMATION:  
APPLICANT:  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING  
NUMBER OF SEQUENCES: 153  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/02121  
FILING DATE: 16-FEB-1995  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/197,484  
FILING DATE: 16-FEB-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/935,811  
FILING DATE: 26-AUG-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/874,491  
FILING DATE: 27-APR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/827,682  
FILING DATE: 29-JAN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/749,568  
FILING DATE: 26-AUG-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Parmelee, Steven W.  
REGISTRATION NUMBER: 31,990  
REFERENCE/DOCKET NUMBER: 14137-26-4PC  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 467-9600  
TELEFAX: (415) 543-5043  
INFORMATION FOR SEQ ID NO: 101:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1..20  
OTHER INFORMATION: /note="HTL-Inducing peptide  
OTHER INFORMATION: specific for HBV, HBC50-69"  
PCT-US95-02121-101

Query Match 29.2%; Score 28; DB 4; Length 20;  
Best Local Similarity 50.0%; Pred. No. 3.9e+02;  
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 5 PHGYLTAHV 14  
Db 1 PHHYALRQAI 10

RESULT 62  
US-08-652-877-52  
Sequence 52, Application US/08652877  
Patent No. 6187548  
GENERAL INFORMATION:  
APPLICANT: Akersstrom, Goran  
APPLICANT: Junlin, Claes  
APPLICANT: Raak, Lars  
APPLICANT: Crumley, Gregg R.  
APPLICANT: Morse, Clarence C.  
APPLICANT: Murray, Edward M.  
TITLE OF INVENTION: Human Calcium Sensor Protein, Fragments  
NUMBER OF SEQUENCES: 106  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Rhone-Poulenc Rorer Inc.  
STREET: 500 Arcola Rd., 3043  
CITY: Collegeville  
STATE: PA  
COUNTRY: USA  
ZIP: 19426-0107  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Macintosh  
OPERATING SYSTEM: System 7.5.1  
SOFTWARE: Word 6.0 (Patentin)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/652,877  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/15203  
FILING DATE: 22-NOV-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/344,836  
FILING DATE: 23-NOV-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/487,314  
FILING DATE: 07-JUNE-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Savitzky, Martin  
REGISTRATION NUMBER: 29,699  
REFERENCE/DOCKET NUMBER: A1355E-US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 610-454-3816  
TELEFAX: 610-454-3808  
INFORMATION FOR SEQ ID NO: 52:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHEICAL: NO  
FRAGMENT TYPE: internal  
US-08-652-877-52

Query Match 28.6%; Score 27.5; DB 2; Length 11;  
Best Local Similarity 38.5%; Pred. No. 2.3e+02;  
Matches 5; Conservative 5; Mismatches 0; Indels 3; Gaps 1;

Qy 4 EPHGYLTAHVSP 16

Db :||: :||  
2 DPNGYMM--MSP 11

## RESULT 63

US-08-476-515A-52  
; Sequence 52, Application US/08476515A  
; Patent No. 6239270  
; GENERAL INFORMATION:  
; APPLICANT: Akerschem, Goran  
; APPLICANT: Junlin, Claes  
; APPLICANT: Raek, Lars  
; APPLICANT: Crumley, Gregg R.  
; APPLICANT: Morse, Clarence C.  
; APPLICANT: Murray, Edward M.  
; APPLICANT: Hjaln, Goran  
; TITLE OF INVENTION: Human Calcium Sensor Protein, Fragments  
; NUMBER OF SEQUENCES: 84  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: Martin Savitzky  
; STREET: Rhone-Poulenc Rorer Inc., 500 Arcola Rd.,  
; STREET: 3C43,  
; CITY: Collegeville  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19426-0107  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: Windows 95  
; SOFTWARE: Word 7.0 (Patentin)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/476,515A  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/344,836  
; FILING DATE: 23-NOV-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/SE94/00483  
; FILING DATE: 24-MAY-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: SE 9301764-8  
; FILING DATE: 24-MAY-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Savitzky, Martin  
; REGISTRATION NUMBER: 29,699  
; REFERENCE/DOCKET NUMBER: A1355D  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 610-454-3816  
; TELEFAX: 610-454-3808  
; INFORMATION FOR SEQ ID NO: 52:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
; FRAGMENT TYPE: internal  
US-08-476-515A-52

Query Match 28.6%; Score 27.5; DB 2; Length 11;  
Best Local Similarity 38.5%; Pred. No. 2.3e+02;  
Matches 5; Conservative 5; Mismatches 0; Indels 3; Gaps 1;

Qy 4 EPHGYLTAVSP 16  
Db 2 DPNGYMM--MSP 11

RESULT 64

US-08-408-604A-27  
; Sequence 27, Application US/08408604A  
; Patent No. 580149  
; GENERAL INFORMATION:  
; APPLICANT: Shoelston, Steven  
; TITLE OF INVENTION: INHIBITION OF SIGNAL TRANSDUCTION MOLECULES  
; NUMBER OF SEQUENCES: 211  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: LAHIVE & COCKFIELD  
; STREET: 60 State Street, Suite 510  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02109-1875  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: IBM PC compatible  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/408,604A  
; FILING DATE: 21-MAR-1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/134,558  
; FILING DATE: 08-OCT-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/959,949  
; FILING DATE: 09-OCT-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/722,359  
; FILING DATE: 19-JUNE-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Myers, Louis  
; REGISTRATION NUMBER: 35,965  
; REFERENCE/DOCKET NUMBER: JDP-014CP3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617)227-7400  
; TELEFAX: (617)227-5941  
; INFORMATION FOR SEQ ID NO: 27:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 17  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-408-604A-27

Query Match 28.6%; Score 27.5; DB 1; Length 17;  
Best Local Similarity 38.5%; Pred. No. 3.9e+02;  
Matches 5; Conservative 5; Mismatches 0; Indels 3; Gaps 1;

Qy 4 EPHGYLTAVSP 16  
Db 5 DPNGYMM--MSP 14

## RESULT 65

PCT-US93-09626-27  
; Sequence 27, Application PCT/US9309626  
; GENERAL INFORMATION:  
; APPLICANT:  
; NUMBER OF SEQUENCES: 48  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: IBM PC compatible  
; SOFTWARE: ASCII (text)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US93/09626  
; APPLICATION NUMBER: 07/959,949  
; FILING DATE: October 9, 1992

APPLICATION NUMBER: 07/722,359  
FILING DATE: June 19, 1991  
INFORMATION FOR SEQ ID NO: 27:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
PCT-US93-09626-27

Query Match 28.6%; Score 27.5; DB 4; Length 17;  
Best Local Similarity 38.5%; Pred. No. 3.9e+02;  
Matches 5; Conservative 5; Mismatches 0; Indels 3; Gaps 1;

QY 4 EPHGYLTAIVSP 16  
DB 5 DPNGYMM--MSP 14

RESULT 66  
US-08-256-747C-15  
Sequence 15, Application US/08256747C  
Patent No. 6037448  
GENERAL INFORMATION:  
APPLICANT: CHONG, Pele  
APPLICANT: GILLAM, Shirley  
APPLICANT: OU, Dawei  
APPLICANT: TINGLE, Aubrey  
TITLE OF INVENTION: SYNTHETIC PEPTIDES FOR A RUBELLA VACCINE  
NUMBER OF SEQUENCES: 78  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: 6th Floor, 330 University Avenue  
STREET: 6th Floor 701, 330 University Avenue  
CITY: Toronto  
STATE: Ontario  
COUNTRY: Canada  
ZIP: M5G 1R7  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/256,747C  
FILING DATE: 06-OCT-1994  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Stewart, Michael I.  
REGISTRATION NUMBER: 24,973  
REFERENCE/DOCKET NUMBER: 1038-370  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (416) 595-1155  
TELEFAX: (416) 595-1163  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-256-747C-15

Query Match 28.6%; Score 27.5; DB 2; Length 20;  
Best Local Similarity 44.4%; Pred. No. 4.7e+02;  
Matches 8; Conservative 2; Mismatches 5; Indels 3; Gaps 1;

QY 1 DAEPPHYLTAIVSPK 18  
DB 4 DADDP---LIRTA PGPE 18

RESULT 67  
US-08-834-130A-15  
Sequence 15, Application US/08834130A

Patent No. 6180758  
GENERAL INFORMATION:  
APPLICANT: CHONG, Pele  
APPLICANT: GILLAM, Shirley  
APPLICANT: OU, Dawei  
APPLICANT: TINGLE, Aubrey  
TITLE OF INVENTION: SYNTHETIC PEPTIDES FOR A RUBELLA VACCINE  
NUMBER OF SEQUENCES: 75  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: 6th Floor, 330 University Avenue  
STREET: 6th Floor, 330 University Avenue  
CITY: Toronto  
STATE: Ontario  
COUNTRY: Canada  
ZIP: M5G 1R7  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/834,130A  
FILING DATE: 14-APR-1997  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: STEWART, Michael I.  
REGISTRATION NUMBER: 24,973  
REFERENCE/DOCKET NUMBER: 1038-686 MIS:jb  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (416) 595-1155  
TELEFAX: (416) 595-1163  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-834-130A-15

Query Match 28.6%; Score 27.5; DB 2; Length 20;  
Best Local Similarity 44.4%; Pred. No. 4.7e+02;  
Matches 8; Conservative 2; Mismatches 5; Indels 3; Gaps 1;

QY 1 DAEPPHYLTAIVSPK 18  
DB 4 DADDP---LIRTA PGPE 18

RESULT 68  
5164481-6  
Patent No. 5164481  
APPLICANT: LACHROIX, MARTIAL/ZREIN, MAAN/DIONNE, GERVAIS  
TITLE OF INVENTION: PEPTIDES AND ANALOGUES AND MIXTURES  
FOR DETECTING AND ELICITING ANTIBODIES TO RUBELLA VIRUS  
NUMBER OF SEQUENCES: 11  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/397,767  
FILING DATE: 23-AUG-1989  
SEQ ID NO: 6  
LENGTH: 20  
5164481-6

Query Match 28.6%; Score 27.5; DB 6; Length 20;  
Best Local Similarity 44.4%; Pred. No. 4.7e+02;  
Matches 8; Conservative 2; Mismatches 5; Indels 3; Gaps 1;

QY 1 DAEPPHYLTAIVSPK 18  
DB 2 DADDP---LIRTA PGPE 16

RESULT 69  
US-08-822-586-19

```
/ Sequence 19, Application US/08822586
/ Patent No. 6015890
/ GENERAL INFORMATION:
/ APPLICANT: WILLIAM R. JACOBS, JR., JAMES M. MUSSER AND
/ TITLE OF INVENTION: AN EMBICAB OPERON OF MYCOBACTERIA AND
/ TITLE OF INVENTION: MUTANTS THEREOF
/ NUMBER OF SEQUENCES: 57
/ CORRESPONDENCE ADDRESS:
/ ADDRESSER: AMSTER, ROTHSTEIN & EBENSTEIN
/ STREET: 90 PARK AVENUE
/ CITY: NEW YORK
/ STATE: NEW YORK
/ COUNTRY: U.S.A.
/ ZIP: 10016
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 3.5 INCH 1.44 MB STORAGE
/ MEDIUM TYPE: DISKETTE
/ COMPUTER: IBM PC COMPATIBLE
/ OPERATING SYSTEM: MS-DOS
/ SOFTWARE: ASCII
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/822,586
/ FILING DATE: MARCH 20, 1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: ELIZABETH A. BOGOSIAN
/ REGISTRATION NUMBER: 39,911
/ REFERENCE/DOCKET NUMBER: 96700/437
/ TELEPHONE: (212) 697-5995
/ TELEFAX: (212) 286-0854 or 286-0082
/ TELEX: TWX 710-581-4766
/ INFORMATION FOR SEQ ID NO: 19:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 10 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE:
/ DESCRIPTION: peptide
/ HYPOTHETICAL: NO
/ FRAGMENT TYPE: Internal fragment
/ US-08-822-586-19

Query Match      28.1%; Score 27; DB 2; Length 10;
Best Local Similarity 71.4%; Pred. No. 2.5e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      7 GYLTTAA 13
       ||:|||
Db      4 GYLTTAA 10
```

```
RESULT 70
US-08-822-586-23
/ Sequence 23, Application US/08822586
/ Patent No. 6015890
/ GENERAL INFORMATION:
/ APPLICANT: WILLIAM R. JACOBS, JR., JAMES M. MUSSER AND
/ APPLICANT: AMALIO TELENTE
/ TITLE OF INVENTION: AN EMBICAB OPERON OF MYCOBACTERIA AND
/ TITLE OF INVENTION: MUTANTS THEREOF
/ NUMBER OF SEQUENCES: 57
/ CORRESPONDENCE ADDRESS:
/ ADDRESSER: AMSTER, ROTHSTEIN & EBENSTEIN
/ STREET: 90 PARK AVENUE
/ CITY: NEW YORK
/ STATE: NEW YORK
/ COUNTRY: U.S.A.
/ ZIP: 10016
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 3.5 INCH 1.44 MB STORAGE
/ MEDIUM TYPE: DISKETTE
```

```
/ COMPUTER: IBM PC COMPATIBLE
/ OPERATING SYSTEM: MS-DOS
/ SOFTWARE: ASCII
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/822,586
/ FILING DATE: MARCH 20, 1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: ELIZABETH A. BOGOSIAN
/ REGISTRATION NUMBER: 39,911
/ REFERENCE/DOCKET NUMBER: 96700/437
/ TELEPHONE: (212) 697-5995
/ TELEFAX: (212) 286-0854 or 286-0082
/ TELEX: TWX 710-581-4766
/ INFORMATION FOR SEQ ID NO: 23:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 10 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE:
/ DESCRIPTION: peptide
/ HYPOTHETICAL: NO
/ FRAGMENT TYPE: Internal fragment
/ US-08-822-586-23
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```
Query Match      28.1%; Score 27; DB 2; Length 10;
Best Local Similarity 71.4%; Pred. No. 2.5e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      7 GYLTTAA 13
       ||:|||
Db      4 GYLTTAA 10
```

```
RESULT 71
US-08-822-586-27
/ Sequence 27, Application US/08822586
/ Patent No. 6015890
/ GENERAL INFORMATION:
/ APPLICANT: WILLIAM R. JACOBS, JR., JAMES M. MUSSER AND
/ APPLICANT: AMALIO TELENTE
/ TITLE OF INVENTION: AN EMBICAB OPERON OF MYCOBACTERIA AND
/ TITLE OF INVENTION: MUTANTS THEREOF
/ NUMBER OF SEQUENCES: 57
/ CORRESPONDENCE ADDRESS:
/ ADDRESSER: AMSTER, ROTHSTEIN & EBENSTEIN
/ STREET: 90 PARK AVENUE
/ CITY: NEW YORK
/ STATE: NEW YORK
/ COUNTRY: U.S.A.
/ ZIP: 10016
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 3.5 INCH 1.44 MB STORAGE
/ MEDIUM TYPE: DISKETTE
/ COMPUTER: IBM PC COMPATIBLE
/ OPERATING SYSTEM: MS-DOS
/ SOFTWARE: ASCII
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/822,586
/ FILING DATE: MARCH 20, 1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: ELIZABETH A. BOGOSIAN
/ REGISTRATION NUMBER: 39,911
/ REFERENCE/DOCKET NUMBER: 96700/437
/ TELEPHONE: (212) 697-5995
/ TELEFAX: (212) 286-0854 or 286-0082
/ TELEX: TWX 710-581-4766
/ INFORMATION FOR SEQ ID NO: 27:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 10 amino acids
/ TYPE: amino acid
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STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
DESCRIPTION: NO  
HYPOTHETICAL: NO  
FRAGMENT TYPE: Internal fragment  
US-08-822-586-27

Query Match 28.1%; Score 27; DB 2; Length 10;  
Best Local Similarity 71.4%; Pred. No. 2.5e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 GYLTTAA 13  
DB 4 GYLTTAA 10

RESULT 72  
US-08-802-981-161  
Sequence 161, Application US/08802981  
Patent No. 6037137  
GENERAL INFORMATION:  
APPLICANT: Komoriya, Akira  
TITLE OF INVENTION: Packard, Beverly S.  
TITLE OF INVENTION: Compositions for the Detection of Enzyme  
TITLE OF INVENTION: Activity in Biological Samples and Methods of Use Thereof  
NUMBER OF SEQUENCES: 231  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
City: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/802,981  
FILING DATE: 20-FEB-1997  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Hunter, Tom  
REGISTRATION NUMBER: 38,498  
REFERENCE/DOCKET NUMBER: 016865-000300US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 161:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 1  
OTHER INFORMATION: /product= "OTHER"  
OTHER INFORMATION: /note= "Xaa = Fluorophore 1 linked to the alpha-amino group C  
OTHER INFORMATION: Asp"  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 9  
OTHER INFORMATION: /product= "OTHER"  
OTHER INFORMATION: /note= "Xaa = Fluorophore 1 linked to the epsilon-amino group  
OTHER INFORMATION: Lys"  
US-08-802-981-161  
Query Match 28.1%; Score 27; DB 2; Length 11;  
Best Local Similarity 50.0%; Pred. No. 2.8e+02;

Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DAFEPHGY 8  
DB 4 DGIDPXYG 11

RESULT 73  
US-09-747-287A-215  
Sequence 215, Application US/09747287A  
Patent No. 6893868  
GENERAL INFORMATION:  
APPLICANT: KOMORIYA, AKIRA  
TITLE OF INVENTION: HOWE-DOUBLY LABELED COMPOSITIONS FOR THE DETECTION OF ENZYME  
TITLE OF INVENTION: ACTIVITY IN BIOLOGICAL SAMPLES  
FILE REFERENCE: 300-948600US  
CURRENT APPLICATION NUMBER: US/09/747,287A  
CURRENT FILING DATE: 2000-12-22  
PRIOR APPLICATION NUMBER: US 09/349,019  
PRIOR FILING DATE: 1999-09-10  
PRIOR APPLICATION NUMBER: US08/802,981  
PRIOR FILING DATE: 1997-02-20  
PRIOR APPLICATION NUMBER: PCT/US00/24882  
PRIOR FILING DATE: 2000-09-11  
NUMBER OF SEQ ID NOS: 246  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 215  
LENGTH: 11  
TYPE: PRT  
ORGANISM: Artificial  
FEATURE:  
OTHER INFORMATION: Synthetic peptide. Artificial protease substrate.  
US-09-747-287A-215

Query Match 28.1%; Score 27; DB 2; Length 11;  
Best Local Similarity 50.0%; Pred. No. 2.8e+02;  
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DAFEPHGY 8  
DB 4 DGIDPXYG 11

RESULT 74  
US-09-394-019C-169  
Sequence 169, Application US/09394019C  
Patent No. 6936687  
GENERAL INFORMATION:  
APPLICANT: OncoImmune, Inc.  
APPLICANT: Komoriya, Akira  
TITLE OF INVENTION: Packard, Beverly  
TITLE OF INVENTION: COMPOSITIONS FOR THE DETECTION OF ENZYME ACTIVITY IN BIOLOGICAL  
FILE REFERENCE: 300-903820US  
CURRENT APPLICATION NUMBER: US/09/394,019C  
CURRENT FILING DATE: 1999-09-10  
PRIOR APPLICATION NUMBER: PCT/US98/00300  
PRIOR FILING DATE: 1998-02-20  
PRIOR APPLICATION NUMBER: US 08/802,981  
PRIOR FILING DATE: 1997-02-20  
NUMBER OF SEQ ID NOS: 405  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 169  
LENGTH: 11  
TYPE: PRT  
ORGANISM: Artificial  
FEATURE:  
OTHER INFORMATION: Synthetic peptide substrate  
FEATURE:  
NAME/KEY: misc feature  
OTHER INFORMATION: Artificial = synthetic protease indicator

NAME/KEY: MOD\_RES  
LOCATION: (1)-(1)  
OTHER INFORMATION: D is derivatized with fluorophore  
FEATURE:  
NAME/KEY: MOD\_RES  
LOCATION: (9)-(9)  
OTHER INFORMATION: K is derivatized with fluorophore  
US-09-394-019C-169

Query Match 28.1%; Score 27; DB 2; Length 11;  
Best Local Similarity 50.0%; Pred. No. 2.8e+02;  
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DAFPHGY 8  
DB 4 DGIDPKGY 11

## RESULT 75

US-08-802-981-162  
Sequence 162, Application US/08802981

Patent No. 6037137  
GENERAL INFORMATION:  
APPLICANT: Komoriya, Akira  
TITLE OF INVENTION: Compositions for the Detection of Enzyme  
TITLE OF INVENTION: Activity in Biological Samples and Methods of Use Thereof  
NUMBER OF SEQUENCES: 231  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/802,981  
FILING DATE: 20-FEB-1997  
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:  
NAME: Hunter, Tom

REGISTRATION NUMBER: 38,498  
REFERENCE/DOCKET NUMBER: 016865-000300US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 162:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid

STRANDEDNESS:  
TOPOLOGY: linear

MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Modified-site

LOCATION: 1  
OTHER INFORMATION: /product= "OTHER"  
OTHER INFORMATION: /note= "Xaa = fluorophore 1 linked to the alpha-amino group of  
OTHER INFORMATION: Ptc"  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 10  
OTHER INFORMATION: /product= "OTHER"  
OTHER INFORMATION: /note= "Xaa = fluorophore 1 linked to the epsilon-amino group  
OTHER INFORMATION: Lys"

US-08-802-981-162

Query Match 28.1%; Score 27; DB 2; Length 12;

Best Local Similarity 50.0%; Pred. No. 3.1e+02;  
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DAFPHGY 8  
DB 5 DGIDPKGY 12

## RESULT 76

US-09-929-266-13

Sequence 13, Application US/09929266  
Patent No. 6824981

GENERAL INFORMATION:  
APPLICANT: Brian T. Chait  
APPLICANT: Darin R. Latimer  
APPLICANT: Paul M. Lizardi  
APPLICANT: Eric R. Kershner  
APPLICANT: Jon S. Morrow  
APPLICANT: Matthew B. Roth  
APPLICANT: Martin J. Matresich  
APPLICANT: Kevin J. McConnell

TITLE OF INVENTION: ULTRA-SENSITIVE DETECTION SYSTEMS  
FILE REFERENCE: 01173.000302

CURRENT APPLICATION NUMBER: US/09/929,266  
CURRENT FILING DATE: 2001-08-13

PRIOR APPLICATION NUMBER: 60/224,939  
PRIOR FILING DATE: 2000-08-11

PRIOR APPLICATION NUMBER: 60/283,498  
PRIOR FILING DATE: 2000-04-12

NUMBER OF SEQ ID NOS: 33  
SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 13

LENGTH: 12

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence; No. 6824981e=synthetic

US-09-929-266-13

Query Match 28.1%; Score 27; DB 2; Length 12;  
Best Local Similarity 40.0%; Pred. No. 3.1e+02;

Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 8 YLTAASRG 17  
DB 1 YFTSGCDPG 10

## RESULT 77

US-09-747-287A-216

Sequence 216, Application US/09747287A  
Patent No. 6893868

GENERAL INFORMATION:  
APPLICANT: KOMORIYA, AKIRA

TITLE OF INVENTION: HOMO-DOUBLY LABELED COMPOSITIONS FOR THE DETECTION OF ENZYME

TITLE OF INVENTION: ACTIVITY IN BIOLOGICAL SAMPLES  
FILE REFERENCE: 300-948600US

CURRENT APPLICATION NUMBER: US/09/747,287A  
CURRENT FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: US 09/349,019  
PRIOR FILING DATE: 1999-09-10

PRIOR APPLICATION NUMBER: US08/802,981  
PRIOR FILING DATE: 1997-02-20

PRIOR APPLICATION NUMBER: PCT/US00/24882  
PRIOR FILING DATE: 2000-09-11

NUMBER OF SEQ ID NOS: 246  
SOFTWARE: Patentin version 3.3

SEQ ID NO 216

LENGTH: 12

TYPE: PRT

ORGANISM: Artificial



FEATURE:  
OTHER INFORMATION: Synthetic peptide.  
US-09-747-287A-216

Query Match 28.1%; Score 27; DB 2; Length 12;  
Best Local Similarity 50.0%; Pred. No. 3.1e+02;  
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DAFEPHGY 8  
DB 5 DGIDPKGY 12

RESULT 78  
US-09-394-019C-170  
Sequence 170, Application US/09394019C  
Patent No. 6936687  
GENERAL INFORMATION:  
APPLICANT: Oncoimmun, Inc.  
APPLICANT: Komoriya, Akira  
APPLICANT: Packard, Beverly  
TITLE OF INVENTION: COMPOSITIONS FOR THE DETECTION OF ENZYME ACTIVITY IN BIOLOGICAL  
FILE REFERENCE: 300-903820US  
CURRENT FILING DATE: 1999-09-10  
PCT/US98/00300  
PRIOR FILING DATE: 1998-02-20  
PRIOR APPLICATION NUMBER: US 08/802,981  
PRIOR FILING DATE: 1997-02-20  
NUMBER OF SEQ ID NOS: 405  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 170  
LENGTH: 12  
TYPE: PRT  
ORGANISM: Artificial  
FEATURE:  
OTHER INFORMATION: Synthetic peptide substrate  
NAME/KEY: misc\_feature  
OTHER INFORMATION: Artificial = synthetic protease indicator  
FEATURE:  
NAME/KEY: MOD RES  
LOCATION: (1)..(1)  
OTHER INFORMATION: P is derivatized with fluorophore  
FEATURE:  
NAME/KEY: MOD RES  
LOCATION: (10)..(10)  
OTHER INFORMATION: K is derivatized with fluorophore  
US-09-394-019C-170

Query Match 28.1%; Score 27; DB 2; Length 12;  
Best Local Similarity 50.0%; Pred. No. 3.1e+02;  
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DAFEPHGY 8  
DB 5 DGIDPKGY 12

RESULT 79  
US-08-802-981-42  
Sequence 42, Application US/08802981  
Patent No. 6037137  
GENERAL INFORMATION:  
APPLICANT: Komoriya, Akira  
APPLICANT: Packard, Beverly S.  
TITLE OF INVENTION: Compositions for the Detection of Enzyme  
ACTIVITY IN BIOLOGICAL SAMPLES AND METHODS OF USE THEREOF  
NUMBER OF SEQUENCES: 231  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/802,981  
FILING DATE: 20-FEB-1997  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Hunter, Tom  
REGISTRATION NUMBER: 38,498  
REFERENCE/DOCKET NUMBER: 016865-000300US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 42:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 13 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 3  
OTHER INFORMATION: /product= "Alb"  
US-08-802-981-42

Query Match 28.1%; Score 27; DB 2; Length 13;  
Best Local Similarity 50.0%; Pred. No. 3.4e+02;  
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DAFEPHGY 8  
DB 6 DGIDPKGY 13

RESULT 80  
US-08-802-981-43  
Sequence 43, Application US/08802981  
Patent No. 6037137  
GENERAL INFORMATION:  
APPLICANT: Komoriya, Akira  
APPLICANT: Packard, Beverly S.  
TITLE OF INVENTION: Compositions for the Detection of Enzyme  
ACTIVITY IN BIOLOGICAL SAMPLES AND METHODS OF USE THEREOF  
NUMBER OF SEQUENCES: 231  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/802,981  
FILING DATE: 20-FEB-1997  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Hunter, Tom  
REGISTRATION NUMBER: 38,498  
REFERENCE/DOCKET NUMBER: 016865-000300US  
TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 43:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 13 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 4  
OTHER INFORMATION: /product= "A1b"  
US-08-802-981-43

Query Match 28.1%; Score 27; DB 2; Length 13;  
Best Local Similarity 50.0%; Pred. No. 3.4e+02;  
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DAFPHGY 8  
| : | | |  
Db 6 DGIIDPKGY 13

RESULT 81  
US-08-802-981-46  
Sequence 46, Application US/08802981  
Patent No. 6037137  
GENERAL INFORMATION:  
APPLICANT: Komoriya, Akira  
APPLICANT: Packard, Beverly S.  
TITLE OF INVENTION: Compositions for the Detection of Enzyme  
TITLE OF INVENTION: Activity in Biological Samples and Methods of Use Thereof  
NUMBER OF SEQUENCES: 231  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/802,981  
FILING DATE: 20-FEB-1997  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Hunter, Tom  
REGISTRATION NUMBER: 38,498  
REFERENCE/DOCKET NUMBER: 016865-000300US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 46:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 13 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 1  
OTHER INFORMATION: /product= "OTHER"  
OTHER INFORMATION: /note= "Xaa = 9-fluorenylmethoxycarbonyl (Fmoc) group attached  
OTHER INFORMATION: to the alpha-amino group of Lys"  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 3

OTHER INFORMATION: /product= "A1b"  
US-08-802-981-46

Query Match 28.1%; Score 27; DB 2; Length 13;  
Best Local Similarity 50.0%; Pred. No. 3.4e+02;  
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DAFPHGY 8  
| : | | |  
Db 6 DGIIDPKGY 13

RESULT 82  
US-08-802-981-51  
Sequence 51, Application US/08802981  
Patent No. 6037137  
GENERAL INFORMATION:  
APPLICANT: Komoriya, Akira  
APPLICANT: Packard, Beverly S.  
TITLE OF INVENTION: Compositions for the Detection of Enzyme  
TITLE OF INVENTION: Activity in Biological Samples and Methods of Use Thereof  
NUMBER OF SEQUENCES: 231  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/802,981  
FILING DATE: 20-FEB-1997  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Hunter, Tom  
REGISTRATION NUMBER: 38,498  
REFERENCE/DOCKET NUMBER: 016865-000300US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 51:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 13 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 1  
OTHER INFORMATION: /product= "OTHER"  
OTHER INFORMATION: /note= "Xaa = 9-fluorenylmethoxycarbonyl (Fmoc) group attached  
OTHER INFORMATION: to the alpha-amino group of Lys"  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 4  
OTHER INFORMATION: /product= "A1b"  
US-08-802-981-51

Query Match 28.1%; Score 27; DB 2; Length 13;  
Best Local Similarity 50.0%; Pred. No. 3.4e+02;  
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DAFPHGY 8  
| : | | |  
Db 6 DGIIDPKGY 13

RESULT 83  
US-08-802-981-170  
Sequence 170, Application US/08802981  
Patent No. 6037137  
GENERAL INFORMATION:  
APPLICANT: Komoriya, Akira  
APPLICANT: Packard, Beverly S.  
TITLE OF INVENTION: Compositions for the Detection of Enzyme  
NUMBER OF SEQUENCES: 231  
TITLE OF INVENTION: Activity in Biological Samples and Methods of Use Thereof  
CORRESPONDENCE ADDRESSES:  
ADDRESSER: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/802,981  
FILING DATE: 20-FEB-1997  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Hunter, Tom  
REGISTRATION NUMBER: 38,498  
REFERENCE/DOCKET NUMBER: 016865-000300US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 170:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 13 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 1  
OTHER INFORMATION: /product= "OTHER"  
OTHER INFORMATION: /note= "Xaa = 9-fluorenylmethoxycarbonyl (Fmoc) group attached  
OTHER INFORMATION: the alpha-amino group and 5'-carboxytetramethylrhodamine  
OTHER INFORMATION: attached to the epsilon-amino group of Lys"  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 3  
OTHER INFORMATION: /product= "Alb"  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 11  
OTHER INFORMATION: /product= "OTHER"  
OTHER INFORMATION: /note= "Xaa = 5'-carboxytetramethylrhodamine attached to the  
OTHER INFORMATION: epsilon-amino group of Lys"  
US-08-802-981-170  
Query Match 28.1%; Score 27; DB 2; Length 13;  
Best Local Similarity 50.0%; Pred. No. 3,4e+02;  
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
Qy 1 DAFEPHGY 8  
Db 6 DGIDPKGY 13  
RESULT 84  
US-08-802-981-171  
Sequence 171, Application US/08802981  
Patent No. 6037137  
GENERAL INFORMATION:

APPLICANT: Komoriya, Akira  
APPLICANT: Packard, Beverly S.  
TITLE OF INVENTION: Compositions for the Detection of Enzyme  
NUMBER OF SEQUENCES: 231  
TITLE OF INVENTION: Activity in Biological Samples and Methods of Use Thereof  
CORRESPONDENCE ADDRESSES:  
ADDRESSER: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/802,981  
FILING DATE: 20-FEB-1997  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Hunter, Tom  
REGISTRATION NUMBER: 38,498  
REFERENCE/DOCKET NUMBER: 016865-000300US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 171:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 13 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 1  
OTHER INFORMATION: /product= "OTHER"  
OTHER INFORMATION: /note= "Xaa = 5'-carboxytetramethylrhodamine attached to the  
OTHER INFORMATION: epsilon-amino group of Lys"  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 4  
OTHER INFORMATION: /product= "Alb"  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 11  
OTHER INFORMATION: /product= "OTHER"  
OTHER INFORMATION: /note= "Xaa = 5'-carboxytetramethylrhodamine attached to the  
OTHER INFORMATION: epsilon-amino group of Lys"  
US-08-802-981-171  
Query Match 28.1%; Score 27; DB 2; Length 13;  
Best Local Similarity 50.0%; Pred. No. 3,4e+02;  
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
Qy 1 DAFEPHGY 8  
Db 6 DGIDPKGY 13  
RESULT 85  
US-08-802-981-175  
Sequence 175, Application US/08802981  
Patent No. 6037137  
GENERAL INFORMATION:  
APPLICANT: Komoriya, Akira  
APPLICANT: Packard, Beverly S.  
TITLE OF INVENTION: Compositions for the Detection of Enzyme  
NUMBER OF SEQUENCES: 231  
TITLE OF INVENTION: Activity in Biological Samples and Methods of Use Thereof  
CORRESPONDENCE ADDRESSES:

ADDRESSER: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/802,981  
FILING DATE: 20-FEB-1997  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Hunter, Tom  
REGISTRATION NUMBER: 38,498  
REFERENCE/DOCKET NUMBER: 016865-000300US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 175:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 13 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 1  
OTHER INFORMATION: /product= "OTHER"  
OTHER INFORMATION: /note= "Xaa = 9-fluorenylmethoxycarbonyl (Fmoc) group attached to the alpha-amino group and 5'-carboxytetramethylrhodamine  
OTHER INFORMATION: attached to the epsilon-amino group of Lys"  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 4  
OTHER INFORMATION: /product= "Aib"  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 11  
OTHER INFORMATION: /product= "OTHER"  
OTHER INFORMATION: /note= "Xaa = 5'-carboxytetramethylrhodamine attached to the  
OTHER INFORMATION: epsilon-amino group of Lys"  
US-08-802-981-175  
Query Match 28.1%; Score 27; DB 2; Length 13;  
Best Local Similarity 50.0%; Pred. No. 3.4e+02;  
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
QY 1 DAFEPHGY 8  
DB 6 DGIDPXGY 13  
RESULT 86  
US-08-802-981-176  
Sequence 176, Application US/08802981  
Patent No. 6037137  
GENERAL INFORMATION:  
APPLICANT: KOMORIYA, AKIRA  
APPLICANT: Packard, Beverly S.  
TITLE OF INVENTION: Compositions for the Detection of Enzyme  
TITLE OF INVENTION: Activity in Biological Samples and Methods of Use Thereof  
NUMBER OF SEQUENCES: 231  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA

ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/802,981  
FILING DATE: 20-FEB-1997  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Hunter, Tom  
REGISTRATION NUMBER: 38,498  
REFERENCE/DOCKET NUMBER: 016865-000300US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 176:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 13 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 1  
OTHER INFORMATION: /product= "OTHER"  
OTHER INFORMATION: /note= "Xaa = 5'-carboxytetramethylrhodamine attached to the  
OTHER INFORMATION: epsilon-amino group of Lys"  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 3  
OTHER INFORMATION: /product= "Aib"  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 11  
OTHER INFORMATION: /product= "OTHER"  
OTHER INFORMATION: /note= "Xaa = 5'-carboxytetramethylrhodamine attached to the  
OTHER INFORMATION: epsilon-amino group of Lys"  
US-08-802-981-176  
Query Match 28.1%; Score 27; DB 2; Length 13;  
Best Local Similarity 50.0%; Pred. No. 3.4e+02;  
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
QY 1 DAFEPHGY 8  
DB 6 DGIDPXGY 13  
RESULT 87  
US-09-747-287A-40  
Sequence 40, Application US/09747287A  
Patent No. 6893868  
GENERAL INFORMATION:  
APPLICANT: KOMORIYA, AKIRA  
APPLICANT: PACKARD, BEVERLY S.  
TITLE OF INVENTION: HOWO-DOUBLY LABELED COMPOSITIONS FOR THE DETECTION OF ENZYME  
TITLE OF INVENTION: ACTIVITY IN BIOLOGICAL SAMPLES  
FILE REFERENCE: 300-948600US  
CURRENT APPLICATION NUMBER: US/09/747,287A  
CURRENT FILING DATE: 2000-12-22  
PRIOR APPLICATION NUMBER: US 09/349,019  
PRIOR FILING DATE: 1999-09-10  
PRIOR APPLICATION NUMBER: US08/802,981  
PRIOR FILING DATE: 1997-02-20  
PRIOR APPLICATION NUMBER: PCT/US00/24882  
PRIOR FILING DATE: 2000-09-11  
NUMBER OF SEQ ID NOS: 246  
SOFTWARE: Patent In version 3.3  
SEQ ID NO 40  
LENGTH: 13

TYPE: PRT  
ORGANISM: Artificial  
FEATURE:  
OTHER INFORMATION: Synthetic peptide.  
US-09-747-287A-40

Query Match 28.1%; Score 27; DB 2; Length 13;  
Best Local Similarity 50.0%; Pred. No. 3.4e+02;  
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DAFEPHGX 8  
DB 6 DGIDPKGX 13

RESULT 88  
US-09-747-287A-41  
Sequence 41, Application US/09747287A  
Patent No. 6893868  
GENERAL INFORMATION:  
APPLICANT: KOMORIYA, AKIRA  
TITLE OF INVENTION: HOMO-DOUBLY LABELED COMPOSITIONS FOR THE DETECTION OF ENZYME  
FILE REFERENCE: 300-948600US  
CURRENT APPLICATION NUMBER: US/09/747,287A  
PRIOR FILING DATE: 2000-12-22  
PRIOR APPLICATION NUMBER: US 09/349,019  
PRIOR FILING DATE: 1999-09-10  
PRIOR APPLICATION NUMBER: US08/802,981  
PRIOR FILING DATE: 1997-02-20  
PRIOR APPLICATION NUMBER: PCT/US00/24882  
NUMBER OF SEQ ID NOS: 246  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 41  
LENGTH: 13  
TYPE: PRT  
ORGANISM: Artificial  
FEATURE:  
OTHER INFORMATION: Synthetic peptide.  
US-09-747-287A-41

Query Match 28.1%; Score 27; DB 2; Length 13;  
Best Local Similarity 50.0%; Pred. No. 3.4e+02;  
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DAFEPHGX 8  
DB 6 DGIDPKGX 13

RESULT 89  
US-09-747-287A-44  
Sequence 44, Application US/09747287A  
Patent No. 6893868  
GENERAL INFORMATION:  
APPLICANT: KOMORIYA, AKIRA  
TITLE OF INVENTION: HOMO-DOUBLY LABELED COMPOSITIONS FOR THE DETECTION OF ENZYME  
FILE REFERENCE: 300-948600US  
CURRENT APPLICATION NUMBER: US/09/747,287A  
PRIOR FILING DATE: 2000-12-22  
PRIOR APPLICATION NUMBER: US 09/349,019  
PRIOR FILING DATE: 1999-09-10  
PRIOR APPLICATION NUMBER: US08/802,981  
PRIOR FILING DATE: 1997-02-20  
PRIOR APPLICATION NUMBER: PCT/US00/24882  
NUMBER OF SEQ ID NOS: 246  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 44

LENGTH: 13  
TYPE: PRT  
ORGANISM: Artificial  
FEATURE:  
OTHER INFORMATION: Synthetic peptide.  
US-09-747-287A-44

Query Match 28.1%; Score 27; DB 2; Length 13;  
Best Local Similarity 50.0%; Pred. No. 3.4e+02;  
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DAFEPHGX 8  
DB 6 DGIDPKGX 13

RESULT 90  
US-09-747-287A-50  
Sequence 50, Application US/09747287A  
Patent No. 6893868  
GENERAL INFORMATION:  
APPLICANT: KOMORIYA, AKIRA  
TITLE OF INVENTION: HOMO-DOUBLY LABELED COMPOSITIONS FOR THE DETECTION OF ENZYME  
FILE REFERENCE: 300-948600US  
CURRENT APPLICATION NUMBER: US/09/747,287A  
PRIOR FILING DATE: 2000-12-22  
PRIOR APPLICATION NUMBER: US 09/349,019  
PRIOR FILING DATE: 1999-09-10  
PRIOR APPLICATION NUMBER: US08/802,981  
PRIOR FILING DATE: 1997-02-20  
PRIOR APPLICATION NUMBER: PCT/US00/24882  
NUMBER OF SEQ ID NOS: 246  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 50  
LENGTH: 13  
TYPE: PRT  
ORGANISM: Artificial  
FEATURE:  
OTHER INFORMATION: Synthetic peptide.  
US-09-747-287A-50

Query Match 28.1%; Score 27; DB 2; Length 13;  
Best Local Similarity 50.0%; Pred. No. 3.4e+02;  
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DAFEPHGX 8  
DB 6 DGIDPKGX 13

RESULT 91  
US-09-747-287A-224  
Sequence 224, Application US/09747287A  
Patent No. 6893868  
GENERAL INFORMATION:  
APPLICANT: KOMORIYA, AKIRA  
TITLE OF INVENTION: HOMO-DOUBLY LABELED COMPOSITIONS FOR THE DETECTION OF ENZYME  
FILE REFERENCE: 300-948600US  
CURRENT APPLICATION NUMBER: US/09/747,287A  
PRIOR FILING DATE: 2000-12-22  
PRIOR APPLICATION NUMBER: US 09/349,019  
PRIOR FILING DATE: 1999-09-10  
PRIOR APPLICATION NUMBER: US08/802,981  
PRIOR FILING DATE: 1997-02-20  
PRIOR APPLICATION NUMBER: PCT/US00/24882  
NUMBER OF SEQ ID NOS: 246  
SOFTWARE: PatentIn version 3.3

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/ SEQ ID NO 224
/ LENGTH: 13
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: Synthetic peptide.
/ NAME/KEY: misc_feature
/ LOCATION: (3)..(3)
/ OTHER INFORMATION: Xaa is aminobutyric acid
US-09-747-287A-224
```

```
Query Match          28.1%; Score 27; DB 2; Length 13;
Best Local Similarity 50.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      1 DAEPPHY 8
      | : | | |
DB      6 DGIDPKGY 13
```

```
RESULT 92
US-09-747-287A-225
/ Sequence 225, Application US/09747287A
/ Patent No. 6893868
/ GENERAL INFORMATION:
/ APPLICANT: KOMORIYA, AKIRA
/ TITLE OF INVENTION: HOWO-DOUBLY LABELED COMPOSITIONS FOR THE DETECTION OF ENZYME
/ FILE REFERENCE: 300-948600US
/ CURRENT APPLICATION NUMBER: US/09/747,287A
/ PRIOR FILING DATE: 2000-12-22
/ PRIOR APPLICATION NUMBER: US 09/349,019
/ PRIOR FILING DATE: 1999-09-10
/ PRIOR APPLICATION NUMBER: US08/802,981
/ PRIOR FILING DATE: 1997-02-20
/ PRIOR APPLICATION NUMBER: PCT/US00/24882
/ PRIOR FILING DATE: 2000-09-11
/ NUMBER OF SEQ ID NOS: 246
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 225
/ LENGTH: 13
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: Synthetic peptide.
/ NAME/KEY: misc_feature
/ LOCATION: (4)..(4)
/ OTHER INFORMATION: Xaa is aminobutyric acid
US-09-747-287A-225
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```
Query Match          28.1%; Score 27; DB 2; Length 13;
Best Local Similarity 50.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
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```
QY      1 DAEPPHY 8
      | : | | |
DB      6 DGIDPKGY 13
```

```
RESULT 93
US-09-747-287A-229
/ Sequence 229, Application US/09747287A
/ Patent No. 6893868
/ GENERAL INFORMATION:
/ APPLICANT: KOMORIYA, AKIRA
/ TITLE OF INVENTION: HOWO-DOUBLY LABELED COMPOSITIONS FOR THE DETECTION OF ENZYME
/ FILE REFERENCE: 300-948600US
/ CURRENT APPLICATION NUMBER: US/09/747,287A
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/ CURRENT FILING DATE: 2000-12-22
/ PRIOR APPLICATION NUMBER: US 09/349,019
/ PRIOR FILING DATE: 1999-09-10
/ PRIOR APPLICATION NUMBER: US08/802,981
/ PRIOR FILING DATE: 1997-02-20
/ PRIOR APPLICATION NUMBER: PCT/US00/24882
/ PRIOR FILING DATE: 2000-09-11
/ NUMBER OF SEQ ID NOS: 246
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 229
/ LENGTH: 13
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: Synthetic peptide.
/ NAME/KEY: misc_feature
/ LOCATION: (4)..(4)
/ OTHER INFORMATION: Xaa is aminobutyric acid
US-09-747-287A-229
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Query Match          28.1%; Score 27; DB 2; Length 13;
Best Local Similarity 50.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
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```
QY      1 DAEPPHY 8
      | : | | |
DB      6 DGIDPKGY 13
```

```
RESULT 94
US-09-747-287A-230
/ Sequence 230, Application US/09747287A
/ Patent No. 6893868
/ GENERAL INFORMATION:
/ APPLICANT: KOMORIYA, AKIRA
/ TITLE OF INVENTION: HOWO-DOUBLY LABELED COMPOSITIONS FOR THE DETECTION OF ENZYME
/ FILE REFERENCE: 300-948600US
/ CURRENT APPLICATION NUMBER: US/09/747,287A
/ PRIOR FILING DATE: 2000-12-22
/ PRIOR APPLICATION NUMBER: US 09/349,019
/ PRIOR FILING DATE: 1999-09-10
/ PRIOR APPLICATION NUMBER: US08/802,981
/ PRIOR FILING DATE: 1997-02-20
/ PRIOR APPLICATION NUMBER: PCT/US00/24882
/ PRIOR FILING DATE: 2000-09-11
/ NUMBER OF SEQ ID NOS: 246
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 230
/ LENGTH: 13
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: Synthetic peptide.
/ NAME/KEY: misc_feature
/ LOCATION: (3)..(3)
/ OTHER INFORMATION: Xaa is aminobutyric acid
US-09-747-287A-230
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Query Match          28.1%; Score 27; DB 2; Length 13;
Best Local Similarity 50.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      1 DAEPPHY 8
      | : | | |
DB      6 DGIDPKGY 13
```

```
RESULT 95
US-09-394-019C-5
```

```
/ Sequence 5, Application US/09394019C
/ Patent No. 6936687
/ GENERAL INFORMATION:
/ APPLICANT: Oncolimmunin, Inc.
/ APPLICANT: Komoriya, Akira
/ TITLE OF INVENTION: COMPOSITIONS FOR THE DETECTION OF ENZYME ACTIVITY IN BIOLOGICAL
/ FILE REFERENCE: 300-903820US
/ CURRENT APPLICATION NUMBER: US/09/394,019C
/ PRIOR FILING DATE: 1999-09-10
/ PRIOR APPLICATION NUMBER: PCT/US98/00300
/ PRIOR FILING DATE: 1998-02-20
/ PRIOR APPLICATION NUMBER: US 08/802,981
/ PRIOR FILING DATE: 1997-02-20
/ NUMBER OF SEQ ID NOS: 405
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 5
/ LENGTH: 13
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: Synthetic peptide substrate
/ NAME/KEY: MOD_RES
/ LOCATION: (3)..(3)
/ OTHER INFORMATION: X is Alb or Pro
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (3)..(3)
/ OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-09-394-019C-5
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Query Match      28.1%; Score 27; DB 2; Length 13;
Best Local Similarity 50.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
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```
QY      1 DAFEPHGY 8
Db       6 DGIDPKGY 13
```

```
RESULT 96
US-09-394-019C-6
/ Sequence 6, Application US/09394019C
/ Patent No. 6936687
/ GENERAL INFORMATION:
/ APPLICANT: Oncolimmunin, Inc.
/ APPLICANT: Komoriya, Akira
/ TITLE OF INVENTION: COMPOSITIONS FOR THE DETECTION OF ENZYME ACTIVITY IN BIOLOGICAL
/ FILE REFERENCE: 300-903820US
/ CURRENT APPLICATION NUMBER: US/09/394,019C
/ PRIOR FILING DATE: 1999-09-10
/ PRIOR APPLICATION NUMBER: PCT/US98/00300
/ PRIOR FILING DATE: 1998-02-20
/ PRIOR APPLICATION NUMBER: US 08/802,981
/ PRIOR FILING DATE: 1997-02-20
/ NUMBER OF SEQ ID NOS: 405
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 6
/ LENGTH: 13
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: Synthetic peptide substrate
/ NAME/KEY: MOD_RES
/ LOCATION: (4)..(4)
/ OTHER INFORMATION: X is Alb or Pro
/ FEATURE:
/ NAME/KEY: misc_feature
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```
/ LOCATION: (4)..(4)
/ OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-09-394-019C-6
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Query Match      28.1%; Score 27; DB 2; Length 13;
Best Local Similarity 50.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
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```
QY      1 DAFEPHGY 8
Db       6 DGIDPKGY 13
```

```
RESULT 97
US-09-394-019C-9
/ Sequence 9, Application US/09394019C
/ Patent No. 6936687
/ GENERAL INFORMATION:
/ APPLICANT: Oncolimmunin, Inc.
/ APPLICANT: Komoriya, Akira
/ TITLE OF INVENTION: COMPOSITIONS FOR THE DETECTION OF ENZYME ACTIVITY IN BIOLOGICAL
/ FILE REFERENCE: 300-903820US
/ CURRENT APPLICATION NUMBER: US/09/394,019C
/ PRIOR FILING DATE: 1999-09-10
/ PRIOR APPLICATION NUMBER: PCT/US98/00300
/ PRIOR FILING DATE: 1998-02-20
/ PRIOR APPLICATION NUMBER: US 08/802,981
/ PRIOR FILING DATE: 1997-02-20
/ NUMBER OF SEQ ID NOS: 405
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 9
/ LENGTH: 13
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: Synthetic peptide substrate
/ NAME/KEY: MOD_RES
/ LOCATION: (1)..(1)
/ OTHER INFORMATION: BLOCKED with Fmoc
/ FEATURE:
/ NAME/KEY: MOD_RES
/ LOCATION: (3)..(3)
/ OTHER INFORMATION: X is Alb or Pro
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (3)..(3)
/ OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-09-394-019C-9
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```
Query Match      28.1%; Score 27; DB 2; Length 13;
Best Local Similarity 50.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
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```
QY      1 DAFEPHGY 8
Db       6 DGIDPKGY 13
```

```
RESULT 98
US-09-394-019C-15
/ Sequence 15, Application US/09394019C
/ Patent No. 6936687
/ GENERAL INFORMATION:
/ APPLICANT: Oncolimmunin, Inc.
/ APPLICANT: Komoriya, Akira
/ TITLE OF INVENTION: COMPOSITIONS FOR THE DETECTION OF ENZYME ACTIVITY IN BIOLOGICAL
/ FILE REFERENCE: 300-903820US
/ CURRENT APPLICATION NUMBER: US/09/394,019C
```

/ CURRENT FILING DATE: 1999-09-10  
/ PRIOR APPLICATION NUMBER: PCT/US98/00300  
/ PRIOR FILING DATE: 1998-02-20  
/ PRIOR APPLICATION NUMBER: US 08/802,981  
/ PRIOR FILING DATE: 1997-02-20  
/ NUMBER OF SEQ ID NOS: 405  
/ SOFTWARE: PatentIn version 3.2  
/ SEQ ID NO 15  
/ LENGTH: 13  
/ TYPE: PRT  
/ ORGANISM: Artificial  
/ FEATURE:  
/ OTHER INFORMATION: Synthetic peptide substrate  
/ FEATURE:  
/ NAME/KEY: MOD\_RES  
/ LOCATION: (1)..(1)  
/ OTHER INFORMATION: BLOCKED with Fmoc  
US-09-394-019C-15

Query Match 28.1%; Score 27; DB 2; Length 13;  
Best Local Similarity 50.0%; Pred. No. 3.4e+02;  
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DAFEPHG 8  
| : | | |  
Db 6 DGIDPKGY 13

RESULT 99  
US-09-394-019C-178  
/ Sequence 178, Application US/09394019C  
/ Patent No. 6936687  
/ GENERAL INFORMATION:  
/ APPLICANT: Oncoimmunin, Inc.  
/ APPLICANT: Komoriya, Akira  
/ TITLE OF INVENTION: COMPOSITIONS FOR THE DETECTION OF ENZYME ACTIVITY IN BIOLOGICAL  
/ FILE REFERENCE: 300-903820US  
/ CURRENT APPLICATION NUMBER: US/09/394,019C  
/ CURRENT FILING DATE: 1999-09-10  
/ PRIOR APPLICATION NUMBER: PCT/US98/00300  
/ PRIOR FILING DATE: 1998-02-20  
/ PRIOR APPLICATION NUMBER: US 08/802,981  
/ PRIOR FILING DATE: 1997-02-20  
/ NUMBER OF SEQ ID NOS: 405  
/ SOFTWARE: PatentIn version 3.2  
/ SEQ ID NO 178  
/ LENGTH: 13  
/ TYPE: PRT  
/ ORGANISM: Artificial  
/ FEATURE:  
/ OTHER INFORMATION: Synthetic peptide substrate  
/ FEATURE:  
/ NAME/KEY: misc.feature  
/ OTHER INFORMATION: ARTIFICIAL/UNKNOWN = synthetic protease indicator  
/ FEATURE:  
/ NAME/KEY: MOD\_RES  
/ LOCATION: (1)..(1)  
/ OTHER INFORMATION: K is blocked with Fmoc  
/ FEATURE:  
/ NAME/KEY: MOD\_RES  
/ LOCATION: (11)..(11)  
/ OTHER INFORMATION: K is derivatized with fluorophore  
US-09-394-019C-178

Query Match 28.1%; Score 27; DB 2; Length 13;  
Best Local Similarity 50.0%; Pred. No. 3.4e+02;  
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DAFEPHG 8  
| : | | |  
Db 6 DGIDPKGY 13

RESULT 100  
US-09-394-019C-179  
/ Sequence 179, Application US/09394019C  
/ Patent No. 6936687  
/ GENERAL INFORMATION:  
/ APPLICANT: Oncoimmunin, Inc.  
/ APPLICANT: Komoriya, Akira  
/ TITLE OF INVENTION: COMPOSITIONS FOR THE DETECTION OF ENZYME ACTIVITY IN BIOLOGICAL  
/ FILE REFERENCE: 300-903820US  
/ CURRENT APPLICATION NUMBER: US/09/394,019C  
/ CURRENT FILING DATE: 1999-09-10  
/ PRIOR APPLICATION NUMBER: PCT/US98/00300  
/ PRIOR FILING DATE: 1998-02-20  
/ PRIOR APPLICATION NUMBER: US 08/802,981  
/ PRIOR FILING DATE: 1997-02-20  
/ NUMBER OF SEQ ID NOS: 405  
/ SOFTWARE: PatentIn version 3.2  
/ SEQ ID NO 179  
/ LENGTH: 13  
/ TYPE: PRT  
/ ORGANISM: Artificial  
/ FEATURE:  
/ OTHER INFORMATION: Synthetic peptide substrate  
/ FEATURE:  
/ NAME/KEY: misc.feature  
/ OTHER INFORMATION: ARTIFICIAL/UNKNOWN = synthetic protease indicator  
/ FEATURE:  
/ NAME/KEY: MOD\_RES  
/ LOCATION: (1)..(1)  
/ OTHER INFORMATION: K is derivatized with fluorophore  
/ FEATURE:  
/ NAME/KEY: MOD\_RES  
/ LOCATION: (11)..(11)  
/ OTHER INFORMATION: K is derivatized with fluorophore  
US-09-394-019C-179

Query Match 28.1%; Score 27; DB 2; Length 13;  
Best Local Similarity 50.0%; Pred. No. 3.4e+02;  
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DAFEPHG 8  
| : | | |  
Db 6 DGIDPKGY 13

Search completed: January 20, 2006, 19:14:15  
OOD time : 19.8654 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 20, 2006, 19:11:21 ! Search time 64,9038 Seconds  
(without alignments)  
115,878 Million cell updates/sec

Title: US-09-662-293-6

Perfect score: 96

Sequence: 1 DAFPHGYLTLTAVSPGK 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 380452

Minimum DB seq length: 0  
Maximum DB seq length: 20

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Published Applications AA\_Main:  
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2: /cgn2\_6/ptodaca/1/pubpaa/US08\_PUBCOMB.pep:\*  
3: /cgn2\_6/ptodaca/1/pubpaa/US09\_PUBCOMB.pep:\*  
4: /cgn2\_6/ptodaca/1/pubpaa/US10A\_PUBCOMB.pep:\*  
5: /cgn2\_6/ptodaca/1/pubpaa/US10B\_PUBCOMB.pep:\*  
6: /cgn2\_6/ptodaca/1/pubpaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	35.5	37.0	19	4	US-10-603-566-43
3	35.5	37.0	19	5	US-10-893-485-43
4	33	34.4	6	4	US-10-689-088-957
5	33	34.4	6	5	US-10-689-088-957
6	33	34.4	6	5	US-10-689-088-957
7	33	34.4	6	5	US-10-689-088-957
8	33	34.4	6	5	US-10-689-088-957
9	33	34.4	6	5	US-10-689-088-957
10	33	34.4	6	5	US-10-689-088-957
11	33	34.4	6	5	US-10-689-088-957
12	33	34.4	6	5	US-10-689-088-957
13	33	34.4	6	5	US-10-689-088-957
14	33	34.4	6	5	US-10-689-088-957
15	33	34.4	6	5	US-10-689-088-957
16	33	34.4	6	5	US-10-689-088-957
17	33	34.4	6	5	US-10-689-088-957
18	33	34.4	6	5	US-10-689-088-957
19	33	34.4	6	5	US-10-689-088-957
20	33	34.4	6	5	US-10-689-088-957
21	33	34.4	6	5	US-10-689-088-957
22	33	34.4	6	5	US-10-689-088-957
23	33	34.4	6	5	US-10-689-088-957
24	33	34.4	6	5	US-10-689-088-957
25	33	34.4	6	5	US-10-689-088-957
26	33	34.4	6	5	US-10-689-088-957
27	33	34.4	6	5	US-10-689-088-957

28	29	30.2	11	4	US-10-671-134-210	Sequence 210, App
29	29	30.2	11	4	US-10-673-098-210	Sequence 210, App
30	29	30.2	11	4	US-10-673-127-210	Sequence 210, App
31	29	30.2	11	4	US-10-673-127-210	Sequence 210, App
32	29	30.2	11	4	US-10-673-127-210	Sequence 210, App
33	29	30.2	11	4	US-10-673-127-210	Sequence 210, App
34	29	30.2	11	4	US-10-673-127-210	Sequence 210, App
35	29	30.2	11	4	US-10-673-127-210	Sequence 210, App
36	29	30.2	11	4	US-10-673-127-210	Sequence 210, App
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40	29	30.2	11	4	US-10-673-127-210	Sequence 210, App
41	29	30.2	11	4	US-10-673-127-210	Sequence 210, App
42	29	30.2	11	4	US-10-673-127-210	Sequence 210, App
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44	29	30.2	11	4	US-10-673-127-210	Sequence 210, App
45	29	30.2	11	4	US-10-673-127-210	Sequence 210, App
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51	29	30.2	11	4	US-10-673-127-210	Sequence 210, App
52	29	30.2	11	4	US-10-673-127-210	Sequence 210, App
53	29	30.2	11	4	US-10-673-127-210	Sequence 210, App
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59	29	30.2	11	4	US-10-673-127-210	Sequence 210, App
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64	29	30.2	11	4	US-10-673-127-210	Sequence 210, App
65	29	30.2	11	4	US-10-673-127-210	Sequence 210, App
66	29	30.2	11	4	US-10-673-127-210	Sequence 210, App
67	29	30.2	11	4	US-10-673-127-210	Sequence 210, App
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81	29	30.2	11	4	US-10-673-127-210	Sequence 210, App
82	29	30.2	11	4	US-10-673-127-210	Sequence 210, App
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85	29	30.2	11	4	US-10-673-127-210	Sequence 210, App
86	29	30.2	11	4	US-10-673-127-210	Sequence 210, App
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90	29	30.2	11	4	US-10-673-127-210	Sequence 210, App
91	29	30.2	11	4	US-10-673-127-210	Sequence 210, App
92	29	30.2	11	4	US-10-673-127-210	Sequence 210, App
93	29	30.2	11	4	US-10-673-127-210	Sequence 210, App
94	29	30.2	11	4	US-10-673-127-210	Sequence 210, App
95	29	30.2	11	4	US-10-673-127-210	Sequence 210, App
96	29	30.2	11	4	US-10-673-127-210	Sequence 210, App
97	29	30.2	11	4	US-10-673-127-210	Sequence 210, App
98	29	30.2	11	4	US-10-673-127-210	Sequence 210, App
99	29	30.2	11	4	US-10-673-127-210	Sequence 210, App
100	29	30.2	11	4	US-10-673-127-210	Sequence 210, App

## ALIGNMENTS

RESULT 1  
US-10-218-743-6

```
; Sequence 6, Application US/10218743
; Publication No. US20030096779A1
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine A.
; APPLICANT: Hunter, Shirley Wu
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: AL-2-C3
; CURRENT APPLICATION NUMBER: US/10/218,743
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: US/09/292,225
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: 60/098,909
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/085,295
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/098,565
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: 09/062,013
; PRIOR FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Dermatophagoides farinae
US-10-218-743-6
```

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Query Match          100.0%; Score 96; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.2e+08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 DAEPPHYLTAAVSPGK 18
        |||||
Db       1 DAEPPHYLTAAVSPGK 18
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RESULT 2  
US-10-603-566-43

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; Sequence 43, Application US/10603566
; Publication No. US20040086966A1
; GENERAL INFORMATION:
; APPLICANT: Wiltamer, Valerie
; APPLICANT: Communi, David
; APPLICANT: Vandenbergaeerde, Ann
; APPLICANT: Detheux, Michel
; APPLICANT: Parentier, Marc
; TITLE OF INVENTION: Compositions and Methods Comprising a Ligand of Chemerin
; FILE REFERENCE: 9409/22212
; CURRENT APPLICATION NUMBER: US/10/603,566
; CURRENT FILING DATE: 2003-06-25
; PRIOR APPLICATION NUMBER: US 60/303,858
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US 09/905,253
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 10/201,187
; PRIOR FILING DATE: 2001-07-23
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 43
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-603-566-43
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```
Query Match          37.0%; Score 35.5; DB 4; Length 19;
Best Local Similarity 46.7%; Pred. No. 1.2e+02;
Matches 7; Conservative 2; Mismatches 1; Indels 5; Gaps 1;
```

```
QY      4 EPHGYLTAAVSPGK 18
        :|||
Db       6 DPHGYFL-----PGQ 15
```

RESULT 3  
US-10-893-485-43

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; Sequence 43, Application US/10893485
; Publication No. US20050155090A1
; GENERAL INFORMATION:
; APPLICANT: Wiltamer, Valerie
; APPLICANT: Communi, David
; APPLICANT: Vandenbergaeerde, Ann
; APPLICANT: Detheux, Michel
; APPLICANT: Parentier, Marc
; TITLE OF INVENTION: Compositions and Methods Comprising a Ligand of Chemerin
; FILE REFERENCE: 9409/2045C
; CURRENT APPLICATION NUMBER: US/10/893,485
; CURRENT FILING DATE: 2004-07-16
; PRIOR APPLICATION NUMBER: US 60/303,858
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US10/603,566
; PRIOR FILING DATE: 2003-06-25
; PRIOR APPLICATION NUMBER: US 09/905,253
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 10/201,187
; PRIOR FILING DATE: 2001-07-23
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 43
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-893-485-43
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Query Match          37.0%; Score 35.5; DB 5; Length 19;
Best Local Similarity 46.7%; Pred. No. 1.2e+02;
Matches 7; Conservative 2; Mismatches 1; Indels 5; Gaps 1;
```

```
QY      4 EPHGYLTAAVSPGK 18
        :|||
Db       6 DPHGYFL-----PGQ 15
```

RESULT 4  
US-10-699-088-957

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; Sequence 957, Application US/10699088
; Publication No. US20040209282A1
; GENERAL INFORMATION:
; APPLICANT: Dana Ault-Riche
; APPLICANT: Bruce Atkinson
; TITLE OF INVENTION: METHODS FOR PRODUCING POLYPEPTIDE-TAGGED COLLECTIONS AND CAPTURE
; TITLE OF INVENTION: SYSTEMS CONTAINING THE TAGGED POLYPEPTIDES
; FILE REFERENCE: 25865-1754
; CURRENT APPLICATION NUMBER: US/10/699,088
; CURRENT FILING DATE: 2003-10-30
; PRIOR APPLICATION NUMBER: 60/422,923
; PRIOR FILING DATE: 2002-10-30
; PRIOR APPLICATION NUMBER: 60/423,018
; PRIOR FILING DATE: 2002-10-30
; NUMBER OF SEQ ID NOS: 1094
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 957
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-10-699-088-957
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Query Match 34.4%; Score 33; DB 4; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EPHGY 8  
|||||  
Db 1 EPHGY 5

RESULT 5  
US-10-699-113-46  
; Sequence 46, Application US/10699113  
; Publication No. US20040241748A1  
; GENERAL INFORMATION:  
; APPLICANT: Ault-Riche, Dana  
; APPLICANT: Kumble, Krishnanand  
; APPLICANT: Schultz, Rainer  
; APPLICANT: Schultz, Kenneth  
; TITLE OF INVENTION: Self-Assembling Arrays and Uses Thereof  
; FILE REFERENCE: 25885-1755  
; CURRENT APPLICATION NUMBER: US/10/699,113  
; PRIOR FILING DATE: 2003-10-30  
; PRIOR APPLICATION NUMBER: 60/446,687  
; PRIOR FILING DATE: 2003-02-10  
; NUMBER OF SEQ ID NOS: 948  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 46  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; OTHER INFORMATION: synthetic peptide  
US-10-699-113-46

Query Match 34.4%; Score 33; DB 5; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EPHGY 8  
|||||  
Db 1 EPHGY 5

RESULT 6  
US-10-699-114-957  
; Sequence 957, Application US/10699114  
; Publication No. US20050042623A1  
; GENERAL INFORMATION:  
; APPLICANT: Dana Ault-Riche  
; APPLICANT: Bruce Atkinson  
; APPLICANT: Krishnanand Kumble  
; APPLICANT: Lynne Jersaltis  
; APPLICANT: Glazette Sperinde  
; TITLE OF INVENTION: SYSTEMS FOR CAPTURE AND ANALYSIS OF BIOLOGICAL PARTICLES AND METH  
; FILE OF INVENTION: USING THE SYSTEMS  
; FILE REFERENCE: 25885-1759  
; CURRENT APPLICATION NUMBER: US/10/699,114  
; PRIOR FILING DATE: 2003-10-30  
; PRIOR APPLICATION NUMBER: 60/423,018  
; PRIOR FILING DATE: 2002-10-30  
; PRIOR APPLICATION NUMBER: 60/422,923  
; PRIOR FILING DATE: 2002-10-30  
; NUMBER OF SEQ ID NOS: 1094  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 957  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic peptide  
US-10-699-114-957

Query Match 34.4%; Score 33; DB 5; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EPHGY 8  
|||||  
Db 1 EPHGY 5

RESULT 7  
US-10-806-924-9  
; Sequence 9, Application US/10806924  
; Publication No. US20050095648A1  
; GENERAL INFORMATION:  
; APPLICANT: Geyesen, H. Mario  
; APPLICANT: Ault-Riche, Dana  
; TITLE OF INVENTION: Method for designing linear epitopes and algorithm therefor  
; TITLE OF INVENTION: Method for designing linear epitopes and algorithm therefor  
; FILE REFERENCE: 25885-1760  
; CURRENT APPLICATION NUMBER: US/10/806,924  
; CURRENT FILING DATE: 2004-03-22  
; NUMBER OF SEQ ID NOS: 911  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 9  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic peptide  
US-10-806-924-9

Query Match 34.4%; Score 33; DB 5; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EPHGY 8  
|||||  
Db 1 EPHGY 5

RESULT 8  
US-09-932-161-8  
; Sequence 8, Application US/09932161  
; Patent No. US20020037533A1  
; GENERAL INFORMATION:  
; APPLICANT: Clivell, Olivier  
; APPLICANT: Ian, Steven  
; TITLE OF INVENTION: Screening and Therapeutic Methods For  
; TITLE OF INVENTION: Promoting Wakefulness and Sleep  
; FILE REFERENCE: P-UC 4679  
; CURRENT APPLICATION NUMBER: US/09/932,161  
; CURRENT FILING DATE: 2001-08-17  
; PRIOR APPLICATION NUMBER: US 09/560,915  
; PRIOR FILING DATE: 2000-04-28  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 8  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: human GPR10 variant  
US-09-932-161-8

Query Match 34.4%; Score 33; DB 3; Length 12;  
Best Local Similarity 60.0%; Pred. No. 1.9e+02;  
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 PHGYLTAAY 14  
|||:|:|  
Db 1 PHGQNNYASY 10

```
RESULT 9
US-10-096-777-8
; Sequence 8, Application US/10096777
; Publication No. US2003017270A1
; GENERAL INFORMATION:
; APPLICANT: Clivell, Olivier
; APPLICANT: Lin, Steven
; TITLE OF INVENTION: Therapeutic Compositions and Methods
; FILE REFERENCE: P-UC 3534
; CURRENT APPLICATION NUMBER: US/10/096,777
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: US/09/560,915
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: human GPR10 variant
US-10-096-777-8

Query Match          34.4%; Score 33; DB 4; Length 12;
Best Local Similarity 60.0%; Pred. No. 1.9e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 PHGYLTTAAV 14
DB 1 PHGQNMVTAV 10

RESULT 10
US-09-932-161-9
; Sequence 9, Application US/09932161
; Patent No. US20020037533A1
; GENERAL INFORMATION:
; APPLICANT: Clivell, Olivier
; APPLICANT: Lin, Steven
; TITLE OF INVENTION: Screening and Therapeutic Methods For
; FILE REFERENCE: P-UC 4679
; CURRENT APPLICATION NUMBER: US/09/932,161
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: US 09/560,915
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: human GPR10 variant
US-09-932-161-9

Query Match          33.3%; Score 32; DB 3; Length 12;
Best Local Similarity 60.0%; Pred. No. 2.7e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 5 PHGYLTTAAV 14
DB 1 PHGQNMVTAV 10

RESULT 11
US-10-096-777-9
; Sequence 9, Application US/10096777
; Publication No. US2003017270A1
; GENERAL INFORMATION:
; APPLICANT: Clivell, Olivier
; APPLICANT: Lin, Steven
```

```
; TITLE OF INVENTION: Therapeutic Compositions and Methods
; FILE REFERENCE: P-UC 3534
; CURRENT APPLICATION NUMBER: US/10/096,777
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: US/09/560,915
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: human GPR10 variant
US-10-096-777-9

Query Match          33.3%; Score 32; DB 4; Length 12;
Best Local Similarity 60.0%; Pred. No. 2.7e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 5 PHGYLTTAAV 14
DB 1 PHGQNMVTAV 10

RESULT 12
US-09-870-089B-13
; Sequence 13, Application US/09870089B
; Publication No. US20030175252A1
; GENERAL INFORMATION:
; APPLICANT: Charles A. Nicolette
; TITLE OF INVENTION: THERAPEUTIC COMPOUNDS FOR OVARIAN CANCER
; FILE REFERENCE: 68126881209900
; CURRENT APPLICATION NUMBER: US/09/870,089B
; CURRENT FILING DATE: 2001-05-30
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: ATP4/CREB-2
US-09-870-089B-13

Query Match          32.3%; Score 31; DB 3; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.7e+06;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 FEPHGV 8
DB 3 FEPHGF 8

RESULT 13
US-10-813-859-13
; Sequence 13, Application US/10813859
; Publication No. US20050048068A1
; GENERAL INFORMATION:
; APPLICANT: Genzyme Corporation
; APPLICANT: Charles, Nicolette A.
; TITLE OF INVENTION: THERAPEUTIC COMPOUNDS FOR OVARIAN CANCER
; FILE REFERENCE: 5032US-DIV
; CURRENT APPLICATION NUMBER: US/10/813,859
; CURRENT FILING DATE: 2004-03-31
; PRIOR APPLICATION NUMBER: US 09/870,089
; PRIOR FILING DATE: 2001-05-31
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 13
; LENGTH: 9
; TYPE: PRT
```

/ ORGANISM: Homo sapiens  
US-10-813-859-13

Query Match 32.3%; Score 31; DB 5; Length 9;  
Best Local Similarity 66.7%; Pred. No. 1.7e+06;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 FEBPHY 8  
|:|:|:  
DB 3 FKPHGF 8

RESULT 14  
US-10-661-156-133

/ Sequence 133, Application US/10661156  
/ Publication No. US20050100963A1

/ GENERAL INFORMATION:

/ APPLICANT: Sato, Aaron K.

/ APPLICANT: Sexton, Daniel J.

/ APPLICANT: Dransfield, Daniel T.

/ APPLICANT: Ladner, Robert C.

/ APPLICANT: Arbogast, Christophe

/ APPLICANT: Bussat, Philippe

/ APPLICANT: Fan, Hong

/ APPLICANT: Khurana, Sudha

/ APPLICANT: Linder, Karen B.

/ APPLICANT: Marinelli, Edmund R.

/ APPLICANT: Nanjappan, Palaniappa

/ APPLICANT: Nunn, Adrian

/ APPLICANT: Pillai, Radhakrishna

/ APPLICANT: Pochon, Sibylle

/ APPLICANT: Ramalingam, Kondareddiar

/ APPLICANT: Shrivastava, Ajay

/ APPLICANT: Song, Bo

/ APPLICANT: Swenson, Rolf E.

/ APPLICANT: Von Wronski, Matthew A.

/ TITLE OF INVENTION: KDR and VEGF/KDR Binding Peptides and  
/ FILE REFERENCE: D0617.70012US00

/ CURRENT APPLICATION NUMBER: US/10/661,156

/ CURRENT FILING DATE: 2003-09-11

/ PRIOR APPLICATION NUMBER: US 10/382,082

/ PRIOR FILING DATE: 2003-03-03

/ PRIOR APPLICATION NUMBER: PCT/US03/06731

/ PRIOR FILING DATE: 2003-03-03

/ PRIOR APPLICATION NUMBER: US 60/440,411

/ PRIOR FILING DATE: 2003-01-15

/ PRIOR APPLICATION NUMBER: US 60/360,851

/ PRIOR FILING DATE: 2002-03-01

/ NUMBER OF SEQ ID NOS: 617

/ SOFTWARE: FASTSEQ for Windows Version 4.0

/ SEQ ID NO 133

/ LENGTH: 18

/ TYPE: PRT

/ ORGANISM: Artificial Sequence

/ FEATURE:

/ OTHER INFORMATION: Library Isolate

US-10-661-156-133

Query Match 32.3%; Score 31; DB 5; Length 18;  
Best Local Similarity 55.6%; Pred. No. 6.3e+02;  
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 FEBPHYLT 11  
|:|:|:|:  
DB 6 YEDHTYMLT 14

RESULT 15  
US-09-839-884-63

/ Sequence 63, Application US/09839884

/ Patent No. US20020076739A1

/ GENERAL INFORMATION:

/ APPLICANT: Aebersold, Rudolf H.

/ APPLICANT: Gelb, Michael H

/ APPLICANT: Gygli, Steven

/ APPLICANT: Scott, C R

/ APPLICANT: Turecek, Frantisek

/ APPLICANT: Gerber, Scott A

/ APPLICANT: Rist, Beate

/ TITLE OF INVENTION: Rapid Quantitative Analysis of Proteins or Protein

/ FUNCTION: Function in Complex Mixture

/ FILE REFERENCE: 64-98A

/ CURRENT APPLICATION NUMBER: US/09/839,884

/ CURRENT FILING DATE: 2001-04-20

/ PRIOR APPLICATION NUMBER: 09/383,062

/ PRIOR FILING DATE: 1999-08-25

/ PRIOR APPLICATION NUMBER: 60/097,788

/ PRIOR FILING DATE: 1998-08-25

/ NUMBER OF SEQ ID NOS: 64

/ SOFTWARE: PatentIn Ver. 2.0

/ SEQ ID NO 63

/ LENGTH: 19

/ TYPE: PRT

/ ORGANISM: Unknown

/ FEATURE:

/ OTHER INFORMATION: Description of Unknown Organism: Unidentified

US-09-839-884-63  
Query Match 32.3%; Score 31; DB 3; Length 19;  
Best Local Similarity 54.5%; Pred. No. 6.7e+02;  
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 DAFBPHYLT 11  
|:|:|:|:  
DB 7 DABGPHGFVT 17

RESULT 16  
US-09-839-884-63

/ Sequence 63, Application US/09839884

/ Publication No. US2003008732A9

/ GENERAL INFORMATION:

/ APPLICANT: Aebersold, Rudolf H.

/ APPLICANT: Gelb, Michael H

/ APPLICANT: Gygli, Steven

/ APPLICANT: Scott, C R

/ APPLICANT: Turecek, Frantisek

/ APPLICANT: Gerber, Scott A

/ APPLICANT: Rist, Beate

/ TITLE OF INVENTION: Rapid Quantitative Analysis of Proteins or Protein

/ FUNCTION: Function in Complex Mixture

/ FILE REFERENCE: 64-98A

/ CURRENT APPLICATION NUMBER: US/09/839,884

/ CURRENT FILING DATE: 2001-04-20

/ PRIOR APPLICATION NUMBER: 09/383,062

/ PRIOR FILING DATE: 1999-08-25

/ PRIOR APPLICATION NUMBER: 60/097,788

/ PRIOR FILING DATE: 1998-08-25

/ NUMBER OF SEQ ID NOS: 64

/ SOFTWARE: PatentIn Ver. 2.0

/ SEQ ID NO 63

/ LENGTH: 19

/ TYPE: PRT

/ ORGANISM: Unknown

/ FEATURE:

/ OTHER INFORMATION: Description of Unknown Organism: Unidentified

US-09-839-884-63  
Query Match 32.3%; Score 31; DB 3; Length 19;  
Best Local Similarity 54.5%; Pred. No. 6.7e+02;  
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 DAFBPHYLT 11  
|:|:|:|:  
DB 7 DABGPHGFVT 17

RESULT 17  
US-10-994-815-63  
Sequence 63, Application US/10994815  
Publication No. US20050233399A1  
GENERAL INFORMATION:  
APPLICANT: Aebbersold, Rudolf H.  
APPLICANT: Galb, Michael H  
APPLICANT: Gysel, Steven  
APPLICANT: Scott, C R  
APPLICANT: Turecek, Frantisek  
APPLICANT: Gerber, Scott A  
APPLICANT: Rist, Beate  
TITLE OF INVENTION: Rapid Quantitative Analysis of Proteins or Protein  
TITLE OF INVENTION: Function in Complex Mixture  
FILE REFERENCE: 64-98A  
CURRENT APPLICATION NUMBER: US/10/994,815  
CURRENT FILING DATE: 2004-11-23  
PRIOR APPLICATION NUMBER: US/09/839,884  
PRIOR FILING DATE: 2001-04-20  
PRIOR APPLICATION NUMBER: 09/383,062  
PRIOR FILING DATE: 1999-08-25  
PRIOR APPLICATION NUMBER: 60/097,788  
PRIOR FILING DATE: 1998-08-25  
NUMBER OF SEQ ID NOS: 64  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 63  
LENGTH: 19  
TYPE: PRT  
ORGANISM: Unknown  
FEATURE:  
OTHER INFORMATION: Description of Unknown Organism: Unidentified  
US-10-994-815-63

Query Match 32.3%; Score 31; DB 5; Length 19;  
Best Local Similarity 54.5%; Pred. No. 6.7e+02;  
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 DAEPHGYLIT 11  
DB 7 DAEPHGYLIT 17

RESULT 18  
US-10-235-483-66  
Sequence 66, Application US/10235483  
Publication No. US20030087407A1  
GENERAL INFORMATION:  
APPLICANT: SOTO-JARA, Claudio  
BAUMANN, Marc  
FRANIGONE, Blas  
TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL  
COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES  
ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE  
DEPOSITS  
NUMBER OF SEQUENCES: 69  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROWDY AND NEIMARK  
STREET: 419 Seventh Street, N.W., Suite 400  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/235,483  
FILING DATE: 06-Sep-2002  
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/766,596  
FILING DATE: <Unknown>  
APPLICATION NUMBER: US 08/630,645  
FILING DATE: 10-APR-1996  
APPLICATION NUMBER: US 08/478,326  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: YUN, Allen C.  
REGISTRATION NUMBER: 37,971  
REFERENCE/DOCKET NUMBER: SOTO-JARA-1A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
INFORMATION FOR SEQ ID NO: 66:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 66:  
US-10-235-483-66

Query Match 31.2%; Score 30; DB 4; Length 11;  
Best Local Similarity 63.6%; Pred. No. 5.3e+02;  
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 7 GYLTVAAVPRG 17  
DB 1 GYLTVAAVPRG 11

RESULT 19  
US-09-932-161-11  
Sequence 11, Application US/09932161  
Patent No. US20020037533A1  
GENERAL INFORMATION:  
APPLICANT: Civeilli, Olivier  
APPLICANT: Lin, Steven  
TITLE OF INVENTION: Screening and Therapeutic Methods For  
FILE REFERENCE: P-UC 4679  
CURRENT APPLICATION NUMBER: US/09/932,161  
CURRENT FILING DATE: 2001-08-17  
PRIOR APPLICATION NUMBER: US 09/560,915  
PRIOR FILING DATE: 2000-04-28  
NUMBER OF SEQ ID NOS: 24  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 11  
LENGTH: 12  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: human GPR10 variant  
US-09-932-161-11

Query Match 31.2%; Score 30; DB 3; Length 12;  
Best Local Similarity 45.5%; Pred. No. 5.9e+02;  
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 5 PHGYLTTAAYS 15  
DB 1 PHGYLTTAAYS 11

RESULT 20  
US-10-096-777-11  
Sequence 11, Application US/10096777  
Publication No. US20030171270A1  
GENERAL INFORMATION:  
APPLICANT: Civeilli, Olivier  
APPLICANT: Lin, Steven

```
/ TITLE OF INVENTION: Therapeutic Compositions and Methods
/ TITLE OF INVENTION: Relating to Protectin Releasing Peptide (Prnp)
/ FILE REFERENCE: P-UC 3534
/ CURRENT APPLICATION NUMBER: US/10/096,777
/ PRIOR FILING DATE: 2002-03-12
/ PRIOR APPLICATION NUMBER: US/09/560,915
/ PRIOR FILING DATE: 2000-04-28
/ NUMBER OF SEQ ID NOS: 24
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 11
/ LENGTH: 12
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: human GPR10 variant
US-10-096-777-11

Query Match          31.2%; Score 30; DB 4; Length 12;
Best Local Similarity 45.5%; Pred. No. 5.9e+02;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 5 PHGYLTVAVS 15
   ||| : |||
   1 PHGQNTVSYVA 11

Db

RESULT 21
US-10-699-088-758
/ Sequence 758, Application US/10699088
/ Publication No. US20040209282A1
/ GENERAL INFORMATION:
/ APPLICANT: Dana Ault-Riche
/ APPLICANT: Bruce Atkinson
/ TITLE OF INVENTION: METHODS FOR PRODUCING POLYPEPTIDE-TAGGED COLLECTIONS AND CAPTURE
/ FILE REFERENCE: 25885-1754
/ CURRENT APPLICATION NUMBER: US/10/699,088
/ CURRENT FILING DATE: 2003-10-30
/ PRIOR APPLICATION NUMBER: 60/422,923
/ PRIOR FILING DATE: 2002-10-30
/ PRIOR APPLICATION NUMBER: 60/423,018
/ PRIOR FILING DATE: 2002-10-30
/ NUMBER OF SEQ ID NOS: 1094
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 758
/ LENGTH: 6
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: synthetic peptide
US-10-699-088-758

Query Match          30.2%; Score 29; DB 4; Length 6;
Best Local Similarity 80.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 EPHGY 8
   : ||||
   1 KPHGY 5

Db

RESULT 22
US-10-699-113-758
/ Sequence 758, Application US/10699113
/ Publication No. US20040241748A1
/ GENERAL INFORMATION:
/ APPLICANT: Ault-Riche, Dana
/ APPLICANT: Kumbale, Krishnamand
/ APPLICANT: Schultz, Rainer
/ APPLICANT: Schultz, Kenneth
/ TITLE OF INVENTION: Self-Assembling Arrays and Uses Thereof
/ FILE REFERENCE: 25885-1755
/ CURRENT APPLICATION NUMBER: US/10/699,113
```

```
/ CURRENT FILING DATE: 2003-10-30
/ PRIOR APPLICATION NUMBER: 60/446,687
/ PRIOR FILING DATE: 2003-02-10
/ NUMBER OF SEQ ID NOS: 948
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 758
/ LENGTH: 6
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: synthetic peptide
US-10-699-113-758

Query Match          30.2%; Score 29; DB 5; Length 6;
Best Local Similarity 80.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 EPHGY 8
   : ||||
   1 KPHGY 5

Db

RESULT 23
US-10-699-114-758
/ Sequence 758, Application US/10699114
/ Publication No. US20050042623A1
/ GENERAL INFORMATION:
/ APPLICANT: Dana Ault-Riche
/ APPLICANT: Bruce Atkinson
/ APPLICANT: Krishnamand Kumbale
/ APPLICANT: Lynne Jersaltis
/ APPLICANT: Gizette Sperinde
/ TITLE OF INVENTION: SYSTEMS FOR CAPTURE AND ANALYSIS OF BIOLOGICAL PARTICLES AND MET
/ FILE REFERENCE: 25885-1759
/ CURRENT APPLICATION NUMBER: US/10/699,114
/ CURRENT FILING DATE: 2003-10-30
/ PRIOR APPLICATION NUMBER: 60/423,018
/ PRIOR FILING DATE: 2002-10-30
/ PRIOR APPLICATION NUMBER: 60/422,923
/ PRIOR FILING DATE: 2002-10-30
/ NUMBER OF SEQ ID NOS: 1094
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 758
/ LENGTH: 6
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: synthetic peptide
US-10-699-114-758

Query Match          30.2%; Score 29; DB 5; Length 6;
Best Local Similarity 80.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 EPHGY 8
   : ||||
   1 KPHGY 5

Db

RESULT 24
US-10-806-924-721
/ Sequence 721, Application US/10806924
/ Publication No. US20050095648A1
/ GENERAL INFORMATION:
/ APPLICANT: Geysen, H. Mario
/ APPLICANT: Ault-Riche, Dana
/ TITLE OF INVENTION: Method for designing linear epitopes and algorithm therefor
/ FILE REFERENCE: 25885-1760
/ CURRENT APPLICATION NUMBER: US/10/806,924
/ CURRENT FILING DATE: 2004-03-22
/ NUMBER OF SEQ ID NOS: 911
```

```
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 721
/ LENGTH: 6
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: synthetic peptide
US-10-806-924-721

Query Match      30.2%; Score 29; DB 5; Length 6;
Best Local Similarity 80.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      4 BPHGY 8
        :||||
Db      1 KPHGY 5

RESULT 25
US-10-671-403-210
/ Sequence 210, Application US/10671403
/ Publication No. US20040038289A1
/ GENERAL INFORMATION:
/ APPLICANT: O'Donnell, Michael E.
/ APPLICANT: Yuzhakov, Alexander
/ APPLICANT: Yurleva, Olga
/ APPLICANT: Jeruzalmi, David
/ APPLICANT: Bruck, Irina
/ APPLICANT: Kurlyan, John
/ TITLE OF INVENTION: ENZYMES DERIVED FROM THERMOPHILIC ORGANISMS THAT
/ TITLE OF INVENTION: FUNCTION AS A CHROMOSOMAL REPLICASE, PREPARATION AND
/ TITLE OF INVENTION: USE THEREOF
/ FILE REFERENCE: 22221/1030
/ CURRENT APPLICATION NUMBER: US/10/671,403
/ CURRENT FILING DATE: 2003-09-25
/ PRIOR APPLICATION NUMBER: US/09/716,964A
/ PRIOR FILING DATE: 2000-11-21
/ PRIOR APPLICATION NUMBER: 60/143,202
/ PRIOR FILING DATE: 1997-04-08
/ PRIOR APPLICATION NUMBER: 08/823,407
/ PRIOR FILING DATE: 1997-04-08
/ PRIOR APPLICATION NUMBER: 09/057,416
/ PRIOR FILING DATE: 1998-04-08
/ NUMBER OF SEQ ID NOS: 212
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 210
/ LENGTH: 11
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: polypeptide
US-10-671-403-210

Query Match      30.2%; Score 29; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 HGYYL 10
        :||||
Db      7 HGYYL 11

RESULT 26
US-10-671-419-210
/ Sequence 210, Application US/10671419
/ Publication No. US20040038290A1
/ GENERAL INFORMATION:
/ APPLICANT: O'Donnell, Michael E.
/ APPLICANT: Yuzhakov, Alexander
/ APPLICANT: Yurleva, Olga
/ APPLICANT: Jeruzalmi, David
/ APPLICANT: Bruck, Irina
/ APPLICANT: Kurlyan, John
```

```
/ TITLE OF INVENTION: ENZYMES DERIVED FROM THERMOPHILIC ORGANISMS THAT
/ TITLE OF INVENTION: FUNCTION AS A CHROMOSOMAL REPLICASE, PREPARATION AND
/ TITLE OF INVENTION: USE THEREOF
/ FILE REFERENCE: 22221/1030
/ CURRENT APPLICATION NUMBER: US/10/671,419
/ CURRENT FILING DATE: 2003-09-25
/ PRIOR APPLICATION NUMBER: US/09/716,964A
/ PRIOR FILING DATE: 2000-11-21
/ PRIOR APPLICATION NUMBER: 60/143,202
/ PRIOR FILING DATE: 1997-04-08
/ PRIOR APPLICATION NUMBER: 08/823,407
/ PRIOR FILING DATE: 1997-04-08
/ PRIOR APPLICATION NUMBER: 09/057,416
/ PRIOR FILING DATE: 1998-04-08
/ NUMBER OF SEQ ID NOS: 212
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 210
/ LENGTH: 11
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: polypeptide
US-10-670-844-210

Query Match      30.2%; Score 29; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 HGYYL 10
        :||||
Db      7 HGYYL 11

RESULT 27
US-10-670-844-210
/ Sequence 210, Application US/10670844
/ Publication No. US20040043414A1
/ GENERAL INFORMATION:
/ APPLICANT: O'Donnell, Michael E.
/ APPLICANT: Yuzhakov, Alexander
/ APPLICANT: Yurleva, Olga
/ APPLICANT: Jeruzalmi, David
/ APPLICANT: Bruck, Irina
/ APPLICANT: Kurlyan, John
/ TITLE OF INVENTION: ENZYMES DERIVED FROM THERMOPHILIC ORGANISMS THAT
/ TITLE OF INVENTION: FUNCTION AS A CHROMOSOMAL REPLICASE, PREPARATION AND
/ TITLE OF INVENTION: USE THEREOF
/ FILE REFERENCE: 22221/1030
/ CURRENT APPLICATION NUMBER: US/10/670,844
/ CURRENT FILING DATE: 2003-09-25
/ PRIOR APPLICATION NUMBER: US/09/716,964A
/ PRIOR FILING DATE: 2000-11-21
/ PRIOR APPLICATION NUMBER: 60/143,202
/ PRIOR FILING DATE: 1997-04-08
/ PRIOR APPLICATION NUMBER: 08/823,407
/ PRIOR FILING DATE: 1997-04-08
/ PRIOR APPLICATION NUMBER: 09/057,416
/ PRIOR FILING DATE: 1998-04-08
/ NUMBER OF SEQ ID NOS: 212
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 210
/ LENGTH: 11
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: polypeptide
US-10-670-844-210

Query Match      30.2%; Score 29; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 HGYYL 10
```





```
/ APPLICANT: Kuriyan, John
/ TITLE OF INVENTION: ENZYMES DERIVED FROM THERMOPHILIC ORGANISMS THAT
/ TITLE OF INVENTION: FUNCTION AS A CHROMOSOMAL REPLICASE, PREPARATION AND
/ TITLE OF INVENTION: USE THEREOF
/ FILE REFERENCE: 22221/1030
/ CURRENT APPLICATION NUMBER: US/10/673,127
/ CURRENT FILING DATE: 2003-09-26
/ PRIOR APPLICATION NUMBER: US/09/716,964A
/ PRIOR FILING DATE: 2000-11-21
/ PRIOR APPLICATION NUMBER: 60/143,202
/ PRIOR FILING DATE: 1997-04-08
/ PRIOR APPLICATION NUMBER: 08/823,407
/ PRIOR FILING DATE: 1997-04-08
/ PRIOR APPLICATION NUMBER: 09/057,416
/ PRIOR FILING DATE: 1998-04-08
/ NUMBER OF SEQ ID NOS: 212
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 210
/ LENGTH: 11
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: polypeptide
US-10-673-127-210
```

```
Query Match          30.2%; Score 29; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6 HGYL 10
       |||||
Db      7 HGYL 11
```

```
RESULT 32
/ Sequence 210, Application US/10670817
/ Publication No. US20040106137A1
/ GENERAL INFORMATION:
/ APPLICANT: O'Donnell, Michael E.
/ APPLICANT: Yuzhakov, Alexander
/ APPLICANT: Yurleva, Olga
/ APPLICANT: Jeruzalmi, David
/ APPLICANT: Bruck, Irina
/ APPLICANT: Kuriyan, John
/ TITLE OF INVENTION: ENZYMES DERIVED FROM THERMOPHILIC ORGANISMS THAT
/ TITLE OF INVENTION: FUNCTION AS A CHROMOSOMAL REPLICASE, PREPARATION AND
/ TITLE OF INVENTION: USE THEREOF
/ FILE REFERENCE: 22221/1030
/ CURRENT APPLICATION NUMBER: US/10/670,817
/ CURRENT FILING DATE: 2003-09-25
/ PRIOR APPLICATION NUMBER: US/09/716,964
/ PRIOR FILING DATE: 2000-11-21
/ PRIOR APPLICATION NUMBER: 60/143,202
/ PRIOR FILING DATE: 1997-04-08
/ PRIOR APPLICATION NUMBER: 08/823,407
/ PRIOR FILING DATE: 1997-04-08
/ PRIOR APPLICATION NUMBER: 09/057,416
/ PRIOR FILING DATE: 1998-04-08
/ NUMBER OF SEQ ID NOS: 212
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 210
/ LENGTH: 11
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: polypeptide
US-10-670-817-210
```

```
Query Match          30.2%; Score 29; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      6 HGYL 10
       |||||
Db      7 HGYL 11
```

```
RESULT 33
/ Sequence 210, Application US/10673119
/ Publication No. US20040110210A1
/ GENERAL INFORMATION:
/ APPLICANT: O'Donnell, Michael E.
/ APPLICANT: Yuzhakov, Alexander
/ APPLICANT: Yurleva, Olga
/ APPLICANT: Jeruzalmi, David
/ APPLICANT: Bruck, Irina
/ APPLICANT: Kuriyan, John
/ TITLE OF INVENTION: ENZYMES DERIVED FROM THERMOPHILIC ORGANISMS THAT
/ TITLE OF INVENTION: FUNCTION AS A CHROMOSOMAL REPLICASE, PREPARATION AND
/ TITLE OF INVENTION: USE THEREOF
/ FILE REFERENCE: 22221/1030
/ CURRENT APPLICATION NUMBER: US/10/673,119
/ CURRENT FILING DATE: 2003-09-26
/ PRIOR APPLICATION NUMBER: US/09/716,964A
/ PRIOR FILING DATE: 2000-11-21
/ PRIOR APPLICATION NUMBER: 60/143,202
/ PRIOR FILING DATE: 1997-04-08
/ PRIOR APPLICATION NUMBER: 08/823,407
/ PRIOR FILING DATE: 1997-04-08
/ PRIOR APPLICATION NUMBER: 09/057,416
/ PRIOR FILING DATE: 1998-04-08
/ NUMBER OF SEQ ID NOS: 212
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 210
/ LENGTH: 11
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: polypeptide
US-10-673-119-210
```

```
Query Match          30.2%; Score 29; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      6 HGYL 10
       |||||
Db      7 HGYL 11
```

```
RESULT 34
/ Sequence 210, Application US/10671207
/ Publication No. US2004019796A1
/ GENERAL INFORMATION:
/ APPLICANT: O'Donnell, Michael E.
/ APPLICANT: Yuzhakov, Alexander
/ APPLICANT: Yurleva, Olga
/ APPLICANT: Jeruzalmi, David
/ APPLICANT: Bruck, Irina
/ APPLICANT: Kuriyan, John
/ TITLE OF INVENTION: ENZYMES DERIVED FROM THERMOPHILIC ORGANISMS THAT
/ TITLE OF INVENTION: FUNCTION AS A CHROMOSOMAL REPLICASE, PREPARATION AND
/ TITLE OF INVENTION: USE THEREOF
/ FILE REFERENCE: 22221/1030
/ CURRENT APPLICATION NUMBER: US/10/671,207
/ CURRENT FILING DATE: 2003-09-25
/ PRIOR APPLICATION NUMBER: US/09/716,964
/ PRIOR FILING DATE: 2000-11-21
/ PRIOR APPLICATION NUMBER: 60/143,202
/ PRIOR FILING DATE: 1997-04-08
/ PRIOR APPLICATION NUMBER: 08/823,407
/ PRIOR FILING DATE: 1997-04-08
/ PRIOR APPLICATION NUMBER: 09/057,416
```

```
/ PRIOR FILING DATE: 1998-04-08
/ NUMBER OF SEQ ID NOS: 212
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 210
/ LENGTH: 11
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURES:
/ OTHER INFORMATION: Description of Artificial Sequence: polypeptide
US-10-671-207-210
```

```
Query Match          30.2%; Score 29; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      6 HGYLE 10
        |||||
Db       7 HGYLE 11
```

```
RESULT 35
US-10-673-120-210
/ Sequence 210, Application US/10673120
/ Publication No. US20050048510A1
/ GENERAL INFORMATION:
/ APPLICANT: O'Donnell, Michael E.
/ APPLICANT: Yuzhakov, Alexander
/ APPLICANT: Yurleva, Olga
/ APPLICANT: Jeruzalim, David
/ APPLICANT: Bruck, Irina
/ APPLICANT: Kuriyan, John
/ TITLE OF INVENTION: ENZYMES DERIVED FROM THERMOPHILIC ORGANISMS THAT
/ TITLE OF INVENTION: FUNCTION AS A CHROMOSOMAL REPLICASE, PREPARATION AND
/ FILE REFERENCE: 22221/1030
/ CURRENT APPLICATION NUMBER: US/10/673,120
/ CURRENT FILING DATE: 2003-09-26
/ PRIOR APPLICATION NUMBER: US/09/716,964A
/ PRIOR FILING DATE: 2000-11-21
/ PRIOR APPLICATION NUMBER: 60/143,202
/ PRIOR FILING DATE: 1997-04-08
/ PRIOR APPLICATION NUMBER: 08/823,407
/ PRIOR FILING DATE: 1997-04-08
/ PRIOR APPLICATION NUMBER: 09/057,416
/ PRIOR FILING DATE: 1998-04-08
/ NUMBER OF SEQ ID NOS: 212
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 210
/ LENGTH: 11
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURES:
/ OTHER INFORMATION: Description of Artificial Sequence: polypeptide
US-10-673-120-210
```

```
Query Match          30.2%; Score 29; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      6 HGYLE 10
        |||||
Db       7 HGYLE 11
```

```
RESULT 36
US-10-257-603A-8
/ Sequence 8, Application US/10257603A
/ Publication No. US20050100551A1
/ GENERAL INFORMATION:
/ APPLICANT: Zieliński, Christoph
/ APPLICANT: Pehamberger, Hubert
/ APPLICANT: Breiteneder, Helmo
/ APPLICANT: Jensen-Jarolim, Erika
```

```
/ APPLICANT: Scheiner, Otto
/ TITLE OF INVENTION: Vaccine Against Cancerous Diseases
/ FILE REFERENCE: 37488-00100
/ CURRENT APPLICATION NUMBER: US/10/257,603A
/ CURRENT FILING DATE: 2002-10-15
/ PRIOR APPLICATION NUMBER: PCT/EP01/04251
/ PRIOR FILING DATE: 2001-04-12
/ PRIOR APPLICATION NUMBER: DE 200 18 403.0
/ PRIOR FILING DATE: 2000-04-13
/ PRIOR APPLICATION NUMBER: DE 100 41 342.0
/ PRIOR FILING DATE: 2000-08-23
/ NUMBER OF SEQ ID NOS: 11
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 8
/ LENGTH: 11
/ TYPE: PRT
/ ORGANISM: homo sapiens
US-10-257-603A-8
```

```
Query Match          30.2%; Score 29; DB 5; Length 11;
Best Local Similarity 71.4%; Pred. No. 7.8e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      1 DAFEPHG 7
        |||||
Db       4 DPFEPHG 10
```

```
RESULT 37
US-10-671-412-210
/ Sequence 210, Application US/10671412
/ Publication No. US20050100920A1
/ GENERAL INFORMATION:
/ APPLICANT: O'Donnell, Michael E.
/ APPLICANT: Yuzhakov, Alexander
/ APPLICANT: Yurleva, Olga
/ APPLICANT: Jeruzalim, David
/ APPLICANT: Bruck, Irina
/ APPLICANT: Kuriyan, John
/ TITLE OF INVENTION: ENZYMES DERIVED FROM THERMOPHILIC ORGANISMS THAT
/ TITLE OF INVENTION: FUNCTION AS A CHROMOSOMAL REPLICASE, PREPARATION AND
/ FILE REFERENCE: 22221/1030
/ CURRENT APPLICATION NUMBER: US/10/671,412
/ CURRENT FILING DATE: 2003-09-25
/ PRIOR APPLICATION NUMBER: US/09/716,964A
/ PRIOR FILING DATE: 2000-11-21
/ PRIOR APPLICATION NUMBER: 60/143,202
/ PRIOR FILING DATE: 1997-04-08
/ PRIOR APPLICATION NUMBER: 08/823,407
/ PRIOR FILING DATE: 1997-04-08
/ PRIOR APPLICATION NUMBER: 09/057,416
/ PRIOR FILING DATE: 1998-04-08
/ NUMBER OF SEQ ID NOS: 212
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 210
/ LENGTH: 11
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURES:
/ OTHER INFORMATION: Description of Artificial Sequence: polypeptide
US-10-671-412-210
```

```
Query Match          30.2%; Score 29; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      6 HGYLE 10
        |||||
Db       7 HGYLE 11
```

RESULT 38

US-10-671-859-210  
; Sequence 210, Application US/10671859  
; Publication No. US20050112580A1  
; GENERAL INFORMATION:  
; APPLICANT: O'Donnell, Michael E.  
; APPLICANT: Yuzhakov, Alexander  
; APPLICANT: Yurileva, Olga  
; APPLICANT: Jeruzalmi, David  
; APPLICANT: Bruck, Irina  
; APPLICANT: Kurlyan, John  
; TITLE OF INVENTION: ENZYMES DERIVED FROM THERMOPHILIC ORGANISMS THAT  
; TITLE OF INVENTION: FUNCTION AS A CHROMOSOMAL REPLICASE, PREPARATION AND  
; FILE REFERENCE: 22221/1030  
; CURRENT APPLICATION NUMBER: US/10/671,859  
; CURRENT FILING DATE: 2003-09-26  
; PRIOR APPLICATION NUMBER: US/09/716,964A  
; PRIOR FILING DATE: 2000-11-21  
; PRIOR APPLICATION NUMBER: 60/143,202  
; PRIOR FILING DATE: 1997-04-08  
; PRIOR APPLICATION NUMBER: 08/823,407  
; PRIOR FILING DATE: 1997-04-08  
; PRIOR APPLICATION NUMBER: 09/057,416  
; PRIOR FILING DATE: 1998-04-08  
; NUMBER OF SEQ ID NOS: 212  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 210  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: polypeptide  
US-10-671-859-210  
  
Query Match 30.2%; Score 29; DB 5; Length 11;  
Best Local Similarity 100.0%; Pred. No. 7.8e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 6 HGYYL 10  
DB 7 HGYYL 11  
  
RESULT 39  
US-10-671-106-210  
; Sequence 210, Application US/10671106  
; Publication No. US20050153299A1  
; GENERAL INFORMATION:  
; APPLICANT: O'Donnell, Michael E.  
; APPLICANT: Yuzhakov, Alexander  
; APPLICANT: Yurileva, Olga  
; APPLICANT: Jeruzalmi, David  
; APPLICANT: Bruck, Irina  
; APPLICANT: Kurlyan, John  
; TITLE OF INVENTION: ENZYMES DERIVED FROM THERMOPHILIC ORGANISMS THAT  
; TITLE OF INVENTION: FUNCTION AS A CHROMOSOMAL REPLICASE, PREPARATION AND  
; FILE REFERENCE: 22221/1030  
; CURRENT APPLICATION NUMBER: US/10/671,106  
; CURRENT FILING DATE: 2003-09-25  
; PRIOR APPLICATION NUMBER: US/09/716,964B  
; PRIOR FILING DATE: 2000-11-21  
; PRIOR APPLICATION NUMBER: 60/143,202  
; PRIOR FILING DATE: 1997-04-08  
; PRIOR APPLICATION NUMBER: 08/823,407  
; PRIOR FILING DATE: 1997-04-08  
; PRIOR APPLICATION NUMBER: 09/057,416  
; PRIOR FILING DATE: 1998-04-08  
; NUMBER OF SEQ ID NOS: 212  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 210  
; LENGTH: 11  
; TYPE: PRT

; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: polypeptide  
US-10-671-106-210  
  
Query Match 30.2%; Score 29; DB 5; Length 11;  
Best Local Similarity 100.0%; Pred. No. 7.8e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 6 HGYYL 10  
DB 7 HGYYL 11  
  
RESULT 40  
US-09-932-161-4  
; Sequence 4, Application US/09932161  
; Patent No. US20020037533A1  
; GENERAL INFORMATION:  
; APPLICANT: Clivelli, Olivier  
; APPLICANT: Lin, Steven  
; TITLE OF INVENTION: Screening and Therapeutic Methods For  
; TITLE OF INVENTION: Promoting Wakefulness and Sleep  
; FILE REFERENCE: P-UC 4679  
; CURRENT APPLICATION NUMBER: US/09/932,161  
; CURRENT FILING DATE: 2001-08-17  
; PRIOR APPLICATION NUMBER: US 09/560,915  
; PRIOR FILING DATE: 2000-04-28  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-09-932-161-4  
  
Query Match 30.2%; Score 29; DB 3; Length 12;  
Best Local Similarity 50.0%; Pred. No. 8.6e+02;  
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
QY 5 PHGYLLTAIV 14  
DB 1 PHGYNNTVSV 10  
  
RESULT 41  
US-09-932-161-12  
; Sequence 12, Application US/09932161  
; Patent No. US20020037533A1  
; GENERAL INFORMATION:  
; APPLICANT: Clivelli, Olivier  
; APPLICANT: Lin, Steven  
; TITLE OF INVENTION: Screening and Therapeutic Methods For  
; TITLE OF INVENTION: Promoting Wakefulness and Sleep  
; FILE REFERENCE: P-UC 4679  
; CURRENT APPLICATION NUMBER: US/09/932,161  
; CURRENT FILING DATE: 2001-08-17  
; PRIOR APPLICATION NUMBER: US 09/560,915  
; PRIOR FILING DATE: 2000-04-28  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 12  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: human GPR10 variant  
US-09-932-161-12  
  
Query Match 30.2%; Score 29; DB 3; Length 12;  
Best Local Similarity 50.0%; Pred. No. 8.6e+02;  
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

```

OY      5 PHGYLLTAAY 14
         ||| : | : |
Db      1 PHGQNMTVSV 10

```

RESULT 42  
US-10-096-777-4

```

1 Sequence 4, Application US/10096777
2 Publication No. US20030171270A1
3
4 GENERAL INFORMATION:
5
6 APPLICANT: Civelli, Olivier
7
8 APPLICANT: Lin, Steven
9
10 TITLE OF INVENTION: Therapeutic Compositions and Methods
11
12 TITLE OF INVENTION: Relating to Prolactin Releasing Peptide (PrRP
13
14 FILE REFERENCE: P-UC 3534
15
16 CURRENT APPLICATION NUMBER: US/10/096,777
17
18 CURRENT FILING DATE: 2002-03-12
19
20 PRIOR APPLICATION NUMBER: US/09/560,915
21
22 PRIOR FILING DATE: 2000-04-28
23
24 NUMBER OF SEQ ID NOS: 24
25
26 SOFTWARE: FastSeq for Windows Version 4.0
27
28 SEQ ID NO 4
29
30 LENGTH: 12
31
32 TYPE: PRT
33
34 ORGANISM: Homo Sapien
35
36 US-10-096-777-4

```

Query Match	30.2%	Score 29;	DB 4;	Length 12;
Best Local Similarity	50.0%	Pred. No. 8.6e+02;		
Matches	5;	Conservative	2;	Mismatches 3;
				Indels 0;
				Gaps 0;

Qy	5	PHGYLLTAAY	14
		:   :	
Db	1	PHGQNMIVSV	10

RESULT 43  
US-10-096-777-1

```

/ Sequence 12, Application US/10096777
/ Publication No. US20030171270A1
/ GENERAL INFORMATION:
/ APPLICANT: Civeall, Oliver
/ APPLICANT: Lin, Steven
/ TITLES OF INVENTION: Therapeutic Compositions and Methods
/ TITLES OF INVENTION: Relating to Prolectin Releasing Peptide (P-RP)
/ FILE REFERENCE: P-UC 3534
/ CURRENT APPLICATION NUMBER: US/10/096,777
/ CURRENT FILING DATE: 2002-03-12
/ PRIOR APPLICATION NUMBER: US/09/560,915
/ PRIOR FILING DATE: 2000-04-28
/ NUMBER OF SEQ ID NOS: 24
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 12
/ LENGTH: 12
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: human GPR10 variant
/ -S-10-096-777-12

```

Query Match	30.2%	Score 29;	DB 4;	Length 12;
Best local similarity	50.0%	Pred. No.	8.6e+02;	
Matches	5;	Conservative	2;	Mismatches 3;
				Indels 0;
				Gaps 0;

```

QY      5  PHGYLLTAAY  14
          |||  :|  :|
DB      1  PHGQNMIVSV  10

```

RESULT 44  
US-09-747-287-205  
; Sequence 205, Application US/09747287  
; Publication No. US20030207264A1

```

? GENERAL INFORMATION:
? APPLICANT: KOMORIYA, AKIRA
? APPLICANT: PACKARD, BEVERLY S.
? TITLE OF INVENTION: HOMO-DOUBLY LABELED COMPOSITIONS FOR THE DETECTION OF ENZYME
? TITLE OF INVENTION: ACTIVITY IN BIOLOGICAL SAMPLES
? FILE REFERENCE: 300-948600US
? CURRENT APPLICATION NUMBER: US/09/747,287
? CURRENT FILING DATE: 2000-12-22
? PRIOR APPLICATION NUMBER: US 09/349,019
? PRIOR FILING DATE: 1999-09-10
? PRIOR APPLICATION NUMBER: US08/802,961
? PRIOR FILING DATE: 1997-02-20
? PRIOR APPLICATION NUMBER: PCT/US00/24882
? PRIOR FILING DATE: 2000-09-11
? NUMBER OF SEQ ID NOS: 242
? SOFTWARE: Patentin version 3.2
? SEQ ID NO 205
? LENGTH: 16
? TYPE: PR1
? ORGANISM: Artificial
? FEATURE:
? OTHER INFORMATION: Synthetic peptide.
? FEATURE:
? NAME/KEY: misc feature
? LOCATION: (4)-(4)
? OTHER INFORMATION: Xaa can be any naturally occurring amino acid
? US-09-747-287-205

```

Query Match	30.2%	Score 29	DB 3	length 16
Best Local Similarity	42.9%	Pred. No.	1 2e+03	
Matches	6	Conservative	2	Mismatches 6
				Indels 0
				Gaps 0

Qy 4 BPHGYLLTAAVSPG 17  
: |||: |||  
Db 2 DPXGYVHDAVPVPG 15

```

RESULT 45
US-10-300-694A-114
/ Sequence 114, Application US/10300694A
/ Publication No. US20030185870A1
/ GENERAL INFORMATION:
/ APPLICANT: Duke University
/ APPLICANT: Grinstaff, Mark W.
/ APPLICANT: Kenan, Daniel J.
/ APPLICANT: Walsh, Elisabeth B.
/ APPLICANT: Middleton, Cristhian
/ TITLE OF INVENTION: INTERFACIAL BIOMATERIALS
/ FILE REFERENCE: 180/143/2
/ CURRENT APPLICATION NUMBER: US/10/300,694A
/ CURRENT FILING DATE: 2003-05-07
/ PRIOR APPLICATION NUMBER: US 60/331,843
/ PRIOR FILING DATE: 2001-11-20
/ NUMBER OF SEQ ID NOS: 117
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 114
/ LENGTH: 19
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: Nylon suture-binding peptide 114
US-10-300-694A-114

```

Query Match	30.2%	Score 29	DB 4	Length 19
Best Local Similarity	62.5%	Pred. No. 1.4e+03		
Matches 5, Conservative	0	Mismatches 3	Indels 0	Gaps 0

Qy	1	DAFBPHGY	8
Db	3	DFPNRHGY	10

## RESULT 46

US-10-918-015A-15  
; Sequence 15, Application US/10918015A  
; Publication No. US20050106653A1  
; GENERAL INFORMATION:  
; APPLICANT: Aventis Pharma Deutschland GmbH  
; APPLICANT: TENNASELS, Norbert  
; APPLICANT: ECKEL, Jürgen  
; APPLICANT: METZGER, Sabine  
; APPLICANT: SOMMERFELD, Mark  
; TITLE OF INVENTION: A METHOD FOR THE IDENTIFICATION OF IRS PROTEIN KINASE INHIBITORS  
; FILE REFERENCE: DE4V2003/0061 US NP  
; CURRENT APPLICATION NUMBER: US/10/918,015A  
; PRIOR FILING DATE: 2004-08-13  
; PRIOR APPLICATION NUMBER: 60/535,139  
; PRIOR FILING DATE: 2004-01-08  
; PRIOR APPLICATION NUMBER: 03018517.7  
; PRIOR FILING DATE: 2003-08-16  
; SOFTWARE: Patent version 3.1  
; SEQ ID NO 15  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Rat IRS-1 fragment  
US-10-918-015A-15

Query Match 29.7%; Score 28.5; DB 5; Length 16;  
Best Local Similarity 40.0%; Pred. No. 1.4e+03;  
Matches 6; Conservative 5; Mismatches 1; Indels 3; Gaps 1;

QY 4 BPHGYL--TAAYS 15  
DB 2 DPHGYMMSPSAAS 16

RESULT 47  
US-10-699-088-232  
; Sequence 232, Application US/10699088  
; Publication No. US20040209282A1  
; GENERAL INFORMATION:  
; APPLICANT: Dana Ault-Riche  
; APPLICANT: Bruce Atkinson  
; TITLE OF INVENTION: METHODS FOR PRODUCING POLYPEPTIDE-TAGGED COLLECTIONS AND CAPTURE  
; FILE REFERENCE: 25885-1754  
; CURRENT APPLICATION NUMBER: US/10/699,088  
; PRIOR FILING DATE: 2003-10-30  
; PRIOR APPLICATION NUMBER: 60/422,923  
; PRIOR FILING DATE: 2002-10-30  
; PRIOR APPLICATION NUMBER: 60/423,018  
; PRIOR FILING DATE: 2002-10-30  
; NUMBER OF SEQ ID NOS: 1094  
; SOFTWARE: FaastSeq for Windows Version 4.0  
; SEQ ID NO 232  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic peptide  
US-10-699-088-232

Query Match 29.2%; Score 28; DB 4; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PHGY 8  
DB 1 PHGY 4

RESULT 48

US-10-699-088-240  
; Sequence 240, Application US/10699088  
; Publication No. US20040209282A1  
; GENERAL INFORMATION:  
; APPLICANT: Dana Ault-Riche  
; APPLICANT: Bruce Atkinson  
; TITLE OF INVENTION: METHODS FOR PRODUCING POLYPEPTIDE-TAGGED COLLECTIONS AND CAPTURE  
; FILE REFERENCE: 25885-1754  
; CURRENT APPLICATION NUMBER: US/10/699,088  
; PRIOR FILING DATE: 2003-10-30  
; PRIOR APPLICATION NUMBER: 60/422,923  
; PRIOR FILING DATE: 2002-10-30  
; PRIOR APPLICATION NUMBER: 60/423,018  
; PRIOR FILING DATE: 2002-10-30  
; NUMBER OF SEQ ID NOS: 1094  
; SOFTWARE: FaastSeq for Windows Version 4.0  
; SEQ ID NO 240  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic peptide  
US-10-699-088-240

Query Match 29.2%; Score 28; DB 4; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PHGY 8  
DB 1 PHGY 4

RESULT 49  
US-10-699-113-232  
; Sequence 232, Application US/10699113  
; Publication No. US20040241748A1  
; GENERAL INFORMATION:  
; APPLICANT: Ault-Riche, Dana  
; APPLICANT: Kumble, Krishnanand  
; APPLICANT: Schultz, Rainer  
; APPLICANT: Schultz, Kenneth  
; TITLE OF INVENTION: Self-Assembling Arrays and Uses Thereof  
; FILE REFERENCE: 25885-1755  
; CURRENT APPLICATION NUMBER: US/10/699,113  
; PRIOR FILING DATE: 2003-10-30  
; PRIOR APPLICATION NUMBER: 60/446,687  
; PRIOR FILING DATE: 2003-02-10  
; NUMBER OF SEQ ID NOS: 948  
; SOFTWARE: FaastSeq for Windows Version 4.0  
; SEQ ID NO 232  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic peptide  
US-10-699-113-232

Query Match 29.2%; Score 28; DB 5; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PHGY 8  
DB 1 PHGY 4

RESULT 50  
US-10-699-113-240  
; Sequence 240, Application US/10699113  
; Publication No. US20040241748A1  
; GENERAL INFORMATION:

```
/ APPLICANT: Ault-Riche, Dana
/ APPLICANT: Kumble, Krishnamand
/ APPLICANT: Schult, Rainer
/ APPLICANT: Schult, Kenneth
/ TITLE OF INVENTION: Self-Assembling Arrays and Uses Thereof
/ FILE REFERENCE: 25885-1755
/ CURRENT APPLICATION NUMBER: US/10/699,113
/ PRIOR FILING DATE: 2003-10-30
/ PRIOR APPLICATION NUMBER: 60/446,687
/ NUMBER OF SEQ ID NOS: 948
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 240
/ LENGTH: 6
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: synthetic peptide
US-10-699-113-240
```

```
Query Match          29.2%; Score 28; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 5 PHGY 8
    ||||
Db 1 PHGY 4
```

```
RESULT 51
US-10-699-114-232
/ Sequence 233, Application US/10699114
/ Publication No. US20050042623A1
/ GENERAL INFORMATION:
/ APPLICANT: Dana Ault-Riche
/ APPLICANT: Bruce Atkinson
/ APPLICANT: Krishnamand Kumble
/ APPLICANT: Lynne Jersaltis
/ APPLICANT: Gizette Sperinde
/ TITLE OF INVENTION: SYSTEMS FOR CAPTURE AND ANALYSIS OF BIOLOGICAL PARTICLES AND MET
/ FILE REFERENCE: 25885-1759
/ CURRENT APPLICATION NUMBER: US/10/699,114
/ PRIOR FILING DATE: 2003-10-30
/ PRIOR APPLICATION NUMBER: 60/423,018
/ PRIOR FILING DATE: 2002-10-30
/ PRIOR APPLICATION NUMBER: 60/422,923
/ PRIOR FILING DATE: 2002-10-30
/ NUMBER OF SEQ ID NOS: 1094
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 232
/ LENGTH: 6
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: synthetic peptide
US-10-699-114-232
```

```
Query Match          29.2%; Score 28; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 5 PHGY 8
    ||||
Db 1 PHGY 4
```

```
RESULT 52
US-10-699-114-240
/ Sequence 240, Application US/10699114
/ Publication No. US20050042623A1
/ GENERAL INFORMATION:
/ APPLICANT: Dana Ault-Riche
```

```
/ APPLICANT: Bruce Atkinson
/ APPLICANT: Krishnamand Kumble
/ APPLICANT: Lynne Jersaltis
/ APPLICANT: Gizette Sperinde
/ TITLE OF INVENTION: SYSTEMS FOR CAPTURE AND ANALYSIS OF BIOLOGICAL PARTICLES AND MET
/ FILE REFERENCE: 25885-1759
/ CURRENT APPLICATION NUMBER: US/10/699,114
/ PRIOR FILING DATE: 2003-10-30
/ PRIOR APPLICATION NUMBER: 60/423,018
/ PRIOR FILING DATE: 2002-10-30
/ PRIOR APPLICATION NUMBER: 60/422,923
/ PRIOR FILING DATE: 2002-10-30
/ NUMBER OF SEQ ID NOS: 1094
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 240
/ LENGTH: 6
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: synthetic peptide
US-10-699-114-240
```

```
Query Match          29.2%; Score 28; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 5 PHGY 8
    ||||
Db 1 PHGY 4
```

```
RESULT 53
US-10-806-924-195
/ Sequence 195, Application US/10806924
/ Publication No. US20050095648A1
/ GENERAL INFORMATION:
/ APPLICANT: Geyzen, H. Mario
/ APPLICANT: Ault-Riche, Dana
/ TITLE OF INVENTION: Method for designing linear epitopes and algorithm therefor
/ FILE REFERENCE: 25885-1760
/ CURRENT APPLICATION NUMBER: US/10/806,924
/ PRIOR FILING DATE: 2004-03-22
/ NUMBER OF SEQ ID NOS: 911
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 195
/ LENGTH: 6
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: synthetic peptide
US-10-806-924-195
```

```
Query Match          29.2%; Score 28; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 5 PHGY 8
    ||||
Db 1 PHGY 4
```

```
RESULT 54
US-10-806-924-203
/ Sequence 203, Application US/10806924
/ Publication No. US20050095648A1
/ GENERAL INFORMATION:
/ APPLICANT: Geyzen, H. Mario
/ APPLICANT: Ault-Riche, Dana
/ TITLE OF INVENTION: Method for designing linear epitopes and algorithm therefor
/ FILE REFERENCE: 25885-1760
```

```
/ CURRENT APPLICATION NUMBER: US/10/806,924
/ CURRENT FILING DATE: 2004-03-22
/ NUMBER OF SEQ ID NOS: 911
/ SOFTWARE: PatSeq for Windows Version 4.0
/ SEQ ID NO 203
/ LENGTH: 6
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: synthetic peptide
US-10-806-924-203
```

```
Query Match          29.2%; Score 28; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      5 PHGY 8
       ||||
Db      1 PHGY 4
```

```
RESULT 55
US-10-862-195-1482
/ Sequence 1482, Application US/10862195
/ Publication No. US20050164324A1
/ GENERAL INFORMATION:
/ APPLICANT: CYGIL STEVEN P.
/ TITLE OF INVENTION: SYSTEMS, METHODS AND KITS FOR CHARACTERIZING PHOSPHOPROTEOMES
/ FILE REFERENCE: 58890 (70207)
/ CURRENT APPLICATION NUMBER: US/10/862,195
/ CURRENT FILING DATE: 2004-06-04
/ PRIOR APPLICATION NUMBER: 60/476,010
/ PRIOR FILING DATE: 2003-06-04
/ NUMBER OF SEQ ID NOS: 2245
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 1482
/ LENGTH: 13
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ OTHER INFORMATION: See specification as filed for preferred embodiments
/ OTHER INFORMATION: and description of phosphorylation sites
US-10-862-195-1482
```

```
Query Match          29.2%; Score 28; DB 5; Length 13;
Best Local Similarity 62.5%; Pred. No. 1.4e+03;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      11 TAAVSPGK 18
       |||||
Db      6 STRLSPGK 13
```

```
RESULT 56
US-09-906-179A-203
/ Sequence 203, Application US/09906179A
/ Publication No. US20030219737A1
/ GENERAL INFORMATION:
/ APPLICANT: Bullard, James M.
/ APPLICANT: Janjic, Nedolija
/ APPLICANT: McHenry, Charles S.
/ TITLE OF INVENTION: NOVEL DNA POLYMERASE III HOLOENZYME DELTA SUBUNIT
/ TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND PROTEINS
/ FILE REFERENCE: RDV03
/ CURRENT APPLICATION NUMBER: US/09/906,179A
/ CURRENT FILING DATE: 2001-07-16
/ PRIOR APPLICATION NUMBER: 60/218,246
/ PRIOR FILING DATE: 2000-07-14
/ PRIOR APPLICATION NUMBER: 09/818,780
/ PRIOR FILING DATE: 2001-03-28
/ PRIOR APPLICATION NUMBER: 60/192,736
/ PRIOR FILING DATE: 2000-03-28
/ NUMBER OF SEQ ID NOS: 230
```

```
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 203
/ LENGTH: 14
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Consensus
/ OTHER INFORMATION: sequence
/ NAME/KEY: UNSURE
/ LOCATION: (1)..(14)
/ OTHER INFORMATION: Xaa at position 14 is Thr or Ser
US-09-906-179A-203
```

```
Query Match          29.2%; Score 28; DB 3; Length 14;
Best Local Similarity 38.5%; Pred. No. 1.5e+03;
Matches 5; Conservative 1; Mismatches 7; Indels 0; Gaps 0;
```

```
Qy      6 HGYLTTAAVSPGK 18
       |||||
Db      1 HAYLFGKXGKXGK 13
```

```
RESULT 57
US-10-447-161-1
/ Sequence 1, Application US/10447161
/ Publication No. US20040023314A1
/ GENERAL INFORMATION:
/ APPLICANT: Wang, Rong-fu
/ TITLE OF INVENTION: Mutant Fibronectin and Tumor Metastasis
/ FILE REFERENCE: HO-P02484US1
/ CURRENT APPLICATION NUMBER: US/10/447,161
/ CURRENT FILING DATE: 2003-05-28
/ PRIOR APPLICATION NUMBER: 60/383,530
/ PRIOR FILING DATE: 2002-05-28
/ NUMBER OF SEQ ID NOS: 148
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 1
/ LENGTH: 14
/ TYPE: PRT
/ ORGANISM: Human
US-10-447-161-1
```

```
Query Match          29.2%; Score 28; DB 4; Length 14;
Best Local Similarity 55.6%; Pred. No. 1.5e+03;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy      3 FEPHGYLLT 11
       |||||
Db      3 FEKHGFRRT 11
```

```
RESULT 58
US-10-103-395-176
/ Sequence 176, Application US/10103395
/ Publication No. US20020160019A1
/ GENERAL INFORMATION:
/ APPLICANT: EPRIMONE, Inc.
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ TITLE OF INVENTION: IDENTIFICATION OF BROADLY REACTIVE DR
/ TITLE OF INVENTION: RESTRICTED EPITOPES
/ FILE REFERENCE: 39963-20016.01
/ CURRENT APPLICATION NUMBER: US/10/103,395
/ CURRENT FILING DATE: 2003-01-03
/ PRIOR APPLICATION NUMBER: US 09/009,953
/ PRIOR FILING DATE: 1998-01-21
/ PRIOR APPLICATION NUMBER: PCT/US98/01373
/ PRIOR FILING DATE: 1998-01-23
/ PRIOR APPLICATION NUMBER: US 60/036,713
/ PRIOR FILING DATE: 1997-01-23
/ PRIOR APPLICATION NUMBER: US 60/037,432
/ PRIOR FILING DATE: 1997-02-07
```



```
/ NUMBER OF SEQ ID NOS: 274
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 176
/ LENGTH: 15
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-103-395-176
```

```
Query Match          29.2%; Score 28; DB 4; Length 15;
Best Local Similarity 66.7%; Pred. No. 1.6e+03;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 9 LPTAAVSPG 17
    |||:||||
Db 6 LPTAIIISP 14
```

```
RESULT 59
US-10-103-395-183
/ Sequence 183, Application US/10103395
/ Publication No. US20020160019A1
/ GENERAL INFORMATION:
/ APPLICANT: EPIMUNE, Inc.
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ TITLE OF INVENTION: IDENTIFICATION OF BROADLY REACTIVE DR
/ FILE REFERENCE: 39963-20016.01
/ CURRENT APPLICATION NUMBER: US/10/103,395
/ PRIOR FILING DATE: 2003-01-03
/ PRIOR APPLICATION NUMBER: US 09/009,953
/ PRIOR FILING DATE: 1998-01-21
/ PRIOR APPLICATION NUMBER: PCT/US98/01373
/ PRIOR FILING DATE: 1998-01-23
/ PRIOR APPLICATION NUMBER: US 60/036,713
/ PRIOR FILING DATE: 1997-01-23
/ PRIOR APPLICATION NUMBER: US 60/037,432
/ PRIOR FILING DATE: 1997-02-07
/ NUMBER OF SEQ ID NOS: 274
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 183
/ LENGTH: 15
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-103-395-183
```

```
Query Match          29.2%; Score 28; DB 4; Length 15;
Best Local Similarity 66.7%; Pred. No. 1.6e+03;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 9 LPTAAVSPG 17
    |||:||||
Db 3 LPTAIIISP 11
```

```
RESULT 60
US-10-203-915A-174
/ Sequence 174, Application US/10203915A
/ Publication No. US20040106159A1
/ GENERAL INFORMATION:
/ APPLICANT: Kern, Florian
/ TITLE OF INVENTION: Method for Antigen-Specific Stimulation of T
/ FILE REFERENCE: 010266wo/JH/ml
/ CURRENT APPLICATION NUMBER: US/10/203,915A
/ CURRENT FILING DATE: 2002-08-15
/ NUMBER OF SEQ ID NOS: 260
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 174
/ LENGTH: 15
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
```

```
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: HCMV pp65
/ OTHER INFORMATION: Fragment
US-10-203-915A-174
```

```
Query Match          29.2%; Score 28; DB 4; Length 15;
Best Local Similarity 46.7%; Pred. No. 1.6e+03;
Matches 7; Conservative 1; Mismatches 7; Indels 0; Gaps 0;
```

```
QY 4 EPHGYLLTAVSPGK 18
    |||:|||||
Db 1 EPDVYTTSAFVFPPTK 15
```

```
RESULT 61
US-10-886-773-49
/ Sequence 49, Application US/10886773
/ Publication No. US20050054107A1
/ GENERAL INFORMATION:
/ APPLICANT: Chulay, Jeffrey D.
/ APPLICANT: Dryga, Sergey A.
/ APPLICANT: Reap, Elizabeth A.
/ APPLICANT: Morris, John S.
/ APPLICANT: Olmsted, Robert A.
/ TITLE OF INVENTION: ALPHAVIRUS-BASED CYTOMEGALOVIRUS VACCINES
/ FILE REFERENCE: 9368-7
/ CURRENT APPLICATION NUMBER: US/10/886,773
/ PRIOR FILING DATE: 2004-07-08
/ PRIOR APPLICATION NUMBER: US 60/486,501
/ PRIOR FILING DATE: 2003-07-11
/ NUMBER OF SEQ ID NOS: 262
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 49
/ LENGTH: 15
/ TYPE: PRT
/ ORGANISM: Human cytomegalovirus
US-10-886-773-49
```

```
Query Match          29.2%; Score 28; DB 5; Length 15;
Best Local Similarity 46.7%; Pred. No. 1.6e+03;
Matches 7; Conservative 1; Mismatches 7; Indels 0; Gaps 0;
```

```
QY 4 EPHGYLLTAVSPGK 18
    |||:|||||
Db 1 EPDVYTTSAFVFPPTK 15
```

```
RESULT 62
US-10-414-522-25
/ Sequence 25, Application US/10414522
/ Publication No. US20050170433A1
/ GENERAL INFORMATION:
/ APPLICANT: The Procter & Gamble Company
/ APPLICANT: Mieling, Glen
/ APPLICANT: Bush, Rodney
/ APPLICANT: Colson, Amy-Odile
/ TITLE OF INVENTION: Three Dimensional Coordinates of Melanin-Concentrating Hormone
/ FILE REFERENCE: 9208
/ CURRENT APPLICATION NUMBER: US/10/414,522
/ CURRENT FILING DATE: 2003-04-15
/ NUMBER OF SEQ ID NOS: 25
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 25
/ LENGTH: 15
/ TYPE: PRT
/ ORGANISM: Homo Sapiens
US-10-414-522-25
```

```
Query Match          29.2%; Score 28; DB 5; Length 15;
Best Local Similarity 60.0%; Pred. No. 1.6e+03;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

Qy 8 YLTTAAVSPG 17  
|||:|  
Db 1 YLYNAAISLG 10

## RESULT 63

US-10-505-929-202  
; Sequence 202, Application US/10505929  
; Publication No. US20050221381A1  
; GENERAL INFORMATION:  
; APPLICANT: KLADE, CHRISTOF  
; APPLICANT: SCHALICH, JULIANE  
; APPLICANT: VYTVYTSKA, ORESTA  
; APPLICANT: AICHINGER, GERALD  
; APPLICANT: OTAVA, ALEXANDER  
; APPLICANT: MATTERN, FRANK  
; TITLE OF INVENTION: METHOD FOR ISOLATING LIGANDS  
; FILE REFERENCE: SONN:055US  
; CURRENT APPLICATION NUMBER: US/10/505,929  
; PRIOR FILING DATE: 2004-08-27  
; PRIOR APPLICATION NUMBER: PCT/EP03/02005  
; PRIOR FILING DATE: 2003-02-27  
; PRIOR APPLICATION NUMBER: A 316/2002  
; PRIOR FILING DATE: 2002-02-28  
; PRIOR APPLICATION NUMBER: A 1376/2002  
; PRIOR FILING DATE: 2002-09-13  
; NUMBER OF SEQ ID NOS: 584  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 202  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Cytoomega1ov1rus  
US-10-505-929-202

Query Match 29.2%; Score 28; DB 5; Length 15;  
Best Local Similarity 46.7%; Pred. No. 1.6e+03;  
Matches 7; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

Qy 4 BPHGYLTTAAVSPGK 18  
|||:|  
Db 1 BPDVYTSAFVFPPTK 15

## RESULT 64

US-10-083-446-188  
; Sequence 188, Application US/10083446  
; Publication No. US20030185790A1  
; GENERAL INFORMATION:  
; APPLICANT: Abrams, Mark A.  
; Bauer, S. C.  
; Bradford-Goldberg, Sarah R.  
; Caparon, Maïre H.  
; Easton, Alan M.  
; Klein, Barbara K.  
; McKearn, John P.  
; Oline, Peter O.  
; Paik, Kumnan  
; Thomas, John W.

TITLE OF INVENTION: Methods Of Ex-Vivo Expansion Of Hematopoietic Cells  
Using Multivariant (IL-3) Hematopoiesis Chimera Proteins  
NUMBER OF SEQUENCES: 197  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: S. Christopher Bauer, Pharmacia Corporation  
Corporate Patent Dept., Mail Zone 04E  
STREET: 800 N. Lindbergh  
CITY: St. Louis  
STATE: Missouri  
COUNTRY: USA  
ZIP: 63167

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/083,446  
FILING DATE: 26-Feb-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/762,227  
FILING DATE: 09-DEC-1996  
APPLICATION NUMBER: US 08/192,325  
FILING DATE: 14-FEB-1994  
APPLICATION NUMBER: US 08/446,872  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: S. Christopher Bauer  
REGISTRATION NUMBER: 42,305  
REFERENCE/DOCKET NUMBER: C-2790/6  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (636)737-6257  
TELEFAX: (636)737-5452  
INFORMATION FOR SEQ ID NO: 188:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 188:  
US-10-083-446-188

Query Match 29.2%; Score 28; DB 4; Length 18;  
Best Local Similarity 40.0%; Pred. No. 2e+03;  
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 8 YLTTAAVSPG 17  
|||:|  
Db 1 YVIEGRISPG 10

## RESULT 65

US-10-083-446-189  
; Sequence 189, Application US/10083446  
; Publication No. US20030185790A1  
; GENERAL INFORMATION:  
; APPLICANT: Abrams, Mark A.  
; Bauer, S. C.  
; Bradford-Goldberg, Sarah R.  
; Caparon, Maïre H.  
; Easton, Alan M.  
; Klein, Barbara K.  
; McKearn, John P.  
; Oline, Peter O.  
; Paik, Kumnan  
; Thomas, John W.

TITLE OF INVENTION: Methods Of Ex-Vivo Expansion Of Hematopoietic Cells  
Using Multivariant (IL-3) Hematopoiesis Chimera Proteins  
NUMBER OF SEQUENCES: 197  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: S. Christopher Bauer, Pharmacia Corporation  
Corporate Patent Dept., Mail Zone 04E  
STREET: 800 N. Lindbergh  
CITY: St. Louis  
STATE: Missouri  
COUNTRY: USA  
ZIP: 63167

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/083,446  
FILING DATE: 26-Feb-2002  
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/762,227  
FILING DATE: 09-DEC-1996  
APPLICATION NUMBER: US 08/192,325  
FILING DATE: 14-FEB-1994  
APPLICATION NUMBER: US 08/446,872  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: S. Christopher Bauer  
REGISTRATION NUMBER: 42,305  
REFERENCE/DOCKET NUMBER: C-2790/6  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (636)737-6257  
TELEFAX: (636)737-5452  
INFORMATION FOR SEQ ID NO: 189:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 189:  
US-10-083-446-189

Query Match 29.2%; Score 28; DB 4; Length 18;  
Best Local Similarity 40.0%; Pred. No. 2e+03; 3; Indels 0; Gaps 0;  
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 8 YLTLAAVSPG 17  
|:::|  
Db 1 YVIEGRISPG 10

RESULT 66  
US-10-948-576-188  
Sequence 188, Application US/10948576  
Publication No. US20050059149A1  
GENERAL INFORMATION:  
APPLICANT: Abrams, Mark A.  
Bauer, S. C.  
Bratford-Goldberg, Sarah R.  
Caparon, Maïre H.  
Easton, Alan M.  
Klein, Barbara K.  
McKearn, John P.  
Oline, Peter O.  
Paik, Kumman  
Thomas, John W.  
TITLE OF INVENTION: Methods Of Ex-Vivo Expansion Of Hematopoietic Cells  
Using Multivariant IL-3 Hematopoiesis Chimera Proteins  
NUMBER OF SEQUENCES: 197  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Carol M. Nielsen, Winstead Sechrest & Minick P.C.  
STREET: P.O. Box 50784  
CITY: Dallas  
STATE: Texas  
COUNTRY: USA  
ZIP: 75201  
COMPUTER READABLE FORM:  
MEDIUM TYPE: CD  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/948,576  
FILING DATE: 22-Sep-2004  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 10/083,446  
FILING DATE: 22-FEB-2002  
APPLICATION NUMBER: 08/762,227  
FILING DATE: 09-DEC-1996  
APPLICATION NUMBER: US 08/192,325

FILING DATE: 14-FEB-1994  
APPLICATION NUMBER: US 08/446,872  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Carol M. Nielsen  
REGISTRATION NUMBER: 37,676  
REFERENCE/DOCKET NUMBER: 2790/7 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 713-650-2722  
TELEFAX: 214-745-5390  
INFORMATION FOR SEQ ID NO: 188:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 188:  
US-10-948-576-188

Query Match 29.2%; Score 28; DB 5; Length 18;  
Best Local Similarity 40.0%; Pred. No. 2e+03; 3; Indels 0; Gaps 0;  
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 8 YLTLAAVSPG 17  
|:::|  
Db 1 YVIEGRISPG 10

RESULT 67  
US-10-948-576-189  
Sequence 189, Application US/10948576  
Publication No. US20050059149A1  
GENERAL INFORMATION:  
APPLICANT: Abrams, Mark A.  
Bauer, S. C.  
Bratford-Goldberg, Sarah R.  
Caparon, Maïre H.  
Easton, Alan M.  
Klein, Barbara K.  
McKearn, John P.  
Oline, Peter O.  
Paik, Kumman  
Thomas, John W.  
TITLE OF INVENTION: Methods Of Ex-Vivo Expansion Of Hematopoietic Cells  
Using Multivariant IL-3 Hematopoiesis Chimera Proteins  
NUMBER OF SEQUENCES: 197  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Carol M. Nielsen, Winstead Sechrest & Minick P.C.  
STREET: P.O. Box 50784  
CITY: Dallas  
STATE: Texas  
COUNTRY: USA  
ZIP: 75201  
COMPUTER READABLE FORM:  
MEDIUM TYPE: CD  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/948,576  
FILING DATE: 22-Sep-2004  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 10/083,446  
FILING DATE: 22-FEB-2002  
APPLICATION NUMBER: 08/762,227  
FILING DATE: 09-DEC-1996  
APPLICATION NUMBER: US 08/192,325  
FILING DATE: 14-FEB-1994  
APPLICATION NUMBER: US 08/446,872  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:

NAME: Carol M. Nielsen  
REGISTRATION NUMBER: 37,676  
REFERENCE/DOCKET NUMBER: 2790/7 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 713-650-2722  
TELEFAX: 214-745-5390  
INFORMATION FOR SEQ ID NO: 189:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 189:  
US-10-948-576-189

Query Match 29.2%; Score 28; DB 5; Length 18;  
Best Local Similarity 40.0%; Pred. No. 2e+03;  
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 8 YLLTAVSPG 17  
DB 1 YVLEKISPG 10

RESULT 68  
US-09-863-054-18  
Sequence 18, Application US/09863054  
Publication No. US20030021809A1  
GENERAL INFORMATION:  
APPLICANT: Chilesi, Francis V.  
TITLE OF INVENTION: Peptide for Inducing Cytotoxic T  
Lymphocyte Responses to Hepatitis B Virus  
NUMBER OF SEQUENCES: 57  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/863,054  
FILING DATE: 21-May-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/935,898  
FILING DATE: 26-AUG-1992  
APPLICATION NUMBER: US 08/024,120  
FILING DATE: 26-FEB-1993  
APPLICATION NUMBER: US 08/396,283  
FILING DATE: 27-FEB-1995  
APPLICATION NUMBER: US 08/463,486  
FILING DATE: 05-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Lockyer, Jean M.  
REGISTRATION NUMBER: 44,879  
REFERENCE/DOCKET NUMBER: 014740-000421US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 18:  
US-09-863-054-18

Query Match 29.2%; Score 28; DB 3; Length 20;  
Best Local Similarity 50.0%; Pred. No. 2.2e+03;  
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 5 PHGYLLTAIV 14  
DB 1 PHRYALRQAI 10

RESULT 69  
US-10-128-711-101  
Sequence 101, Application US/10128711  
Publication No. US2003009634A1  
GENERAL INFORMATION:  
APPLICANT: VITIELLO, Maria A.  
CHESTNUT, Robert W.  
SETTE, Alessandro D.  
CELSI, Beceban  
GRAY, Howard  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING  
CTL IMMUNITY  
NUMBER OF SEQUENCES: 153  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend Kourie and Crew  
STREET: Stewart Street Tower, One Market Plaza  
CITY: San Francisco  
STATE: California  
COUNTRY: US  
ZIP: 94105-1493  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/128,711  
FILING DATE: 22-Apr-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/197,484  
FILING DATE: 16-FEB-1994  
APPLICATION NUMBER: US 07/935,811  
FILING DATE: 26-AUG-1992  
APPLICATION NUMBER: US 07/874,491  
FILING DATE: 27-APR-1992  
APPLICATION NUMBER: US 07/827,682  
FILING DATE: 29-JAN-1992  
APPLICATION NUMBER: US 07/749,568  
FILING DATE: 26-AUG-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Parmelee, Steven W.  
REGISTRATION NUMBER: 31,990  
REFERENCE/DOCKET NUMBER: 14137-26-4  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 467-9600  
TELEFAX: (206) 623-6793  
INFORMATION FOR SEQ ID NO: 101:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1..20  
OTHER INFORMATION: /note= "HTL-inducing peptide  
specific for HBV/ Hbc50-69"  
SEQUENCE DESCRIPTION: SEQ ID NO: 101:  
US-10-128-711-101

Query Match 29.2% Score 28; DB 4; Length 20;  
Best Local Similarity 50.0%; Pred. No. 2.2e+03;  
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 5 PHGYLTAAY 14  
|||  
1 PHHYALRQAI 10

RESULT 70  
US-10-359-431-7

Sequence 7, Application US/10359431  
Publication No. US2003017538A1

GENERAL INFORMATION:

APPLICANT: Chisari, Francis V.

TITLE OF INVENTION: Peptides for inducing Cytotoxic T

NUMBER OF SEQUENCES: 66 Lymphocyte Responses to Hepatitis B Virus

CORRESPONDENCE ADDRESS:

ADDRESSER: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/359,431

FILING DATE: 05-Feb-2003

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/749,540

FILING DATE: 26-AUG-1991

APPLICATION NUMBER: US 07/935,898

FILING DATE: 26-AUG-1992

APPLICATION NUMBER: US 08/100,870

FILING DATE: 02-AUG-1993

APPLICATION NUMBER: WO PCT/US94/08685

FILING DATE: 01-AUG-1994

APPLICATION NUMBER: US 08/591,502

FILING DATE: 20-MAY-1996

ATTORNEY/AGENT INFORMATION:

NAME: Lockyer, Jean M.

REGISTRATION NUMBER: 44,879

TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 20 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: linear

MOLECULAR TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 7:

US-10-359-431-7

Query Match 29.2% Score 28; DB 4; Length 20;  
Best Local Similarity 50.0%; Pred. No. 2.2e+03;  
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 5 PHGYLTAAY 14  
|||  
1 PHHYALRQAI 10

RESULT 71

US-10-397-411-13  
Sequence 13, Application US/10397411  
Publication No. US2003018622A1

GENERAL INFORMATION:

APPLICANT: Immune systems

TITLE OF INVENTION: CD4+ T-LYMPHOCYTE-SPECIFIC HEPATITIS C VIRUS-EPIPTOPES

FILE REFERENCE: 029474-5011

CURRENT APPLICATION NUMBER: US/10/397,411

PRIOR FILING DATE: 2003-03-26

PRIOR APPLICATION NUMBER: PCT/EP01/11263

PRIOR FILING DATE: 2001-09-28

PRIOR APPLICATION NUMBER: EP 00121138.2

PRIOR FILING DATE: 2000-09-28

NUMBER OF SEQ ID NOS: 21

SOFTWARE: Patentin version 3.2

SEQ ID NO 13

LENGTH: 20

TYPE: PRT

ORGANISM: Hepatitis C virus

US-10-397-411-13

Query Match 29.2% Score 28; DB 4; Length 20;  
Best Local Similarity 66.7%; Pred. No. 2.2e+03;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 LRTAAVSPG 17  
|||  
8 LRPALISPG 16

RESULT 72  
US-10-776-013-250

Sequence 250, Application US/10776013

Publication No. US20040226056A1

GENERAL INFORMATION:

APPLICANT: MYRIAD GENETICS, INC.

APPLICANT: Roch, Jean-Marc

APPLICANT: Bartel, Paul

APPLICANT: Heichman, Karen

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING NEUROLOGICAL DISORDERS AND

FILE REFERENCE: 1600.24

CURRENT APPLICATION NUMBER: US/10/776,013

PRIOR FILING DATE: 2004-02-09

PRIOR APPLICATION NUMBER: 09/948904

PRIOR FILING DATE: 2001-09-10

PRIOR APPLICATION NUMBER: 09/466139

PRIOR FILING DATE: 1999-12-21

PRIOR APPLICATION NUMBER: 60/113534

PRIOR FILING DATE: 1998-12-22

PRIOR APPLICATION NUMBER: 60/124120

PRIOR FILING DATE: 1999-03-12

PRIOR APPLICATION NUMBER: 60/141243

PRIOR FILING DATE: 1999-06-30

PRIOR APPLICATION NUMBER: 09/975072

PRIOR FILING DATE: 2001-10-12

PRIOR APPLICATION NUMBER: 60/240790

PRIOR FILING DATE: 2000-10-17

PRIOR APPLICATION NUMBER: 10/194967

PRIOR FILING DATE: 2002-07-15

PRIOR APPLICATION NUMBER: 60/304775

PRIOR FILING DATE: 2001-07-13

NUMBER OF SEQ ID NOS: 695

SOFTWARE: Patentin version 3.2

SEQ ID NO 250

LENGTH: 20

TYPE: PRT

ORGANISM: Homo sapiens

US-10-776-013-250

Query Match 29.2% Score 28; DB 5; Length 20;  
Best Local Similarity 41.7%; Pred. No. 2.2e+03;  
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 5 PHGYLTAASP 16  
| | | | |  
DB 2 PRRYTAALSP 13

RESULT 73  
US-10-881-453-18  
; Sequence 18, Application US/10881453  
; Publication No. US20040241143A1  
; GENERAL INFORMATION:  
; APPLICANT: Chisari, Francis V.  
; TITLE OF INVENTION: Peptides for Inducing Cytotoxic T Lymphocyte Responses to  
; TITLE OF INVENTION: Hepatitis B Virus  
; FILE REFERENCE: EPI-T101D5  
; CURRENT APPLICATION NUMBER: US/10/881,453  
; PRIOR FILING DATE: 2004-06-29  
; PRIOR APPLICATION NUMBER: 09/863,054  
; PRIOR FILING DATE: 2001-05-21  
; PRIOR APPLICATION NUMBER: 08/463,486  
; PRIOR FILING DATE: 1995-06-05  
; PRIOR APPLICATION NUMBER: 08/396,283  
; PRIOR FILING DATE: 1995-02-27  
; PRIOR APPLICATION NUMBER: 08/024,120  
; PRIOR FILING DATE: 1993-02-26  
; PRIOR APPLICATION NUMBER: 07/935,898  
; PRIOR FILING DATE: 1992-08-26  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 18  
; LENGTH: 20  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: HBC50-69  
US-10-881-453-18

Query Match 29.2%; Score 28; DB 5; Length 20;  
Best Local Similarity 50.0%; Pred. No. 2.2e+03;  
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 5 PHGYLTAASP 14  
| | | | |  
DB 1 PHHYALRQAI 10

RESULT 74  
US-10-621-675-446  
; Sequence 446, Application US/10621675  
; Publication No. US20050049398A1  
; GENERAL INFORMATION:  
; APPLICANT: De Iers, Robert  
; TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES CORRESPONDING  
; TITLE OF INVENTION: TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THEIR USE IN  
; TITLE OF INVENTION: A BIOTINYLATED PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT  
; TITLE OF INVENTION: EPITOPES, A PROCESS FOR PREPARING THEM AND COMPOSITIONS  
; TITLE OF INVENTION: CONTAINING THEM  
; FILE REFERENCE: 2752-11  
; CURRENT APPLICATION NUMBER: US/10/621,675  
; PRIOR FILING DATE: 2003-07-18  
; PRIOR APPLICATION NUMBER: US/09/576,824A  
; PRIOR FILING DATE: 1996-09-30  
; PRIOR APPLICATION NUMBER: 08/723,425  
; PRIOR FILING DATE: 1996-09-30  
; PRIOR APPLICATION NUMBER: 09/146,028  
; PRIOR FILING DATE: 1993-11-22  
; PRIOR APPLICATION NUMBER: PCT/EP93/00517  
; PRIOR FILING DATE: 1993-03-08  
; PRIOR APPLICATION NUMBER: EP 92400598.6  
; PRIOR FILING DATE: 1992-03-06  
; NUMBER OF SEQ ID NOS: 600  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 446

; LENGTH: 20  
; TYPE: PRT  
; ORGANISM: Hepatitis C virus  
US-10-621-675-446

Query Match 29.2%; Score 28; DB 5; Length 20;  
Best Local Similarity 66.7%; Pred. No. 2.2e+03;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 LITAAVSPG 17  
| | | | |  
DB 10 LHPALSPG 18

RESULT 75  
US-10-931-566-22  
; Sequence 22, Application US/10931566  
; Publication No. US20050106137A1  
; GENERAL INFORMATION:  
; APPLICANT: Aphon Corporation  
; APPLICANT: Grimes, Stephen  
; TITLE OF INVENTION: Chimeric Peptide Immunogens  
; FILE REFERENCE: 1102865-0047CIP  
; CURRENT APPLICATION NUMBER: US/10/931,566  
; PRIOR FILING DATE: 2004-08-31  
; PRIOR APPLICATION NUMBER: 09/848,834  
; PRIOR FILING DATE: 2001-05-04  
; PRIOR APPLICATION NUMBER: 60/202,328  
; PRIOR FILING DATE: 2000-05-05  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 22  
; LENGTH: 20  
; TYPE: PRT  
; ORGANISM: Hepatitis B virus  
US-10-931-566-22

Query Match 29.2%; Score 28; DB 5; Length 20;  
Best Local Similarity 50.0%; Pred. No. 2.2e+03;  
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 5 PHGYLTAASP 14  
| | | | |  
DB 1 PHHYALRQAI 10

RESULT 76  
US-11-068-710-18  
; Sequence 18, Application US/11068710  
; Publication No. US20050232935A1  
; GENERAL INFORMATION:  
; APPLICANT: Chisari, Francis V.  
; TITLE OF INVENTION: Peptides for Inducing Cytotoxic T Lymphocyte Responses to  
; TITLE OF INVENTION: Hepatitis B Virus  
; FILE REFERENCE: EPI-T101D5  
; CURRENT APPLICATION NUMBER: US/11/068,710  
; PRIOR FILING DATE: 2005-02-28  
; PRIOR APPLICATION NUMBER: US/10/861,453  
; PRIOR FILING DATE: 2004-06-29  
; PRIOR APPLICATION NUMBER: 09/863,054  
; PRIOR FILING DATE: 2001-05-21  
; PRIOR APPLICATION NUMBER: 08/463,486  
; PRIOR FILING DATE: 1995-06-05  
; PRIOR APPLICATION NUMBER: 08/396,283  
; PRIOR FILING DATE: 1995-02-27  
; PRIOR APPLICATION NUMBER: 08/024,120  
; PRIOR FILING DATE: 1993-02-26  
; PRIOR APPLICATION NUMBER: 07/935,898  
; PRIOR FILING DATE: 1992-08-26  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 18  
; LENGTH: 20

TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: HBC50-69  
US-11-068-710-18

Query Match 29.2%; Score 28; DB 6; Length 20;  
Best Local Similarity 50.0%; Pred. No. 2.2e+03;  
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 5 PHGYLTAAY 14  
DB 1 PHHYALRQAI 10

RESULT 77  
US-10-461-864-5  
Sequence 5, Application US/10461864  
Publication No. US20040208919A1  
GENERAL INFORMATION:  
APPLICANT: Nicotian, Yves Claude  
TITLE OF INVENTION: Vaccination Against Prion Diseases  
FILE REFERENCE: 49918-0123 (49918-286753)  
CURRENT APPLICATION NUMBER: US/10/461,864  
CURRENT FILING DATE: 2003-06-13  
PRIOR APPLICATION NUMBER: US 60/388,795  
PRIOR FILING DATE: 2002-06-13  
NUMBER OF SEQ ID NOS: 7  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 5  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic  
US-10-461-864-5

Query Match 28.1%; Score 27; DB 4; Length 9;  
Best Local Similarity 55.6%; Pred. No. 1.7e+06;  
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 7 GYLLTAAYS 15  
DB 1 GYMLGSAMS 9

RESULT 78  
US-09-747-287-215  
Sequence 215, Application US/09747287  
Publication No. US20030207264A1  
GENERAL INFORMATION:  
APPLICANT: KOMORIYA, AKIRA  
TITLE OF INVENTION: HOMO-DOUBLY LABELED COMPOSITIONS FOR THE DETECTION OF ENZYME  
FILE REFERENCE: 300-948600US  
CURRENT APPLICATION NUMBER: US/09/747,287  
CURRENT FILING DATE: 2000-12-22  
PRIOR APPLICATION NUMBER: US 09/349,019  
PRIOR FILING DATE: 1999-09-10  
PRIOR APPLICATION NUMBER: US08/802,981  
PRIOR FILING DATE: 1997-02-20  
PRIOR APPLICATION NUMBER: PCT/US00/24882  
PRIOR FILING DATE: 2000-09-11  
NUMBER OF SEQ ID NOS: 242  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 215  
LENGTH: 11  
TYPE: PRT  
ORGANISM: Artificial  
FEATURE:  
OTHER INFORMATION: Synthetic peptide. Artificial protease substrate.  
US-09-747-287-215

Query Match 28.1%; Score 27; DB 3; Length 11;  
Best Local Similarity 50.0%; Pred. No. 1.7e+03;  
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DAFEPHGY 8  
DB 4 DGIIDPKGY 11

RESULT 79  
US-09-874-350A-186  
Sequence 186, Application US/09874350A  
Publication No. US20040096926A1  
GENERAL INFORMATION:  
APPLICANT: Oncolmmunin, Inc.  
APPLICANT: Komoriya, Akira  
TITLE OF INVENTION: COMPOSITIONS FOR THE DETECTION OF ENZYME ACTIVITY IN BIOLOGICAL  
FILE REFERENCE: 300-903840US  
CURRENT APPLICATION NUMBER: US/09/874,350A  
CURRENT FILING DATE: 2001-06-04  
PRIOR APPLICATION NUMBER: PCT/US98/00300  
PRIOR FILING DATE: 1998-02-20  
PRIOR APPLICATION NUMBER: PCT/US00/24882  
PRIOR FILING DATE: 2000-09-11  
PRIOR APPLICATION NUMBER: US 09/394,019  
PRIOR FILING DATE: 1999-09-10  
PRIOR APPLICATION NUMBER: US 08/802,981  
PRIOR FILING DATE: 1997-02-20  
NUMBER OF SEQ ID NOS: 221  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 186  
LENGTH: 11  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic peptide substrate  
NAME/KEY: misc feature  
OTHER INFORMATION: Artificial = synthetic protease indicator  
NAME/KEY: MOD\_RES  
LOCATION: (9)-(9)  
OTHER INFORMATION: K is derivatized with fluorophore  
NAME/KEY: MOD\_RES  
LOCATION: (1)-(1)  
OTHER INFORMATION: D is derivatized with fluorophore  
US-09-874-350A-186

Query Match 28.1%; Score 27; DB 3; Length 11;  
Best Local Similarity 50.0%; Pred. No. 1.7e+03;  
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DAFEPHGY 8  
DB 4 DGIIDPKGY 11

RESULT 80  
US-10-014-340-731  
Sequence 731, Application US/10014340  
Publication No. US20030064411A1  
GENERAL INFORMATION:  
APPLICANT: Herath, et al  
TITLE OF INVENTION: Nucleic Acid Molecules, Polypeptides and Uses Therefor, Including  
FILE REFERENCE: 9195-078  
CURRENT APPLICATION NUMBER: US/10/014,340  
CURRENT FILING DATE: 2001-12-10  
NUMBER OF SEQ ID NOS: 823  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 731  
LENGTH: 11

TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-014-340-731

Query Match 28.1%; Score 27; DB 4; Length 11;  
Best Local Similarity 50.0%; Pred. No. 1.7e+03;  
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 FEBPGYL 10  
DB 2 FIPHGLIM 9

RESULT 81  
US-10-285-394-364  
Sequence 364, Application US/10285394  
Publication No. US20030228583A1  
GENERAL INFORMATION:  
APPLICANT: AMACHER, DAVID E.  
APPLICANT: PASULO, LISA M.  
APPLICANT: HERATH, HERATH MUDIYANSELAGE ATHULA CHANDRASIRI  
APPLICANT: HOLT, GORDON DUANE  
APPLICANT: STIGER, THOMAS R.  
TITLE OF INVENTION: BIOMARKERS OF LIVER RESPONSE  
FILE REFERENCE: POA-003.01  
CURRENT APPLICATION NUMBER: US/10/285,394  
CURRENT FILING DATE: 2003-02-07  
PRIOR APPLICATION NUMBER: 60/335,964  
PRIOR FILING DATE: 2001-10-31  
NUMBER OF SEQ ID NOS: 412  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 364  
LENGTH: 11  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-285-394-364

Query Match 28.1%; Score 27; DB 4; Length 11;  
Best Local Similarity 50.0%; Pred. No. 1.7e+03;  
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 FEBPGYL 10  
DB 2 FIPHGLIM 9

RESULT 82  
US-10-468-543-79  
Sequence 79, Application US/10468543  
Publication No. US20040091938A1  
GENERAL INFORMATION:  
APPLICANT: Irimura, Tetsuro  
APPLICANT: Matsumoto, Mariko  
APPLICANT: Yim, Mijung  
APPLICANT: Ono, Takashi  
TITLE OF INVENTION: Lectins for Analyzing Sugar Chains and Method of Using the Same  
FILE REFERENCE: 03-786  
CURRENT APPLICATION NUMBER: US/10/468,543  
CURRENT FILING DATE: 2003-08-20  
PRIOR APPLICATION NUMBER: JP 2001-044221  
PRIOR FILING DATE: 2001-02-20  
NUMBER OF SEQ ID NOS: 95  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 79  
LENGTH: 11  
TYPE: PRT  
ORGANISM: Artificial  
FEATURE:  
OTHER INFORMATION: Generated from randomly recombinant DNA part of MAH.  
US-10-468-543-79

Query Match 28.1%; Score 27; DB 4; Length 11;  
Best Local Similarity 57.1%; Pred. No. 1.7e+03;

Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DAFEPHG 7  
DB 1 DTYLPHG 7

RESULT 83  
US-09-486-734A-28  
Sequence 28, Application US/09486734A  
Patent No. US20020164732A1  
GENERAL INFORMATION:  
APPLICANT: Chopin, Marie-Christine  
APPLICANT: Clier, Florence  
APPLICANT: Erlich, S. Dusko  
APPLICANT: Gautier, Michel  
APPLICANT: Schouler, Catherine  
TITLE OF INVENTION: Institut National de la Recherche Agronomique  
TITLE OF INVENTION: Resistance Mechanisms to  $\alpha$  Type R/M  
FILE REFERENCE: 33339/196048  
CURRENT APPLICATION NUMBER: US/09/486,734A  
CURRENT FILING DATE: 2000-05-03  
PRIOR APPLICATION NUMBER: PCT/FR98/01873  
PRIOR FILING DATE: 1998-09-01  
PRIOR APPLICATION NUMBER: FR 97/10885  
PRIOR FILING DATE: 1997-09-02  
NUMBER OF SEQ ID NOS: 40  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 28  
LENGTH: 12  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Hcdm subunit  
US-09-486-734A-28

Query Match 28.1%; Score 27; DB 3; Length 12;  
Best Local Similarity 55.6%; Pred. No. 1.8e+03;  
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 PHGYLTTAA 13  
DB 2 PHGVLPFGA 10

RESULT 84  
US-09-929-266-13  
Sequence 13, Application US/09929266  
Publication No. US20030045594A1  
GENERAL INFORMATION:  
APPLICANT: Brian T. Chait  
APPLICANT: Datin R. Latimer  
APPLICANT: Paul M. Lizaradi  
APPLICANT: Eric R. Kershner  
APPLICANT: Jon S. Morrow  
APPLICANT: Matthew E. Roch  
APPLICANT: Martin J. McConnell  
TITLE OF INVENTION: ULTRA-SENSITIVE DETECTION SYSTEMS  
FILE REFERENCE: 01173\_000302  
CURRENT APPLICATION NUMBER: US/09/929,266  
CURRENT FILING DATE: 2001-08-13  
PRIOR APPLICATION NUMBER: 60/224,939  
PRIOR FILING DATE: 2000-08-11  
PRIOR APPLICATION NUMBER: 60/283,498  
PRIOR FILING DATE: 2000-04-12  
NUMBER OF SEQ ID NOS: 33  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 13  
LENGTH: 12  
TYPE: PRT  
ORGANISM: Artificial Sequence



```
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence; No. US20030045694A1e=synthetic
/ OTHER INFORMATION: construct
US-09-929-266-13

Query Match      28.1%; Score 27; DB 3; Length 12;
Best Local Similarity 40.0%; Pred. No. 1.8e+03;
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY      8 YLTAIVSPG 17
      | : | : |
      1 YFMTSGCDPG 10

Db

RESULT 85
US-09-747-287-216
/ Sequence 216, Application US/09747287
/ Publication No. US20030207264A1
/ GENERAL INFORMATION:
/ APPLICANT: KOMORIYA, AKIRA
/ APPLICANT: KOMORIYA, AKIRA
/ TITLE OF INVENTION: HOMO-DOUBLY LABELED COMPOSITIONS FOR THE DETECTION OF ENZYME
/ FILE REFERENCE: 300-948600US
/ CURRENT APPLICATION NUMBER: US/09/747,287
/ CURRENT FILING DATE: 2000-12-22
/ PRIOR APPLICATION NUMBER: US 09/349,019
/ PRIOR FILING DATE: 1999-09-10
/ PRIOR APPLICATION NUMBER: US08/802,981
/ PRIOR FILING DATE: 1997-02-20
/ PRIOR APPLICATION NUMBER: PCT/US00/24882
/ PRIOR FILING DATE: 2000-09-11
/ NUMBER OF SEQ ID NOS: 242
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 216
/ LENGTH: 12
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: Synthetic peptide.
US-09-747-287-216

Query Match      28.1%; Score 27; DB 3; Length 12;
Best Local Similarity 50.0%; Pred. No. 1.8e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      1 DAFEPHGY 8
      | : | : |
      5 DGIDPKGY 12

Db

RESULT 86
US-09-874-350A-187
/ Sequence 187, Application US/09874350A
/ Publication No. US20040096926A1
/ GENERAL INFORMATION:
/ APPLICANT: Oncolmmunln, Inc.
/ APPLICANT: Komoriya, Akira
/ APPLICANT: Packard, Beverly
/ TITLE OF INVENTION: COMPOSITIONS FOR THE DETECTION OF ENZYME ACTIVITY IN BIOLOGICAL S
/ TITLE OF INVENTION: AND METHODS OF USE THEREOF
/ FILE REFERENCE: 300-903840US
/ CURRENT APPLICATION NUMBER: US/09/874,350A
/ CURRENT FILING DATE: 2001-06-04
/ PRIOR APPLICATION NUMBER: PCT/US96/00300
/ PRIOR FILING DATE: 1998-02-20
/ PRIOR APPLICATION NUMBER: PCT/US00/24882
/ PRIOR FILING DATE: 2000-09-11
/ PRIOR APPLICATION NUMBER: US 09/394,019
/ PRIOR FILING DATE: 1999-09-10
/ PRIOR APPLICATION NUMBER: US 08/802,981
/ PRIOR FILING DATE: 1997-02-20
/ NUMBER OF SEQ ID NOS: 221
```

```
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 187
/ LENGTH: 12
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Synthetic peptide substrate
/ NAME/KEY: misc:feature
/ OTHER INFORMATION: Artificial = synthetic protease indicator
/ NAME/KEY: MOD.RES
/ LOCATION: (1)-(1)
/ OTHER INFORMATION: P is derivatized with fluorophore
/ NAME/KEY: MOD.RES
/ LOCATION: (10)-(10)
/ OTHER INFORMATION: K is derivatized with fluorophore
US-09-874-350A-187

Query Match      28.1%; Score 27; DB 3; Length 12;
Best Local Similarity 50.0%; Pred. No. 1.8e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      1 DAFEPHGY 8
      | : | : |
      5 DGIDPKGY 12

Db

RESULT 87
US-10-825-568-13
/ Sequence 13, Application US/10825568
/ Publication No. US20050069916A1
/ GENERAL INFORMATION:
/ APPLICANT: Brian T. Chait
/ APPLICANT: Darin R. Lattimer
/ APPLICANT: Paul M. Lizardi
/ APPLICANT: Eric R. Kershner
/ APPLICANT: Jon S. Morrow
/ APPLICANT: Matthew E. Roth
/ APPLICANT: Martin J. Matlessich
/ APPLICANT: Kevin J. McConnell
/ TITLE OF INVENTION: ULTRA-SENSITIVE DETECTION SYSTEMS
/ FILE REFERENCE: 01173.000302
/ CURRENT APPLICATION NUMBER: US/10/825,568
/ CURRENT FILING DATE: 2004-04-14
/ PRIOR APPLICATION NUMBER: US/09/929,266
/ PRIOR FILING DATE: 2001-08-13
/ PRIOR APPLICATION NUMBER: 60/224,939
/ PRIOR FILING DATE: 2000-08-11
/ PRIOR APPLICATION NUMBER: 60/283,498
/ PRIOR FILING DATE: 2000-04-12
/ NUMBER OF SEQ ID NOS: 33
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 13
/ LENGTH: 12
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence; Note=synthetic
US-10-825-568-13

Query Match      28.1%; Score 27; DB 5; Length 12;
Best Local Similarity 40.0%; Pred. No. 1.8e+03;
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY      8 YLTAIVSPG 17
      | : | : |
      1 YFMTSGCDPG 10

Db

RESULT 88
US-09-747-287-40
/ Sequence 40, Application US/09747287
/ Publication No. US20030207264A1
```

```
/ GENERAL INFORMATION:
/ APPLICANT: KOMORIYA, AKIRA
/ APPLICANT: PACKARD, BEVERLY S.
/ TITLE OF INVENTION: HOMO-DOUBLY LABELED COMPOSITIONS FOR THE DETECTION OF ENZYME
/ FILE REFERENCE: 300-948600US
/ CURRENT APPLICATION NUMBER: US/09/747,287
/ PRIOR FILING DATE: 2000-12-22
/ PRIOR APPLICATION NUMBER: US 09/349,019
/ PRIOR FILING DATE: 1999-09-10
/ PRIOR APPLICATION NUMBER: US08/802,981
/ PRIOR FILING DATE: 1997-02-20
/ PRIOR APPLICATION NUMBER: PCT/US00/24882
/ PRIOR FILING DATE: 2000-09-11
/ NUMBER OF SEQ ID NOS: 242
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 40
/ LENGTH: 13
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: Synthetic peptide.
US-09-747-287-40
```

```
Query Match      28.1%; Score 27; DB 3; Length 13;
Best Local Similarity 50.0%; Pred. No. 2e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      1 DAFEPHGY 8
      | : |||
DB      6 DGDIDPKGY 13
```

```
RESULT 89
US-09-747-287-41
/ Sequence 41, Application US/09747287
/ Publication No. US20030207264A1
/ GENERAL INFORMATION:
/ APPLICANT: KOMORIYA, AKIRA
/ APPLICANT: PACKARD, BEVERLY S.
/ TITLE OF INVENTION: HOMO-DOUBLY LABELED COMPOSITIONS FOR THE DETECTION OF ENZYME
/ FILE REFERENCE: 300-948600US
/ CURRENT APPLICATION NUMBER: US/09/747,287
/ PRIOR FILING DATE: 2000-12-22
/ PRIOR APPLICATION NUMBER: US 09/349,019
/ PRIOR FILING DATE: 1999-09-10
/ PRIOR APPLICATION NUMBER: US08/802,981
/ PRIOR FILING DATE: 1997-02-20
/ PRIOR APPLICATION NUMBER: PCT/US00/24882
/ PRIOR FILING DATE: 2000-09-11
/ NUMBER OF SEQ ID NOS: 242
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 41
/ LENGTH: 13
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: Synthetic peptide.
US-09-747-287-41
```

```
Query Match      28.1%; Score 27; DB 3; Length 13;
Best Local Similarity 50.0%; Pred. No. 2e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      1 DAFEPHGY 8
      | : |||
DB      6 DGDIDPKGY 13
```

```
RESULT 90
US-09-747-287-44
/ Sequence 44, Application US/09747287
```

```
/ Publication No. US20030207264A1
/ GENERAL INFORMATION:
/ APPLICANT: KOMORIYA, AKIRA
/ APPLICANT: PACKARD, BEVERLY S.
/ TITLE OF INVENTION: HOMO-DOUBLY LABELED COMPOSITIONS FOR THE DETECTION OF ENZYME
/ FILE REFERENCE: 300-948600US
/ CURRENT APPLICATION NUMBER: US/09/747,287
/ PRIOR FILING DATE: 2000-12-22
/ PRIOR APPLICATION NUMBER: US 09/349,019
/ PRIOR FILING DATE: 1999-09-10
/ PRIOR APPLICATION NUMBER: US08/802,981
/ PRIOR FILING DATE: 1997-02-20
/ PRIOR APPLICATION NUMBER: PCT/US00/24882
/ PRIOR FILING DATE: 2000-09-11
/ NUMBER OF SEQ ID NOS: 242
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 44
/ LENGTH: 13
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: Synthetic peptide.
US-09-747-287-44
```

```
Query Match      28.1%; Score 27; DB 3; Length 13;
Best Local Similarity 50.0%; Pred. No. 2e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      1 DAFEPHGY 8
      | : |||
DB      6 DGDIDPKGY 13
```

```
RESULT 91
US-09-747-287-50
/ Sequence 50, Application US/09747287
/ Publication No. US20030207264A1
/ GENERAL INFORMATION:
/ APPLICANT: KOMORIYA, AKIRA
/ APPLICANT: PACKARD, BEVERLY S.
/ TITLE OF INVENTION: HOMO-DOUBLY LABELED COMPOSITIONS FOR THE DETECTION OF ENZYME
/ FILE REFERENCE: 300-948600US
/ CURRENT APPLICATION NUMBER: US/09/747,287
/ PRIOR FILING DATE: 2000-12-22
/ PRIOR APPLICATION NUMBER: US 09/349,019
/ PRIOR FILING DATE: 1999-09-10
/ PRIOR APPLICATION NUMBER: US08/802,981
/ PRIOR FILING DATE: 1997-02-20
/ PRIOR APPLICATION NUMBER: PCT/US00/24882
/ PRIOR FILING DATE: 2000-09-11
/ NUMBER OF SEQ ID NOS: 242
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 50
/ LENGTH: 13
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: Synthetic peptide.
US-09-747-287-50
```

```
Query Match      28.1%; Score 27; DB 3; Length 13;
Best Local Similarity 50.0%; Pred. No. 2e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      1 DAFEPHGY 8
      | : |||
DB      6 DGDIDPKGY 13
```

```
RESULT 92
US-09-747-287-224
```

```
/ Sequence 224, Application US/09747287
/ Publication No. US20030207264A1
/ GENERAL INFORMATION:
/ APPLICANT: KOMORIYA, AKIRA
/ APPLICANT: PACKARD, BEVERLY S.
/ TITLE OF INVENTION: HOMO-DOUBLY LABELED COMPOSITIONS FOR THE DETECTION OF ENZYME
/ FILE REFERENCE: 300-948600US
/ CURRENT APPLICATION NUMBER: US/09/747,287
/ PRIOR FILING DATE: 2000-12-22
/ PRIOR APPLICATION NUMBER: US 09/349,019
/ PRIOR FILING DATE: 1999-09-10
/ PRIOR APPLICATION NUMBER: US08/802,981
/ PRIOR FILING DATE: 1997-02-20
/ PRIOR APPLICATION NUMBER: PCT/US00/24882
/ PRIOR FILING DATE: 2000-09-11
/ NUMBER OF SEQ ID NOS: 242
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 224
/ LENGTH: 13
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: Synthetic peptide.
US-09-747-287-224
```

```
Query Match      28.1% Score 27; DB 3; Length 13;
Best Local Similarity 50.0%; Pred. No. 2e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 1 DAEPRGY 8
DB 6 DGIDPRGY 13
```

```
RESULT 93
US-09-747-287-225
/ Sequence 225, Application US/09747287
/ Publication No. US20030207264A1
/ GENERAL INFORMATION:
/ APPLICANT: KOMORIYA, AKIRA
/ APPLICANT: PACKARD, BEVERLY S.
/ TITLE OF INVENTION: HOMO-DOUBLY LABELED COMPOSITIONS FOR THE DETECTION OF ENZYME
/ FILE REFERENCE: 300-948600US
/ CURRENT APPLICATION NUMBER: US/09/747,287
/ PRIOR FILING DATE: 2000-12-22
/ PRIOR APPLICATION NUMBER: US 09/349,019
/ PRIOR FILING DATE: 1999-09-10
/ PRIOR APPLICATION NUMBER: US08/802,981
/ PRIOR FILING DATE: 1997-02-20
/ PRIOR APPLICATION NUMBER: PCT/US00/24882
/ PRIOR FILING DATE: 2000-09-11
/ NUMBER OF SEQ ID NOS: 242
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 225
/ LENGTH: 13
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: Synthetic peptide.
US-09-747-287-225
```

```
Query Match      28.1% Score 27; DB 3; Length 13;
Best Local Similarity 50.0%; Pred. No. 2e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 1 DAEPRGY 8
DB 6 DGIDPRGY 13
```

RESULT 94

```
US-09-747-287-229
/ Sequence 229, Application US/09747287
/ Publication No. US20030207264A1
/ GENERAL INFORMATION:
/ APPLICANT: KOMORIYA, AKIRA
/ APPLICANT: PACKARD, BEVERLY S.
/ TITLE OF INVENTION: HOMO-DOUBLY LABELED COMPOSITIONS FOR THE DETECTION OF ENZYME
/ FILE REFERENCE: 300-948600US
/ CURRENT APPLICATION NUMBER: US/09/747,287
/ PRIOR FILING DATE: 2000-12-22
/ PRIOR APPLICATION NUMBER: US 09/349,019
/ PRIOR FILING DATE: 1999-09-10
/ PRIOR APPLICATION NUMBER: US08/802,981
/ PRIOR FILING DATE: 1997-02-20
/ PRIOR APPLICATION NUMBER: PCT/US00/24882
/ PRIOR FILING DATE: 2000-09-11
/ NUMBER OF SEQ ID NOS: 242
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 229
/ LENGTH: 13
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: Synthetic peptide.
US-09-747-287-229
```

```
Query Match      28.1% Score 27; DB 3; Length 13;
Best Local Similarity 50.0%; Pred. No. 2e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 1 DAEPRGY 8
DB 6 DGIDPRGY 13
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RESULT 95
US-09-747-287-230
/ Sequence 230, Application US/09747287
/ Publication No. US20030207264A1
/ GENERAL INFORMATION:
/ APPLICANT: KOMORIYA, AKIRA
/ APPLICANT: PACKARD, BEVERLY S.
/ TITLE OF INVENTION: HOMO-DOUBLY LABELED COMPOSITIONS FOR THE DETECTION OF ENZYME
/ FILE REFERENCE: 300-948600US
/ CURRENT APPLICATION NUMBER: US/09/747,287
/ PRIOR FILING DATE: 2000-12-22
/ PRIOR APPLICATION NUMBER: US 09/349,019
/ PRIOR FILING DATE: 1999-09-10
/ PRIOR APPLICATION NUMBER: US08/802,981
/ PRIOR FILING DATE: 1997-02-20
/ PRIOR APPLICATION NUMBER: PCT/US00/24882
/ PRIOR FILING DATE: 2000-09-11
/ NUMBER OF SEQ ID NOS: 242
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 230
/ LENGTH: 13
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: Synthetic peptide.
US-09-747-287-230
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Query Match      28.1% Score 27; DB 3; Length 13;
Best Local Similarity 50.0%; Pred. No. 2e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
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QY 1 DAEPRGY 8
DB 6 DGIDPRGY 13
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RESULT 96  
US-09-874-350A-6  
; Sequence 6, Application US/09874350A  
; Publication No. US20040096926A1  
; GENERAL INFORMATION:  
; APPLICANT: Oncoimmunin, Inc.  
; APPLICANT: Komoriya, Akira  
; APPLICANT: Packard, Beverly  
; TITLE OF INVENTION: COMPOSITIONS FOR THE DETECTION OF ENZYME ACTIVITY IN BIOLOGICAL S  
; FILE REFERENCE: 300-903840US  
; CURRENT APPLICATION NUMBER: US/09/874,350A  
; PRIOR FILING DATE: 2001-06-04  
; PRIOR APPLICATION NUMBER: PCT/US98/00300  
; PRIOR FILING DATE: 1998-02-20  
; PRIOR APPLICATION NUMBER: PCT/US00/24882  
; PRIOR FILING DATE: 2000-09-11  
; PRIOR APPLICATION NUMBER: US 09/394,019  
; PRIOR FILING DATE: 1999-09-10  
; PRIOR APPLICATION NUMBER: US 08/802,981  
; PRIOR FILING DATE: 1997-02-20  
; NUMBER OF SEQ ID NOS: 221  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 6  
; LENGTH: 13  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic peptide substrate  
; NAME/KEY: MOD\_RES  
; LOCATION: (3)..(3)  
; OTHER INFORMATION: X is Alb or Pro  
US-09-874-350A-6

Query Match 28.1%; Score 27; DB 3; Length 13;  
Best Local Similarity 50.0%; Pred. No. 2e+03;  
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DAFEPHG 8  
| : | | |  
DB 6 DGIIDPKGY 13

RESULT 97  
US-09-874-350A-7  
; Sequence 7, Application US/09874350A  
; Publication No. US20040096926A1  
; GENERAL INFORMATION:  
; APPLICANT: Oncoimmunin, Inc.  
; APPLICANT: Komoriya, Akira  
; APPLICANT: Packard, Beverly  
; TITLE OF INVENTION: COMPOSITIONS FOR THE DETECTION OF ENZYME ACTIVITY IN BIOLOGICAL S  
; FILE REFERENCE: 300-903840US  
; CURRENT APPLICATION NUMBER: US/09/874,350A  
; PRIOR FILING DATE: 2001-06-04  
; PRIOR APPLICATION NUMBER: PCT/US98/00300  
; PRIOR FILING DATE: 1998-02-20  
; PRIOR APPLICATION NUMBER: PCT/US00/24882  
; PRIOR FILING DATE: 2000-09-11  
; PRIOR APPLICATION NUMBER: US 09/394,019  
; PRIOR FILING DATE: 1999-09-10  
; PRIOR APPLICATION NUMBER: US 08/802,981  
; PRIOR FILING DATE: 1997-02-20  
; NUMBER OF SEQ ID NOS: 221  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 7  
; LENGTH: 13  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic peptide substrate  
; NAME/KEY: MOD\_RES  
; LOCATION: (3)..(3)  
; OTHER INFORMATION: X is Alb or Pro  
US-09-874-350A-7

; LOCATION: (4)..(4)  
; OTHER INFORMATION: X is Alb or Pro  
US-09-874-350A-7

Query Match 28.1%; Score 27; DB 3; Length 13;  
Best Local Similarity 50.0%; Pred. No. 2e+03;  
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DAFEPHG 8  
| : | | |  
DB 6 DGIIDPKGY 13

RESULT 98  
US-09-874-350A-10  
; Sequence 10, Application US/09874350A  
; Publication No. US20040096926A1  
; GENERAL INFORMATION:  
; APPLICANT: Oncoimmunin, Inc.  
; APPLICANT: Komoriya, Akira  
; APPLICANT: Packard, Beverly  
; TITLE OF INVENTION: COMPOSITIONS FOR THE DETECTION OF ENZYME ACTIVITY IN BIOLOGICAL S  
; FILE REFERENCE: 300-903840US  
; CURRENT APPLICATION NUMBER: US/09/874,350A  
; PRIOR FILING DATE: 2001-06-04  
; PRIOR APPLICATION NUMBER: PCT/US98/00300  
; PRIOR FILING DATE: 1998-02-20  
; PRIOR APPLICATION NUMBER: PCT/US00/24882  
; PRIOR FILING DATE: 2000-09-11  
; PRIOR APPLICATION NUMBER: US 09/394,019  
; PRIOR FILING DATE: 1999-09-10  
; PRIOR APPLICATION NUMBER: US 08/802,981  
; PRIOR FILING DATE: 1997-02-20  
; NUMBER OF SEQ ID NOS: 221  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 10  
; LENGTH: 13  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic peptide substrate  
; NAME/KEY: MOD\_RES  
; LOCATION: (1)..(1)  
; OTHER INFORMATION: BLOCKED with Fmoc  
; NAME/KEY: MOD\_RES  
; LOCATION: (3)..(3)  
; OTHER INFORMATION: X is Alb or Pro  
US-09-874-350A-10

Query Match 28.1%; Score 27; DB 3; Length 13;  
Best Local Similarity 50.0%; Pred. No. 2e+03;  
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DAFEPHG 8  
| : | | |  
DB 6 DGIIDPKGY 13

RESULT 99  
US-09-874-350A-16  
; Sequence 16, Application US/09874350A  
; Publication No. US20040096926A1  
; GENERAL INFORMATION:  
; APPLICANT: Oncoimmunin, Inc.  
; APPLICANT: Komoriya, Akira  
; APPLICANT: Packard, Beverly  
; TITLE OF INVENTION: COMPOSITIONS FOR THE DETECTION OF ENZYME ACTIVITY IN BIOLOGICAL S  
; FILE REFERENCE: 300-903840US  
; CURRENT APPLICATION NUMBER: US/09/874,350A  
; PRIOR FILING DATE: 2001-06-04  
; PRIOR APPLICATION NUMBER: PCT/US98/00300

/ PRIOR FILING DATE: 1998-02-20  
 / PRIOR APPLICATION NUMBER: PCT/US00/24882  
 / PRIOR FILING DATE: 2000-09-11  
 / PRIOR APPLICATION NUMBER: US 09/394,019  
 / PRIOR FILING DATE: 1999-09-10  
 / PRIOR APPLICATION NUMBER: US 08/802,981  
 / PRIOR FILING DATE: 1997-02-20  
 / NUMBER OF SEQ ID NOS: 221  
 / SOFTWARE: PatentIn version 3.0  
 / SEQ ID NO 16  
 / LENGTH: 13  
 / TYPE: PRT  
 / ORGANISM: Artificial Sequence  
 / FEATURE:  
 / OTHER INFORMATION: Synthetic peptide substrate  
 / NAME/KEY: MOD\_RES  
 / LOCATION: (1)..(1)  
 / OTHER INFORMATION: BLOCKED with Fmoc  
 US-09-874-350A-16

Query Match 28.1%; Score 27; DB 3; Length 13;  
 Best Local Similarity 50.0%; Pred. No. 2e+03;  
 Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DAFEPHGY 8  
 Db 6 DGIDPKCY 13

RESULT 100  
 US-09-874-350A-195  
 / Sequence 195, Application US/09874350A  
 / Publication No. US20040096926A1  
 / GENERAL INFORMATION:  
 / APPLICANT: Oncolmmunln, Inc.  
 / APPLICANT: Komoriya, Akira  
 / APPLICANT: Packard, Beverly  
 / TITLE OF INVENTION: COMPOSITIONS FOR THE DETECTION OF ENZYME ACTIVITY IN BIOLOGICAL S  
 / TITLE OF INVENTION: AND METHODS OF USE THEREOF  
 / FILE REFERENCE: 300-903840US  
 / CURRENT APPLICATION NUMBER: US/09/874,350A  
 / CURRENT FILING DATE: 2001-06-04  
 / PRIOR APPLICATION NUMBER: PCT/US98/00300  
 / PRIOR FILING DATE: 1998-02-20  
 / PRIOR APPLICATION NUMBER: PCT/US00/24882  
 / PRIOR FILING DATE: 2000-09-11  
 / PRIOR APPLICATION NUMBER: US 09/394,019  
 / PRIOR FILING DATE: 1999-09-10  
 / PRIOR APPLICATION NUMBER: US 08/802,981  
 / PRIOR FILING DATE: 1997-02-20  
 / NUMBER OF SEQ ID NOS: 221  
 / SOFTWARE: PatentIn version 3.0  
 / SEQ ID NO 195  
 / LENGTH: 13  
 / TYPE: PRT  
 / ORGANISM: Artificial Sequence  
 / FEATURE:  
 / OTHER INFORMATION: Synthetic peptide substrate  
 / NAME/KEY: misc feature  
 / OTHER INFORMATION: ARTIFICIAL/UNKNOWN = synthetic protease indicator  
 / NAME/KEY: MOD\_RES  
 / LOCATION: (1)..(1)  
 / OTHER INFORMATION: K 1s blocked with Fmoc  
 / LOCATION: (11)..(11)  
 / OTHER INFORMATION: K 1s derivatized with fluorophore  
 US-09-874-350A-195

Query Match 28.1%; Score 27; DB 3; Length 13;  
 Best Local Similarity 50.0%; Pred. No. 2e+03;  
 Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DAFEPHGY 8

Db 6 DGIDPKCY 13

Search completed: January 20, 2006, 19:45:43  
 Job time : 66.9038 secs

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OM protein - protein search, using sw model

Run on: January 20, 2006, 19:12:21 ; Search time 7.26923 Seconds

(without alignments)  
25.093 Million cell updates/sec

Title: US-09-662-293-6

Perfect score: 96

Sequence: 1 DAFEPHYLTAVSPEK 18

Scoring table: BLOSUM62

Searched: Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 34662

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Maximum Match 100%

Listing first 100 summaries

Database : Published Applications AA New:  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31	32.3	18	6	US-10-939-890-133
2	28	29.2	16	7	US-11-134-046-10
3	27	28.1	19	6	US-10-503-575-224
4	26	27.1	14	7	US-11-054-515-2400
5	26	27.1	14	7	US-11-054-515-2477
6	26	27.1	14	7	US-11-144-630-33
7	25.5	26.6	15	7	US-11-045-024-13324
8	25.5	26.6	15	7	US-11-045-024-13327
9	25	26.0	9	7	US-11-062-186-2
10	25	26.0	9	7	US-11-045-024-3531
11	25	26.0	9	7	US-11-045-024-10473
12	25	26.0	10	7	US-11-045-024-12303
13	25	26.0	9	7	US-11-045-024-3546
14	25	26.0	10	7	US-11-045-024-10479
15	25	26.0	11	7	US-11-045-024-12307
16	25	26.0	11	7	US-11-045-024-3559
17	25	26.0	11	7	US-11-045-024-10483
18	25	26.0	11	7	US-11-045-024-12311
19	25	26.0	15	7	US-11-041-893-2
20	25	26.0	15	7	US-11-041-893-13
21	25	26.0	20	6	US-10-939-890-138
22	25	26.0	20	6	US-10-623-155-247
23	25	26.0	20	7	US-11-022-562-292
24	25	26.0	20	7	US-11-022-562-293
25	25	26.0	20	7	US-11-043-542-42

26	24	25.0	9	7	US-11-152-747-35	Sequence 35, App1
27	24	25.0	11	7	US-11-054-515-3192	Sequence 3192, Ap
28	24	25.0	11	7	US-11-158-723-7	Sequence 7, App1
29	24	25.0	12	6	US-10-507-662-53	Sequence 53, App1
30	24	25.0	14	7	US-11-054-515-2602	Sequence 2602, Ap
31	24	25.0	15	7	US-11-054-515-2909	Sequence 2909, Ap
32	24	25.0	16	6	US-10-467-657-9074	Sequence 9074, Ap
33	24	25.0	16	6	US-10-467-657-9075	Sequence 9075, Ap
34	24	25.0	20	7	US-11-022-562-176	Sequence 176, App
35	24	25.0	20	7	US-11-128-900-1118	Sequence 118, App
36	24	25.0	20	7	US-11-128-900-1119	Sequence 119, App
37	24	25.0	20	7	US-11-128-900-121	Sequence 121, App
38	24	25.0	20	7	US-11-128-900-122	Sequence 122, App
39	24	25.0	20	7	US-11-128-900-123	Sequence 123, App
40	24	25.0	20	7	US-11-128-900-124	Sequence 124, App
41	24	25.0	20	7	US-11-128-900-125	Sequence 125, App
42	23	24.0	8	6	US-10-859-643-31	Sequence 31, App1
43	23	24.0	9	6	US-10-859-643-31	Sequence 31, App1
44	23	24.0	9	6	US-10-859-643-115	Sequence 115, App
45	23	24.0	9	6	US-10-859-643-698	Sequence 698, App
46	23	24.0	9	7	US-11-097-864-31	Sequence 31, App1
47	23	24.0	9	7	US-11-097-864-115	Sequence 115, App
48	23	24.0	9	7	US-11-097-864-698	Sequence 698, App
49	23	24.0	9	7	US-11-097-812-31	Sequence 31, App1
50	23	24.0	9	7	US-11-097-812-115	Sequence 115, App
51	23	24.0	9	7	US-11-097-812-698	Sequence 698, App
52	23	24.0	10	6	US-10-859-643-100	Sequence 100, App
53	23	24.0	10	6	US-10-859-643-433	Sequence 433, App
54	23	24.0	10	6	US-10-859-643-619	Sequence 619, App
55	23	24.0	10	7	US-11-097-864-100	Sequence 100, App
56	23	24.0	10	7	US-11-097-864-433	Sequence 433, App
57	23	24.0	10	7	US-11-097-864-619	Sequence 619, App
58	23	24.0	10	7	US-11-097-912-100	Sequence 100, App
59	23	24.0	10	7	US-11-097-912-433	Sequence 433, App
60	23	24.0	10	7	US-11-097-912-619	Sequence 619, App
61	23	24.0	13	6	US-10-511-559-637	Sequence 637, App
62	23	24.0	14	7	US-10-866-671-14	Sequence 14, App1
63	23	24.0	14	7	US-11-054-515-2916	Sequence 2916, App
64	23	24.0	14	7	US-11-073-347-116	Sequence 116, App
65	23	24.0	15	7	US-11-022-562-35	Sequence 35, App1
66	23	24.0	15	7	US-11-073-347-110	Sequence 110, App
67	23	24.0	15	7	US-11-045-024-13033	Sequence 13033, A
68	23	24.0	15	7	US-11-045-024-13034	Sequence 13034, A
69	23	24.0	15	7	US-11-045-024-13046	Sequence 13046, A
70	23	24.0	15	7	US-11-045-024-14210	Sequence 14210, A
71	23	24.0	15	7	US-11-045-024-14400	Sequence 14400, A
72	23	24.0	15	7	US-11-045-024-14417	Sequence 14417, A
73	23	24.0	15	7	US-11-045-024-14477	Sequence 14477, A
74	23	24.0	15	7	US-11-033-039-581	Sequence 581, App
75	23	24.0	15	7	US-11-041-893-176	Sequence 176, App
76	23	24.0	16	7	US-11-033-039-839	Sequence 839, App
77	23	24.0	17	7	US-11-073-347-118	Sequence 118, App
78	23	24.0	18	7	US-11-033-039-993	Sequence 993, App
79	23	24.0	18	7	US-11-033-039-1048	Sequence 1048, App
80	23	24.0	19	7	US-11-054-515-3036	Sequence 3036, App
81	23	24.0	20	7	US-11-022-562-287	Sequence 287, App
82	23	24.0	20	7	US-11-022-562-286	Sequence 286, App
83	22.5	23.4	11	7	US-11-045-024-3558	Sequence 3558, App
84	22.5	23.4	11	7	US-11-045-024-10541	Sequence 10541, A
85	22.5	23.4	11	7	US-11-045-024-12349	Sequence 12349, A
86	22.5	23.4	15	7	US-11-045-024-13314	Sequence 13314, A
87	22.5	23.4	19	6	US-10-503-575-197	Sequence 197, App
88	22	22.9	8	7	US-11-045-024-1035	Sequence 1035, App
89	22	22.9	8	7	US-11-045-024-3518	Sequence 3518, App
90	22	22.9	8	7	US-11-045-024-4007	Sequence 4007, App
91	22	22.9	8	7	US-11-045-024-6362	Sequence 6362, App
92	22	22.9	8	7	US-11-045-024-10522	Sequence 10522, App
93	22	22.9	8	7	US-11-045-024-12335	Sequence 12335, A
94	22	22.9	8	7	US-11-045-024-12616	Sequence 12616, A
95	22	22.9	8	7	US-11-116-144-73	Sequence 73, App1
96	22	22.9	9	6	US-10-999-866-60	Sequence 60, App1
97	22	22.9	9	7	US-11-045-024-1138	Sequence 1138, App
98	22	22.9	9	7	US-11-045-024-3530	Sequence 3530, App

99 22 22.9 9 7 US-11-045-024-4061 Sequence 4061, Ap  
100 22 22.9 9 7 US-11-045-024-5639 Sequence 5639, Ap

## ALIGNMENTS

## RESULT 1

US-10-939-890-133  
Sequence 133, Application US/10939890  
Publication No. US20050250700A1  
GENERAL INFORMATION:  
APPLICANT: Sato, Aaron K.  
APPLICANT: Sexton, Daniel J.  
APPLICANT: Dransfield, Daniel T.  
APPLICANT: Ladner, Robert C.  
APPLICANT: Arbogast, Christophe  
APPLICANT: Bussat, Philippe  
APPLICANT: Fan, Hong  
APPLICANT: Khurana, Sudha  
APPLICANT: Linder, Karen B.  
APPLICANT: Marinelli, Edmund R.  
APPLICANT: Nanjappa, Palaniappa  
APPLICANT: Nunn, Adrian D.  
APPLICANT: Pillai, Radhakrishna  
APPLICANT: Pochon, Sibylle  
APPLICANT: Ramalingam, Kondareddiar  
APPLICANT: Shrivastava, Ajay  
APPLICANT: Song, Bo  
APPLICANT: Swenson, Rolf E.  
APPLICANT: Von Wronski, Mathew A.  
TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES  
FILE REFERENCE: D0617,70014US00  
CURRENT APPLICATION NUMBER: US/10/939,890  
CURRENT FILING DATE: 2004-09-13  
PRIOR APPLICATION NUMBER: US 10/661,156  
PRIOR FILING DATE: 2003-09-11  
PRIOR APPLICATION NUMBER: US 10/382,082  
PRIOR FILING DATE: 2003-03-03  
PRIOR APPLICATION NUMBER: PCT/US03/06731  
PRIOR FILING DATE: 2003-03-03  
PRIOR APPLICATION NUMBER: US 60/440,411  
PRIOR FILING DATE: 2003-01-15  
PRIOR APPLICATION NUMBER: US 60/360,851  
PRIOR FILING DATE: 2002-03-01  
NUMBER OF SEQ ID NOS: 883  
SOFTWARE: PatSeq for Windows Version 4.0  
SEQ ID NO 133  
LENGTH: 18  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Library Isolate  
US-10-939-890-133

Query Match 32.3%; Score 31; DB 6; Length 18;  
Best Local Similarity 55.6%; Pred. No. 19;  
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 PEPHYLIT 11  
:|:|:|:|

Db 6 YEDHTYMLT 14

## RESULT 2

US-11-134-046-10  
Sequence 10, Application US/11134046  
Publication No. US20050266467A1  
GENERAL INFORMATION:  
APPLICANT: Roy, Susmita  
TITLE OF INVENTION: BLOWMERS FOR MULTIPLE SCLEROSIS AND METHODS OF USE THEREOF  
FILE REFERENCE: 4220-103  
CURRENT APPLICATION NUMBER: US/11/134,046

CURRENT FILING DATE: 2005-05-19  
PRIOR APPLICATION NUMBER: 60/572,655  
PRIOR FILING DATE: 2004-05-19  
NUMBER OF SEQ ID NOS: 26  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 10  
LENGTH: 16  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-11-134-046-10

Query Match 29.2%; Score 28; DB 7; Length 16;  
Best Local Similarity 42.9%; Pred. No. 52;  
Matches 6; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 5 PPHYLITAVSPCK 18  
:|:|:|:|

Db 2 PYSYSTAVVTMPK 15

## RESULT 3

US-10-503-575-224  
Sequence 224, Application US/10503575  
Publication No. US20050244823A1  
GENERAL INFORMATION:  
APPLICANT: Driffoht, Jan Mouter  
APPLICANT: van Veele, Petrus Antonius  
APPLICANT: Konig, Fritz  
TITLE OF INVENTION: NOVEL EPITOPES FOR CELIAC DISEASE AND AUTOIMMUNE DISEASES, METHOD  
TITLE OF INVENTION: DETECTING THOSE AND NOVEL NON-ANTIGENIC FOOD COMPOUNDS  
FILE REFERENCE: 2799/72843-PCT-US  
CURRENT APPLICATION NUMBER: US/10/503,575  
CURRENT FILING DATE: 2004-08-04  
PRIOR APPLICATION NUMBER: PCT/NL03/00077  
PRIOR FILING DATE: 2003-02-04  
PRIOR APPLICATION NUMBER: EP 02075456.0  
PRIOR FILING DATE: 2002-02-04  
NUMBER OF SEQ ID NOS: 340  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 224  
LENGTH: 19  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-503-575-224

Query Match 28.1%; Score 27; DB 6; Length 19;  
Best Local Similarity 50.0%; Pred. No. 93;  
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 BPHYLIT 11  
:|:|:|:|

Db 1 BEYGIYV 8

## RESULT 4

US-11-054-515-2400  
Sequence 2400, Application US/11054515  
Publication No. US20050255532A1  
GENERAL INFORMATION:  
APPLICANT: Ruben et al.  
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys  
FILE REFERENCE: PF52393  
CURRENT APPLICATION NUMBER: US/11/054,515  
CURRENT FILING DATE: 2005-02-10  
PRIOR APPLICATION NUMBER: 60/543,296  
PRIOR FILING DATE: 2004-02-11  
PRIOR APPLICATION NUMBER: 60/580,347  
PRIOR FILING DATE: 2004-06-18  
PRIOR APPLICATION NUMBER: 10/293,418  
PRIOR FILING DATE: 2002-11-14  
PRIOR APPLICATION NUMBER: 60/331,469  
PRIOR FILING DATE: 2001-11-16  
PRIOR APPLICATION NUMBER: 60/340,817



```
/ PRIOR FILING DATE: 2001-12-19
/ PRIOR APPLICATION NUMBER: 09/880,748
/ PRIOR FILING DATE: 2001-06-15
/ PRIOR APPLICATION NUMBER: 60/293,499
/ PRIOR FILING DATE: 2001-05-25
/ PRIOR APPLICATION NUMBER: 60/277,379
/ PRIOR FILING DATE: 2001-03-21
/ PRIOR APPLICATION NUMBER: 60/276,248
/ PRIOR FILING DATE: 2001-03-16
/ PRIOR APPLICATION NUMBER: 60/240,816
/ PRIOR FILING DATE: 2000-10-17
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 3247
/ SEQ ID NO 2400
/ LENGTH: 14
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-054-515-2400
```

```
Query Match      27.1% Score 26; DB 7; Length 14;
Best Local Similarity 83.3%; Pred. No. 97;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      5 PHGYL 10
      |||||
DB      8 PHGPL 13
```

```
RESULT 5
US-11-054-515-2477
/ Sequence 2477, Application US/11054515
/ Publication No. US2005025532A1
/ GENERAL INFORMATION:
/ APPLICANT: Ruben et al.
/ TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
/ FILE REFERENCE: PF523P3
/ CURRENT APPLICATION NUMBER: US/11/054,515
/ CURRENT FILING DATE: 2005-02-10
/ PRIOR APPLICATION NUMBER: 60/543,296
/ PRIOR FILING DATE: 2004-02-11
/ PRIOR APPLICATION NUMBER: 60/580,347
/ PRIOR FILING DATE: 2004-06-18
/ PRIOR APPLICATION NUMBER: 10/293,418
/ PRIOR FILING DATE: 2002-11-14
/ PRIOR APPLICATION NUMBER: 60/331,469
/ PRIOR FILING DATE: 2001-11-16
/ PRIOR APPLICATION NUMBER: 60/340,817
/ PRIOR FILING DATE: 2001-12-19
/ PRIOR APPLICATION NUMBER: 09/880,748
/ PRIOR FILING DATE: 2001-06-15
/ PRIOR APPLICATION NUMBER: 60/293,499
/ PRIOR FILING DATE: 2001-05-25
/ PRIOR APPLICATION NUMBER: 60/277,379
/ PRIOR FILING DATE: 2001-03-21
/ PRIOR APPLICATION NUMBER: 60/276,248
/ PRIOR FILING DATE: 2001-03-16
/ PRIOR APPLICATION NUMBER: 60/240,816
/ PRIOR FILING DATE: 2000-10-17
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 3247
/ SEQ ID NO 2477
/ LENGTH: 14
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-054-515-2477
```

```
Query Match      27.1% Score 26; DB 7; Length 14;
Best Local Similarity 80.0%; Pred. No. 97;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      5 PHGYL 9
      |||||
DB      8 PHSYL 12
```

```
RESULT 6
US-11-144-630-33
/ Sequence 33, Application US/11144630
/ Publication No. US20060010517A1
/ GENERAL INFORMATION:
/ APPLICANT: KALEEN, ZHONGYILI
/ APPLICANT: MORELL, MATTHEW
/ APPLICANT: RAHMAN, SADEOUR
/ TITLE OF INVENTION: REGULATION OF GENE EXPRESSION IN PLANTS
/ FILE REFERENCE: 054270/0126
/ CURRENT APPLICATION NUMBER: US/11/144,630
/ CURRENT FILING DATE: 2005-06-06
/ PRIOR APPLICATION NUMBER: US/09/508,377
/ PRIOR FILING DATE: 2000-06-09
/ PRIOR APPLICATION NUMBER: AU PP 2509
/ PRIOR FILING DATE: 1998-03-20
/ PRIOR APPLICATION NUMBER: PCT/AU98/00743
/ PRIOR FILING DATE: 1998-09-11
/ PRIOR APPLICATION NUMBER: AU PP 9108
/ PRIOR FILING DATE: 1997-09-12
/ NUMBER OF SEQ ID NOS: 71
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 33
/ LENGTH: 20
/ TYPE: PRT
/ ORGANISM: Trifolium trautschii
US-11-144-630-33
```

```
Query Match      27.1% Score 26; DB 7; Length 20;
Best Local Similarity 83.3%; Pred. No. 1,4e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      13 AVSPGK 18
      |||||
DB      1 AASPGK 6
```

```
RESULT 7
US-11-045-024-13324
/ Sequence 13324, Application US/11045024
/ Publication No. US20050271676A1
/ GENERAL INFORMATION:
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Livingston, Brian
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Baker, Denise Marie
/ APPLICANT: Celis, Bastejan
/ APPLICANT: Kubo, Ralph
/ APPLICANT: Grey, Howard M.
/ APPLICANT: Bpimmune Inc.
/ TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
/ TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
/ FILE REFERENCE: 2060.0040007
/ CURRENT APPLICATION NUMBER: US/11/045,024
/ CURRENT FILING DATE: 2005-01-28
/ PRIOR APPLICATION NUMBER: US 09/412,863
/ PRIOR FILING DATE: 1999-10-05
/ PRIOR APPLICATION NUMBER: US 08/027,146
/ PRIOR FILING DATE: 1993-03-05
/ PRIOR APPLICATION NUMBER: US 08/073,205
/ PRIOR FILING DATE: 1993-06-04
/ PRIOR APPLICATION NUMBER: US 08/103,396
/ PRIOR FILING DATE: 1993-08-06
/ PRIOR APPLICATION NUMBER: US 08/159,184
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/159,339
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/205,713
/ PRIOR FILING DATE: 1994-03-04
```

PRIOR APPLICATION NUMBER: US 08/347,610  
PRIOR FILING DATE: 1994-12-01  
NUMBER OF SEQ ID NOS: 14528  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 13324  
LENGTH: 15  
TYPE: PRN  
ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS  
US-11-045-024-13324

Query Match 26.6%; Score 25.5; DB 7; Length 15;  
Best Local Similarity 58.3%; Pred. No. 1.3e+02;  
Matches 7; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

QY 8 YL-LTPAASPK 18  
DB 4 YLATLTKPK 15

## RESULT 8

US-11-045-024-13327  
Sequence 13327, Application US/11045024  
Publication No. US20050271676A1  
GENERAL INFORMATION:  
APPLICANT: Sette, Alessandro  
APPLICANT: Sidney, John  
APPLICANT: Southwood, Scott  
APPLICANT: Livingston, Brian  
APPLICANT: Chesnut, Robert  
APPLICANT: Baker, Denise Marie  
APPLICANT: Celis, Esceban  
APPLICANT: Kubo, Ralph  
APPLICANT: Grey, Howard M.

APPLICANT: Epimmune Inc.  
TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency  
FILE REFERENCE: 2060.0040007  
CURRENT APPLICATION NUMBER: US/11/045,024  
CURRENT FILING DATE: 2005-01-28  
PRIOR APPLICATION NUMBER: US 09/412,863  
PRIOR FILING DATE: 1999-10-05  
PRIOR APPLICATION NUMBER: US 08/027,146  
PRIOR FILING DATE: 1993-03-05  
PRIOR APPLICATION NUMBER: US 08/073,205  
PRIOR FILING DATE: 1993-06-04  
PRIOR APPLICATION NUMBER: US 08/103,396  
PRIOR FILING DATE: 1993-08-06  
PRIOR APPLICATION NUMBER: US 08/159,184  
PRIOR FILING DATE: 1993-11-29  
PRIOR APPLICATION NUMBER: US 08/159,339  
PRIOR FILING DATE: 1993-11-29  
PRIOR APPLICATION NUMBER: US 08/205,713  
PRIOR FILING DATE: 1994-03-04  
PRIOR APPLICATION NUMBER: US 08/347,610  
PRIOR FILING DATE: 1994-12-01  
NUMBER OF SEQ ID NOS: 14528  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 13327  
LENGTH: 15  
TYPE: PRN  
ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS  
US-11-045-024-13327

Query Match 26.6%; Score 25.5; DB 7; Length 15;  
Best Local Similarity 58.3%; Pred. No. 1.3e+02;  
Matches 7; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

QY 8 YL-LTPAASPK 18  
DB 3 YLATLTKPK 14

## RESULT 9

US-11-062-186-2  
Sequence 2, Application US/11062186  
Publication No. US20050272097A1  
GENERAL INFORMATION:  
APPLICANT: CALENOFF, EMANUEL  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING AND TREATING  
FILE REFERENCE: 21417-98470  
CURRENT APPLICATION NUMBER: US/11/062,186  
CURRENT FILING DATE: 2005-02-18  
PRIOR APPLICATION NUMBER: 60/546,062  
PRIOR FILING DATE: 2004-02-18  
PRIOR APPLICATION NUMBER: 60/545,980  
PRIOR FILING DATE: 2004-02-18  
NUMBER OF SEQ ID NOS: 172  
SOFTWARE: Patentin version 3.3  
SEQ ID NO 2  
LENGTH: 8  
TYPE: PRN  
ORGANISM: Homo sapiens  
US-11-062-186-2

Query Match 26.0%; Score 25; DB 7; Length 8;  
Best Local Similarity 80.0%; Pred. No. 5.5e+04;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 14 VSPGK 18  
DB 1 ISPGK 5

## RESULT 10

US-11-045-024-3531  
Sequence 3531, Application US/11045024  
Publication No. US20050271676A1  
GENERAL INFORMATION:  
APPLICANT: Sette, Alessandro  
APPLICANT: Sidney, John  
APPLICANT: Southwood, Scott  
APPLICANT: Livingston, Brian  
APPLICANT: Chesnut, Robert  
APPLICANT: Baker, Denise Marie  
APPLICANT: Celis, Esceban  
APPLICANT: Kubo, Ralph  
APPLICANT: Grey, Howard M.

APPLICANT: Epimmune Inc.  
TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency  
FILE REFERENCE: 2060.0040007  
CURRENT APPLICATION NUMBER: US/11/045,024  
CURRENT FILING DATE: 2005-01-28  
PRIOR APPLICATION NUMBER: US 09/412,863  
PRIOR FILING DATE: 1999-10-05  
PRIOR APPLICATION NUMBER: US 08/027,146  
PRIOR FILING DATE: 1993-03-05  
PRIOR APPLICATION NUMBER: US 08/073,205  
PRIOR FILING DATE: 1993-06-04  
PRIOR APPLICATION NUMBER: US 08/103,396  
PRIOR FILING DATE: 1993-08-06  
PRIOR APPLICATION NUMBER: US 08/159,184  
PRIOR FILING DATE: 1993-11-29  
PRIOR APPLICATION NUMBER: US 08/159,339  
PRIOR FILING DATE: 1993-11-29  
PRIOR APPLICATION NUMBER: US 08/205,713  
PRIOR FILING DATE: 1994-03-04  
PRIOR APPLICATION NUMBER: US 08/347,610  
PRIOR FILING DATE: 1994-12-01  
NUMBER OF SEQ ID NOS: 14528  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 3531  
LENGTH: 9  
TYPE: PRN  
ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS

US-11-045-024-3531

Query Match 26.0%; Score 25; DB 7; Length 9;  
 Best Local Similarity 55.6%; Pred. No. 5.5e+04;  
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 10 LTAASPGK 18  
 |||:|  
 Db 1 LTAALPKPK 9

RESULT 11

US-11-045-024-10473  
 / Sequence 10473, Application US/11045024  
 / Publication No. US20050271676A1  
 / GENERAL INFORMATION:  
 / APPLICANT: Sette, Alessandro  
 / APPLICANT: Sidney, John  
 / APPLICANT: Southwood, Scott  
 / APPLICANT: Livingston, Brian  
 / APPLICANT: Chesnut, Robert  
 / APPLICANT: Baker, Denise Marie  
 / APPLICANT: Kubo, Ralph  
 / APPLICANT: Grey, Howard M.  
 / APPLICANT: Bpimmune Inc.  
 / TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency  
 / TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions  
 / FILE REFERENCE: 2060.0040007  
 / CURRENT APPLICATION NUMBER: US/11/045,024  
 / CURRENT FILING DATE: 2005-01-28  
 / PRIOR APPLICATION NUMBER: US 09/412,863  
 / PRIOR FILING DATE: 1999-10-05  
 / PRIOR APPLICATION NUMBER: US 08/027,146  
 / PRIOR FILING DATE: 1993-03-05  
 / PRIOR APPLICATION NUMBER: US 08/073,205  
 / PRIOR FILING DATE: 1993-06-04  
 / PRIOR APPLICATION NUMBER: US 08/103,396  
 / PRIOR FILING DATE: 1993-08-06  
 / PRIOR APPLICATION NUMBER: US 08/159,184  
 / PRIOR FILING DATE: 1993-11-29  
 / PRIOR APPLICATION NUMBER: US 08/159,339  
 / PRIOR FILING DATE: 1993-11-29  
 / PRIOR APPLICATION NUMBER: US 08/205,713  
 / PRIOR FILING DATE: 1994-03-04  
 / PRIOR APPLICATION NUMBER: US 08/347,610  
 / PRIOR FILING DATE: 1994-12-01  
 / NUMBER OF SEQ ID NOS: 14528  
 / SOFTWARE: FastSeq for Windows Version 4.0  
 / SEQ ID NO 10473  
 / LENGTH: 9  
 / TYPE: PRT  
 / ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS  
 US-11-045-024-10473

Query Match 26.0%; Score 25; DB 7; Length 9;  
 Best Local Similarity 55.6%; Pred. No. 5.5e+04;  
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 10 LTAASPGK 18  
 |||:|  
 Db 1 LTAALPKPK 9

RESULT 12

US-11-045-024-12303  
 / Sequence 12303, Application US/11045024  
 / Publication No. US20050271676A1  
 / GENERAL INFORMATION:  
 / APPLICANT: Sette, Alessandro  
 / APPLICANT: Sidney, John  
 / APPLICANT: Southwood, Scott  
 / APPLICANT: Livingston, Brian

APPLICANT: Chesnut, Robert  
 APPLICANT: Baker, Denise Marie  
 APPLICANT: Celis, Betteban  
 APPLICANT: Kubo, Ralph  
 APPLICANT: Grey, Howard M.  
 APPLICANT: Bpimmune Inc.

US-11-045-024-12303  
 / Sequence 3546, Application US/11045024  
 / Publication No. US20050271676A1  
 / GENERAL INFORMATION:  
 / APPLICANT: Sette, Alessandro  
 / APPLICANT: Sidney, John  
 / APPLICANT: Southwood, Scott  
 / APPLICANT: Livingston, Brian  
 / APPLICANT: Chesnut, Robert  
 / APPLICANT: Baker, Denise Marie  
 / APPLICANT: Kubo, Ralph  
 / APPLICANT: Grey, Howard M.  
 / APPLICANT: Bpimmune Inc.  
 / TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency  
 / TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions  
 / FILE REFERENCE: 2060.0040007  
 / CURRENT APPLICATION NUMBER: US/11/045,024  
 / CURRENT FILING DATE: 2005-01-28  
 / PRIOR APPLICATION NUMBER: US 09/412,863  
 / PRIOR FILING DATE: 1999-10-05  
 / PRIOR APPLICATION NUMBER: US 08/027,146  
 / PRIOR FILING DATE: 1993-03-05  
 / PRIOR APPLICATION NUMBER: US 08/073,205  
 / PRIOR FILING DATE: 1993-06-04  
 / PRIOR APPLICATION NUMBER: US 08/103,396  
 / PRIOR FILING DATE: 1993-08-06  
 / PRIOR APPLICATION NUMBER: US 08/159,184  
 / PRIOR FILING DATE: 1993-11-29  
 / PRIOR APPLICATION NUMBER: US 08/159,339  
 / PRIOR FILING DATE: 1993-11-29  
 / PRIOR APPLICATION NUMBER: US 08/205,713  
 / PRIOR FILING DATE: 1994-03-04  
 / PRIOR APPLICATION NUMBER: US 08/347,610  
 / PRIOR FILING DATE: 1994-12-01  
 / NUMBER OF SEQ ID NOS: 14528  
 / SOFTWARE: FastSeq for Windows Version 4.0  
 / SEQ ID NO 12303  
 / LENGTH: 9  
 / TYPE: PRT  
 / ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS  
 US-11-045-024-12303

Query Match 26.0%; Score 25; DB 7; Length 9;  
 Best Local Similarity 55.6%; Pred. No. 5.5e+04;  
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 10 LTAASPGK 18  
 |||:|  
 Db 1 LTAALPKPK 9

RESULT 13

US-11-045-024-3546  
 / Sequence 3546, Application US/11045024  
 / Publication No. US20050271676A1  
 / GENERAL INFORMATION:  
 / APPLICANT: Sette, Alessandro  
 / APPLICANT: Sidney, John  
 / APPLICANT: Southwood, Scott  
 / APPLICANT: Livingston, Brian  
 / APPLICANT: Chesnut, Robert  
 / APPLICANT: Baker, Denise Marie  
 / APPLICANT: Kubo, Ralph  
 / APPLICANT: Grey, Howard M.  
 / APPLICANT: Bpimmune Inc.  
 / TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency  
 / TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions  
 / FILE REFERENCE: 2060.0040007  
 / CURRENT APPLICATION NUMBER: US/11/045,024  
 / CURRENT FILING DATE: 2005-01-28  
 / PRIOR APPLICATION NUMBER: US 09/412,863  
 / PRIOR FILING DATE: 1999-10-05  
 / PRIOR APPLICATION NUMBER: US 08/027,146  
 / PRIOR FILING DATE: 1993-03-05  
 / PRIOR APPLICATION NUMBER: US 08/073,205  
 / PRIOR FILING DATE: 1993-06-04  
 / PRIOR APPLICATION NUMBER: US 08/103,396  
 / PRIOR FILING DATE: 1993-08-06  
 / PRIOR APPLICATION NUMBER: US 08/159,184

```

; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3546
; LENGTH: 10
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-3546
```

```
Query Match          26.0%; Score 25; DB 7; Length 10;
Best Local Similarity 55.6%; Pred. No. 98;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

```
QY          10 LTRAAVSPGK 18
DB          2 LTRALIKPKK 10
```

```

RESULT 14
US-11-045-024-10479
; Sequence 10479, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chennut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Kubo, Esteban
; APPLICANT: Grey, Howard M.
; APPLICANT: Epiimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; PRIOR FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10479
; LENGTH: 10
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-10479
```

```
Query Match          26.0%; Score 25; DB 7; Length 10;
Best Local Similarity 55.6%; Pred. No. 98;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

```
QY          10 LTRAAVSPGK 18
```

```
DB          2 LTRALIKPKK 10
```

```

RESULT 15
US-11-045-024-12307
; Sequence 12307, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chennut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Kubo, Esteban
; APPLICANT: Grey, Howard M.
; APPLICANT: Epiimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; PRIOR FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12307
; LENGTH: 10
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-12307
```

```
Query Match          26.0%; Score 25; DB 7; Length 10;
Best Local Similarity 55.6%; Pred. No. 98;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

```
QY          10 LTRAAVSPGK 18
DB          2 LTRALIKPKK 10
```

```

RESULT 16
US-11-045-024-3559
; Sequence 3559, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chennut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Kubo, Esteban
; APPLICANT: Grey, Howard M.
; APPLICANT: Epiimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
```

```
/ TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
/ FILE REFERENCE: 2060.0040007
/ CURRENT APPLICATION NUMBER: US/11/045,024
/ CURRENT FILING DATE: 2005-01-28
/ PRIOR APPLICATION NUMBER: US 09/412,863
/ PRIOR FILING DATE: 1999-10-05
/ PRIOR APPLICATION NUMBER: US 08/027,146
/ PRIOR FILING DATE: 1993-03-05
/ PRIOR APPLICATION NUMBER: US 08/073,205
/ PRIOR FILING DATE: 1993-06-04
/ PRIOR APPLICATION NUMBER: US 08/103,396
/ PRIOR FILING DATE: 1993-08-06
/ PRIOR APPLICATION NUMBER: US 08/159,184
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/159,339
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/205,713
/ PRIOR FILING DATE: 1994-03-04
/ PRIOR APPLICATION NUMBER: US 08/347,610
/ PRIOR FILING DATE: 1994-12-01
/ NUMBER OF SEQ ID NOS: 14528
/ SOFTWARE: FASTSEQ for Windows Version 4.0
/ SEQ ID NO 3559
/ LENGTH: 11
/ TYPE: PRT
/ ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-3559

Query Match          26.0%; Score 25; DB 7; Length 11;
Best Local Similarity 55.6%; Pred. No. 1.1e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      10 LTRAVSPK 18
DB      3 LTRALPKPK 11
```

```
RESULT 17
US-11-045-024-10483
/ Sequence 10483, Application US/11045024
/ Publication No. US20050271676A1
/ GENERAL INFORMATION:
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Livingston, Brian
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Baker, Denise Marie
/ APPLICANT: Celis, Betteban
/ APPLICANT: Kubo, Ralph
/ APPLICANT: Grey, Howard M.
/ APPLICANT: EpiImmune Inc.
/ TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
/ TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
/ FILE REFERENCE: 2060.0040007
/ CURRENT APPLICATION NUMBER: US/11/045,024
/ CURRENT FILING DATE: 2005-01-28
/ PRIOR APPLICATION NUMBER: US 09/412,863
/ PRIOR FILING DATE: 1999-10-05
/ PRIOR APPLICATION NUMBER: US 08/027,146
/ PRIOR FILING DATE: 1993-03-05
/ PRIOR APPLICATION NUMBER: US 08/073,205
/ PRIOR FILING DATE: 1993-06-04
/ PRIOR APPLICATION NUMBER: US 08/103,396
/ PRIOR FILING DATE: 1993-08-06
/ PRIOR APPLICATION NUMBER: US 08/159,184
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/159,339
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/205,713
/ PRIOR FILING DATE: 1994-03-04
/ PRIOR APPLICATION NUMBER: US 08/347,610
/ PRIOR FILING DATE: 1994-12-01
```

```
/ NUMBER OF SEQ ID NOS: 14528
/ SOFTWARE: FASTSEQ for Windows Version 4.0
/ SEQ ID NO 10483
/ LENGTH: 11
/ TYPE: PRT
/ ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-10483
```

```
Query Match          26.0%; Score 25; DB 7; Length 11;
Best Local Similarity 55.6%; Pred. No. 1.1e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      10 LTRAVSPK 18
DB      3 LTRALPKPK 11
```

```
RESULT 18
US-11-045-024-12311
/ Sequence 12311, Application US/11045024
/ Publication No. US20050271676A1
/ GENERAL INFORMATION:
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Livingston, Brian
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Baker, Denise Marie
/ APPLICANT: Celis, Betteban
/ APPLICANT: Kubo, Ralph
/ APPLICANT: Grey, Howard M.
/ APPLICANT: EpiImmune Inc.
/ TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
/ TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
/ FILE REFERENCE: 2060.0040007
/ CURRENT APPLICATION NUMBER: US/11/045,024
/ CURRENT FILING DATE: 2005-01-28
/ PRIOR APPLICATION NUMBER: US 09/412,863
/ PRIOR FILING DATE: 1999-10-05
/ PRIOR APPLICATION NUMBER: US 08/027,146
/ PRIOR FILING DATE: 1993-03-05
/ PRIOR APPLICATION NUMBER: US 08/073,205
/ PRIOR FILING DATE: 1993-06-04
/ PRIOR APPLICATION NUMBER: US 08/103,396
/ PRIOR FILING DATE: 1993-08-06
/ PRIOR APPLICATION NUMBER: US 08/159,184
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/159,339
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/205,713
/ PRIOR FILING DATE: 1994-03-04
/ PRIOR APPLICATION NUMBER: US 08/347,610
/ PRIOR FILING DATE: 1994-12-01
/ NUMBER OF SEQ ID NOS: 14528
/ SOFTWARE: FASTSEQ for Windows Version 4.0
/ SEQ ID NO 12311
/ LENGTH: 11
/ TYPE: PRT
/ ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-12311
```

```
Query Match          26.0%; Score 25; DB 7; Length 11;
Best Local Similarity 55.6%; Pred. No. 1.1e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      10 LTRAVSPK 18
DB      3 LTRALPKPK 11
```

```
RESULT 19
US-11-041-893-2
/ Sequence 2, Application US/11041893
```

```
/ Publication No. US20060002941A1
/ GENERAL INFORMATION:
/ APPLICANT: Mahairas, Gregory G.
/ TITLE OF INVENTION: COMPOSITIONS COMPRISING IMMUNE RESPONSE
/ TITLE OF INVENTION: ALTERING AGENTS AND METHODS OF USE
/ FILE REFERENCE: 100123.401
/ CURRENT APPLICATION NUMBER: US/11/041,893
/ PRIOR FILING DATE: 2005-01-24
/ PRIOR APPLICATION NUMBER: US 60/616,855
/ PRIOR FILING DATE: 2004-10-06
/ PRIOR APPLICATION NUMBER: US 60/538,713
/ PRIOR FILING DATE: 2004-01-23
/ NUMBER OF SEQ ID NOS: 295
/ SOFTWARE: FaastSeq for Windows Version 4.0
/ SEQ ID NO 2
/ LENGTH: 15
/ TYPE: PRT
/ ORGANISM: Mycobacterium leprae
US-11-041-893-2
```

```
Query Match      26.0%; Score 25; DB 7; Length 15;
Best Local Similarity 71.4%; Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      11 TAAVSPG 17
      |||:|
Db      6 TAAISNG 12
```

```
RESULT 20
US-11-041-893-13
/ Sequence 13, Application US/11041893
/ Publication No. US20060002941A1
/ GENERAL INFORMATION:
/ APPLICANT: Mahairas, Gregory G.
/ TITLE OF INVENTION: COMPOSITIONS COMPRISING IMMUNE RESPONSE
/ TITLE OF INVENTION: ALTERING AGENTS AND METHODS OF USE
/ FILE REFERENCE: 100123.401
/ CURRENT APPLICATION NUMBER: US/11/041,893
/ PRIOR FILING DATE: 2005-01-24
/ PRIOR APPLICATION NUMBER: US 60/616,855
/ PRIOR FILING DATE: 2004-10-06
/ PRIOR APPLICATION NUMBER: US 60/538,713
/ PRIOR FILING DATE: 2004-01-23
/ NUMBER OF SEQ ID NOS: 295
/ SOFTWARE: FaastSeq for Windows Version 4.0
/ SEQ ID NO 13
/ LENGTH: 15
/ TYPE: PRT
/ ORGANISM: Mycobacterium tuberculosis
US-11-041-893-13
```

```
Query Match      26.0%; Score 25; DB 7; Length 15;
Best Local Similarity 71.4%; Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      11 TAAVSPG 17
      |||:|
Db      6 TAAISNG 12
```

```
RESULT 21
US-10-939-890-138
/ Sequence 138, Application US/10939890
/ Publication No. US20050250700A1
/ GENERAL INFORMATION:
/ APPLICANT: Sato, Aaron K.
/ APPLICANT: Sexton, Daniel J.
/ APPLICANT: Dransfield, Daniel T.
/ APPLICANT: Ladner, Robert C.
/ APPLICANT: Arbogast, Christophe
/ APPLICANT: Busset, Philippe
/ APPLICANT: Fan, Hong
```

```
/ APPLICANT: Khurana, Sudha
/ APPLICANT: Linder, Karen B.
/ APPLICANT: Marinelli, Edmund R.
/ APPLICANT: Nanjappan, Palaniappa
/ APPLICANT: Nunn, Adrian D.
/ APPLICANT: Pillai, Radhakrishna
/ APPLICANT: Pochon, Sibylle
/ APPLICANT: Ramalingam, Kondareddat
/ APPLICANT: Shrivastava, Ajay
/ APPLICANT: Song, Bo
/ APPLICANT: Swenson, Rolf E.
/ APPLICANT: Von Wronski, Mathew A.
/ TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
/ FILE REFERENCE: D0647.70014US00
/ CURRENT APPLICATION NUMBER: US/10/939,890
/ PRIOR FILING DATE: 2004-09-13
/ PRIOR APPLICATION NUMBER: US 10/661,156
/ PRIOR FILING DATE: 2003-09-11
/ PRIOR APPLICATION NUMBER: US 10/382,082
/ PRIOR FILING DATE: 2003-03-03
/ PRIOR APPLICATION NUMBER: PCT/US03/06731
/ PRIOR FILING DATE: 2003-03-03
/ PRIOR APPLICATION NUMBER: US 60/440,411
/ PRIOR FILING DATE: 2003-01-15
/ PRIOR APPLICATION NUMBER: US 60/360,851
/ PRIOR FILING DATE: 2002-03-01
/ NUMBER OF SEQ ID NOS: 883
/ SOFTWARE: FaastSeq for Windows Version 4.0
/ SEQ ID NO 138
/ LENGTH: 20
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Library Isolate
US-10-939-890-138
```

```
Query Match      26.0%; Score 25; DB 6; Length 20;
Best Local Similarity 80.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      4 EPHGY 8
      |||
Db      1 EPEGY 5
```

```
RESULT 22
US-10-623-155-247
/ Sequence 247, Application US/10623155
/ Publication No. US20050261166A1
/ GENERAL INFORMATION:
/ APPLICANT: Wang, Tonglong
/ APPLICANT: Peckham, David W.
/ APPLICANT: Retter, Marc W.
/ APPLICANT: Fanger, Gary R.
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
/ TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
/ FILE REFERENCE: 210121.455C20
/ CURRENT APPLICATION NUMBER: US/10/623,155
/ PRIOR FILING DATE: 2003-07-17
/ NUMBER OF SEQ ID NOS: 560
/ SOFTWARE: FaastSeq for Windows Version 4.0
/ SEQ ID NO 247
/ LENGTH: 20
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-623-155-247
```

```
Query Match      26.0%; Score 25; DB 6; Length 20;
Best Local Similarity 38.5%; Pred. No. 2.1e+02;
Matches 5; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
```

```
Qy      5 PHGYLTTAAVSPG 17
      ||::|||
```

Db 4 PHEPMIVANKOG 16

## RESULT 23

```
US-11-022-562-292
/ Sequence 292, Application US/11022562
/ Publication No. US20050249742A1
/ GENERAL INFORMATION:
/ APPLICANT: Ruprecht, Ruth M.
/ APPLICANT: Shisong, Jiang
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING
/ FILE REFERENCE: DFN-043CN
/ CURRENT APPLICATION NUMBER: US/11/022,562
/ PRIOR FILING DATE: 2004-12-22
/ PRIOR APPLICATION NUMBER: PCT/US03/20322
/ PRIOR FILING DATE: 2003-06-27
/ PRIOR APPLICATION NUMBER: 60/392718
/ PRIOR FILING DATE: 2002-06-27
/ NUMBER OF SEQ ID NOS: 340
/ SOFTWARE: PasteSeq for Windows Version 4.0
/ SEQ ID NO 292
/ LENGTH: 20
/ TYPE: PRT
/ ORGANISM: Human Immunodeficiency Virus
US-11-022-562-292
```

```
Query Match 26.0%; Score 25; DB 7; Length 20;
Best Local Similarity 37.5%; Pred. No. 2.1e+02;
Matches 6; Conservative 3; Mismatches 7; Indels 0; Gaps 0;
```

QY 2 APEPHGYLTAIVSPG 17

Db 3 APEPEVIMPMFSAUSEG 18

## RESULT 24

```
US-11-022-562-293
/ Sequence 293, Application US/11022562
/ Publication No. US20050249742A1
/ GENERAL INFORMATION:
/ APPLICANT: Ruprecht, Ruth M.
/ APPLICANT: Shisong, Jiang
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING
/ FILE REFERENCE: DFN-043CN
/ CURRENT APPLICATION NUMBER: US/11/022,562
/ PRIOR FILING DATE: 2004-12-22
/ PRIOR APPLICATION NUMBER: PCT/US03/20322
/ PRIOR FILING DATE: 2003-06-27
/ PRIOR APPLICATION NUMBER: 60/392718
/ NUMBER OF SEQ ID NOS: 340
/ SOFTWARE: PasteSeq for Windows Version 4.0
/ SEQ ID NO 293
/ LENGTH: 20
/ TYPE: PRT
/ ORGANISM: Human Immunodeficiency Virus
US-11-022-562-293
```

```
Query Match 26.0%; Score 25; DB 7; Length 20;
Best Local Similarity 37.5%; Pred. No. 2.1e+02;
Matches 6; Conservative 3; Mismatches 7; Indels 0; Gaps 0;
```

QY 2 APEPHGYLTAIVSPG 17

Db 3 APEPEVIMPMFSAUSEG 18

## RESULT 25

```
US-11-043-542-42
/ Sequence 42, Application US/11043542
/ Publication No. US20050289664A1
```

```
/ GENERAL INFORMATION:
/ APPLICANT: MOSHIRI, Parhad
/ APPLICANT: HAO, Ming
/ APPLICANT: KARUNANANDAA, Balasubramini
```

```
/ APPLICANT: VALENTIN, Henry E.
/ APPLICANT: VENKATESH, Tyagagondlu V.
/ APPLICANT: WONG, Yun-Hua Huang
/ TITLE OF INVENTION: Genes Encoding 4-Hydroxyphenylpyruvate Dioxygenase (HPPD) Enzyme
/ FILE REFERENCE: REN-02-123
/ CURRENT APPLICATION NUMBER: US/11/043,542
/ PRIOR FILING DATE: 2005-01-26
/ PRIOR APPLICATION NUMBER: US 60/539,309
/ PRIOR FILING DATE: 2004-01-26
/ NUMBER OF SEQ ID NOS: 44
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 42
/ LENGTH: 20
/ TYPE: PRT
/ ORGANISM: Bacillus thuringiensis
US-11-043-542-42
```

```
Query Match 26.0%; Score 25; DB 7; Length 20;
Best Local Similarity 38.5%; Pred. No. 2.1e+02;
Matches 5; Conservative 1; Mismatches 7; Indels 0; Gaps 0;
```

QY 4 EPHGYLTAIVSP 16

Db 7 DDEGYLQIFTKP 19

## RESULT 26

```
US-11-152-747-35
/ Sequence 35, Application US/11152747
/ Publication No. US20050251881A1
/ GENERAL INFORMATION:
/ APPLICANT: E. I. du Pont de Nemours, Inc.
/ APPLICANT: Cheng, Olong
/ APPLICANT: Tao, Luan
/ TITLE OF INVENTION: CAROTENOID KETOYLASE GENE
/ FILE REFERENCE: CL-1849 US NA
/ CURRENT APPLICATION NUMBER: US/11/152,747
/ PRIOR FILING DATE: 2005-06-14
/ PRIOR APPLICATION NUMBER:
/ PRIOR FILING DATE:
/ NUMBER OF SEQ ID NOS: 47
/ SOFTWARE: Microsoft Office 97
/ SEQ ID NO 35
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Deinococcus radiodurans
US-11-152-747-35
```

```
Query Match 25.0%; Score 24; DB 7; Length 9;
Best Local Similarity 62.5%; Pred. No. 5.5e+04;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

QY 6 HGYLTPA 13

Db 1 HNALVTAA 8

## RESULT 27

```
US-11-054-515-3192
/ Sequence 3192, Application US/11054515
/ Publication No. US20050255532A1
/ GENERAL INFORMATION:
/ APPLICANT: Ruben et al.
/ TITLE OF INVENTION: Antibodies that Immunospecifically Bind BlyS
/ FILE REFERENCE: PF523P3
/ CURRENT APPLICATION NUMBER: US/11/054,515
/ PRIOR FILING DATE: 2005-02-10
/ PRIOR APPLICATION NUMBER: 60/543,296
```

```
/ PRIOR FILING DATE: 2004-02-11
/ PRIOR APPLICATION NUMBER: 60/580,347
/ PRIOR FILING DATE: 2004-06-18
/ PRIOR APPLICATION NUMBER: 10/293,418
/ PRIOR FILING DATE: 2002-11-14
/ PRIOR APPLICATION NUMBER: 60/331,469
/ PRIOR FILING DATE: 2001-11-16
/ PRIOR APPLICATION NUMBER: 60/340,817
/ PRIOR FILING DATE: 2001-12-19
/ PRIOR APPLICATION NUMBER: 09/880,748
/ PRIOR FILING DATE: 2001-06-15
/ PRIOR APPLICATION NUMBER: 60/293,499
/ PRIOR FILING DATE: 2001-05-25
/ PRIOR APPLICATION NUMBER: 60/277,379
/ PRIOR FILING DATE: 2001-03-21
/ PRIOR APPLICATION NUMBER: 60/276,248
/ PRIOR FILING DATE: 2001-03-16
/ PRIOR APPLICATION NUMBER: 60/240,816
/ PRIOR FILING DATE: 2000-10-17
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 3247
/ SEQ ID NO 3192
/ LENGTH: 11
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-054-515-3192
```

```
Query Match      25.0%; Score 24; DB 7; Length 11;
Best Local Similarity 55.6%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      1 DAVEPHGYL 9
Db      1 DVPPPDGYL 9
```

```
RESULT 28
US-11-158-723-7
/ Sequence 7; Application US/11158723
/ Publication No. US20060002938A1
/ GENERAL INFORMATION:
/ APPLICANT: Gomer, Richard
/ APPLICANT: Pilling, Darrell
/ TITLE OF INVENTION: METHOD OF DETECTING THE INHIBITION OF
/ TITLE OF INVENTION: FIBROCYTE FORMATION AND METHODS AND COMPOSITIONS FOR
/ TITLE OF INVENTION: ENHANCING FIBROCYTE FORMATION
/ FILE REFERENCE: 002376.1029
/ CURRENT APPLICATION NUMBER: US/11/158,723
/ PRIOR FILING DATE: 2005-06-22
/ PRIOR APPLICATION NUMBER: 60/436,046
/ PRIOR FILING DATE: 2002-12-23
/ PRIOR APPLICATION NUMBER: 60/436,027
/ PRIOR FILING DATE: 2002-12-23
/ PRIOR APPLICATION NUMBER: 60/515,776
/ PRIOR FILING DATE: 2003-10-30
/ PRIOR APPLICATION NUMBER: 60/519,467
/ PRIOR FILING DATE: 2003-11-12
/ PRIOR APPLICATION NUMBER: 60/525,175
/ PRIOR FILING DATE: 2003-11-26
/ PRIOR APPLICATION NUMBER: PCT/US03/41183
/ PRIOR FILING DATE: 2003-12-22
/ NUMBER OF SEQ ID NOS: 8
/ SOFTWARE: FaastSeq for Windows Version 4.0
/ SEQ ID NO 7
/ LENGTH: 11
/ TYPE: PRT
/ ORGANISM: Human
US-11-158-723-7
```

```
Query Match      25.0%; Score 24; DB 7; Length 11;
Best Local Similarity 50.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy      5 PHGYLTA 12
Db      1 PGGYFVEA 8
```

```
RESULT 29
US-10-507-662-53
/ Sequence 53; Application US/10507662
/ Publication No. US20050255102A1
/ GENERAL INFORMATION:
/ APPLICANT: BIOGEN, INC.
/ APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
/ TITLE OF INVENTION: ANTI-ALPHA-V BETA-6 ANTIBODIES
/ FILE REFERENCE: A136PCT
/ CURRENT APPLICATION NUMBER: US/10/507,662
/ PRIOR FILING DATE: 2004-09-13
/ PRIOR APPLICATION NUMBER: 60/364,991
/ PRIOR FILING DATE: 2002-03-13
/ PRIOR APPLICATION NUMBER: 60/426,286
/ PRIOR FILING DATE: 2002-11-13
/ NUMBER OF SEQ ID NOS: 64
/ SOFTWARE: Patencin Ver. 2.1
/ SEQ ID NO 53
/ LENGTH: 12
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-507-662-53
```

```
Query Match      25.0%; Score 24; DB 6; Length 12;
Best Local Similarity 37.5%; Pred. No. 1.8e+02;
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy      3 FEPHGYL 10
Db      3 YGPHSYAM 10
```

```
RESULT 30
US-11-054-515-2602
/ Sequence 2602; Application US/11054515
/ Publication No. US2005025532A1
/ GENERAL INFORMATION:
/ APPLICANT: Ruben et al.
/ TITLE OF INVENTION: Antibodies that Immunosepecifically Bind Blys
/ FILE REFERENCE: PFS23p3
/ CURRENT APPLICATION NUMBER: US/11/054,515
/ PRIOR FILING DATE: 2005-02-10
/ PRIOR APPLICATION NUMBER: 60/543,296
/ PRIOR FILING DATE: 2004-02-11
/ PRIOR APPLICATION NUMBER: 60/580,347
/ PRIOR FILING DATE: 2004-06-18
/ PRIOR APPLICATION NUMBER: 10/293,418
/ PRIOR FILING DATE: 2002-11-14
/ PRIOR APPLICATION NUMBER: 60/331,469
/ PRIOR FILING DATE: 2001-11-16
/ PRIOR APPLICATION NUMBER: 60/340,817
/ PRIOR FILING DATE: 2001-12-19
/ PRIOR APPLICATION NUMBER: 09/880,748
/ PRIOR FILING DATE: 2001-06-15
/ PRIOR APPLICATION NUMBER: 60/293,499
/ PRIOR FILING DATE: 2001-05-25
/ PRIOR APPLICATION NUMBER: 60/277,379
/ PRIOR FILING DATE: 2001-03-21
/ PRIOR APPLICATION NUMBER: 60/276,248
/ PRIOR FILING DATE: 2001-03-16
/ PRIOR APPLICATION NUMBER: 60/240,816
/ PRIOR FILING DATE: 2000-10-17
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 3247
/ SEQ ID NO 2602
/ LENGTH: 14
/ TYPE: PRT
/ ORGANISM: Homo sapiens
```



US-11-054-515-2602

Query Match 25.0%; Score 24; DB 7; Length 14;  
Best Local Similarity 66.7%; Pred. No. 2.1e+02;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 PHGYLL 10  
|:|:|  
DB 8 PHDHL 13

RESULT 31

US-11-054-515-2909  
Sequence 2909, Application US/11054515  
Publication No. US2005025532A1  
GENERAL INFORMATION:

APPLICANT: Ruben et al.  
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BlyS  
FILE REFERENCE: P523P3  
CURRENT APPLICATION NUMBER: US/11/054,515

CURRENT FILING DATE: 2005-02-10  
PRIOR APPLICATION NUMBER: 60/543,296

PRIOR FILING DATE: 2004-02-11  
PRIOR APPLICATION NUMBER: 60/580,347

PRIOR FILING DATE: 2004-06-18  
PRIOR APPLICATION NUMBER: 10/293,418

PRIOR FILING DATE: 2002-11-14  
PRIOR APPLICATION NUMBER: 60/331,469

PRIOR FILING DATE: 2001-11-16  
PRIOR APPLICATION NUMBER: 60/340,817

PRIOR FILING DATE: 2001-12-19  
PRIOR APPLICATION NUMBER: 09/880,748

PRIOR FILING DATE: 2001-06-15  
PRIOR APPLICATION NUMBER: 60/293,499

PRIOR FILING DATE: 2001-05-25  
PRIOR APPLICATION NUMBER: 60/277,379

PRIOR FILING DATE: 2001-03-21  
PRIOR APPLICATION NUMBER: 60/276,248

PRIOR FILING DATE: 2001-03-16  
PRIOR APPLICATION NUMBER: 60/240,816

PRIOR FILING DATE: 2000-10-17  
Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 3247  
SEQ ID NO 2909  
LENGTH: 15  
TYPE: PRT  
ORGANISM: Homo sapiens

US-11-054-515-2309

Query Match 25.0%; Score 24; DB 7; Length 15;  
Best Local Similarity 66.7%; Pred. No. 2.3e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 8 YLLTAA 13  
|:|:|  
DB 4 YMTTAA 9

RESULT 32

US-10-467-657-9074  
Sequence 9074, Application US/10467657  
Publication No. US20050260581A1  
GENERAL INFORMATION:

APPLICANT: CHIRON SPA  
APPLICANT: FONTANA Maria Rita  
APPLICANT: PIZZA Mariagrazia  
APPLICANT: MASIGNANI Vega  
APPLICANT: MONACI Elisabetta  
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS  
FILE REFERENCE:  
CURRENT APPLICATION NUMBER: US/10/467,657  
CURRENT FILING DATE: 2003-08-11  
PRIOR APPLICATION NUMBER: GB-0103424.8

PRIOR FILING DATE: 2001-02-12

NUMBER OF SEQ ID NOS: 9218  
SOFTWARE: SeqMin99, version 1.04  
SEQ ID NO 9074  
LENGTH: 16  
TYPE: PRT  
ORGANISM: Neisseria gonorrhoeae

US-10-467-657-9074

Query Match 25.0%; Score 24; DB 6; Length 16;  
Best Local Similarity 36.4%; Pred. No. 2.4e+02;  
Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 6 HGVLTAASP 16  
|:|:|:|  
DB 2 HNFLEPSADTP 12

RESULT 33

US-10-467-657-9075  
Sequence 9075, Application US/10467657  
Publication No. US20050260581A1  
GENERAL INFORMATION:

APPLICANT: CHIRON SPA  
APPLICANT: PIZZA Mariagrazia  
APPLICANT: MASIGNANI Vega  
APPLICANT: MONACI Elisabetta  
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS  
FILE REFERENCE:

CURRENT APPLICATION NUMBER: US/10/467,657  
CURRENT FILING DATE: 2003-08-11  
PRIOR APPLICATION NUMBER: GB-0103424.8

PRIOR FILING DATE: 2001-02-12  
NUMBER OF SEQ ID NOS: 9218  
SOFTWARE: SeqMin99, version 1.04  
SEQ ID NO 9075  
LENGTH: 16  
TYPE: PRT  
ORGANISM: Neisseria gonorrhoeae

US-10-467-657-9075

Query Match 25.0%; Score 24; DB 6; Length 16;  
Best Local Similarity 36.4%; Pred. No. 2.4e+02;  
Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 6 HGVLTAASP 16  
|:|:|:|  
DB 2 HNFLEPSADTP 12

RESULT 34

US-11-022-562-176  
Sequence 176, Application US/11022562  
Publication No. US20050249742A1  
GENERAL INFORMATION:

APPLICANT: Ruprecht, Ruth M.  
APPLICANT: Shisong, Jiang  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING  
TITLE OF INVENTION: A CYTOTOXIC T LYMPHOCYTE IMMUNE RESPONSE  
FILE REFERENCE: DFN-043CN  
CURRENT APPLICATION NUMBER: US/11/022,562

CURRENT FILING DATE: 2004-12-22  
PRIOR APPLICATION NUMBER: PCT/US03/20322  
PRIOR FILING DATE: 2003-06-27  
PRIOR APPLICATION NUMBER: 60/392718

PRIOR FILING DATE: 2002-06-27  
NUMBER OF SEQ ID NOS: 340  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 176  
LENGTH: 20  
TYPE: PRT  
ORGANISM: Simian Immunodeficiency Virus

US-11-022-562-176

Query Match 25.0%; Score 24; DB 6; Length 16;  
Best Local Similarity 36.4%; Pred. No. 2.4e+02;  
Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 6 HGVLTAASP 16  
|:|:|:|  
DB 2 HNFLEPSADTP 12

RESULT 34

US-11-022-562-176  
Sequence 176, Application US/11022562  
Publication No. US20050249742A1  
GENERAL INFORMATION:

APPLICANT: Ruprecht, Ruth M.  
APPLICANT: Shisong, Jiang  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING  
TITLE OF INVENTION: A CYTOTOXIC T LYMPHOCYTE IMMUNE RESPONSE  
FILE REFERENCE: DFN-043CN  
CURRENT APPLICATION NUMBER: US/11/022,562

CURRENT FILING DATE: 2004-12-22  
PRIOR APPLICATION NUMBER: PCT/US03/20322  
PRIOR FILING DATE: 2003-06-27  
PRIOR APPLICATION NUMBER: 60/392718

PRIOR FILING DATE: 2002-06-27  
NUMBER OF SEQ ID NOS: 340  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 176  
LENGTH: 20  
TYPE: PRT  
ORGANISM: Simian Immunodeficiency Virus

US-11-022-562-176

## Query Match

Best Local Similarity 25.0%; Score 24; DB 7; Length 20;  
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;QY 7 GYLTAAPSPG 17  
|:|:|:|:|

DB 4 GPLATAGSAMG 14

## RESULT 35

US-11-128-900-118

; Sequence 118, Application US/11128900  
; Publication No. US20050287136A1

## GENERAL INFORMATION:

; APPLICANT: HANSON, DOUGLAS C.

; APPLICANT: NEVEU, MARK J.

; APPLICANT: MUELLER, EILEEN E.

; APPLICANT: HANKE, JEFFREY H.

; APPLICANT: GILMAN, STEVEN C.

; APPLICANT: DAVIS, C. GEOFFREY

; APPLICANT: CORVALAN, JOSE R.

; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4

; FILE REFERENCE: ABX-PF1 DIV3

; CURRENT APPLICATION NUMBER: US/11/128,900

; PRIOR FILING DATE: 2005-05-12

; PRIOR APPLICATION NUMBER: US 10/776649

; PRIOR FILING DATE: 2004-02-10

; PRIOR APPLICATION NUMBER: US 10/612497

; PRIOR APPLICATION NUMBER: 2003-07-01

; PRIOR FILING DATE: 1999-12-23

; PRIOR APPLICATION NUMBER: US 60/113647

; PRIOR FILING DATE: 1998-12-23

; NUMBER OF SEQ ID NOS: 147

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 118

; LENGTH: 20

; TYPE: PRT

; ORGANISM: Homo sapiens

US-11-128-900-118

## Query Match

Best Local Similarity 25.0%; Score 24; DB 7; Length 20;  
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;QY 11 TAAVSPGK 18  
|:|:|:|:|

DB 10 TSLSPGE 17

## RESULT 36

US-11-128-900-119

; Sequence 119, Application US/11128900  
; Publication No. US20050287136A1

## GENERAL INFORMATION:

; APPLICANT: HANSON, DOUGLAS C.

; APPLICANT: NEVEU, MARK J.

; APPLICANT: MUELLER, EILEEN E.

; APPLICANT: HANKE, JEFFREY H.

; APPLICANT: GILMAN, STEVEN C.

; APPLICANT: DAVIS, C. GEOFFREY

; APPLICANT: CORVALAN, JOSE R.

; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4

; FILE REFERENCE: ABX-PF1 DIV3

; CURRENT APPLICATION NUMBER: US/11/128,900

; PRIOR FILING DATE: 2005-05-12

; PRIOR APPLICATION NUMBER: US 10/776649

; PRIOR FILING DATE: 2004-02-10

; PRIOR APPLICATION NUMBER: US 10/612497

; PRIOR APPLICATION NUMBER: 2003-07-01

; PRIOR APPLICATION NUMBER: US 09/472087

; PRIOR FILING DATE: 1999-12-23

; PRIOR APPLICATION NUMBER: US 60/113647

; PRIOR FILING DATE: 1998-12-23

; NUMBER OF SEQ ID NOS: 147

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 119

; LENGTH: 20

; TYPE: PRT

; ORGANISM: Homo sapiens

US-11-128-900-119

Query Match  
Best Local Similarity 25.0%; Score 24; DB 7; Length 20;  
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;QY 11 TAAVSPGK 18  
|:|:|:|:|

DB 10 TSLSPGE 17

## RESULT 37

US-11-128-900-121

; Sequence 121, Application US/11128900  
; Publication No. US20050287136A1

## GENERAL INFORMATION:

; APPLICANT: HANSON, DOUGLAS C.

; APPLICANT: NEVEU, MARK J.

; APPLICANT: MUELLER, EILEEN E.

; APPLICANT: HANKE, JEFFREY H.

; APPLICANT: GILMAN, STEVEN C.

; APPLICANT: DAVIS, C. GEOFFREY

; APPLICANT: CORVALAN, JOSE R.

; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4

; FILE REFERENCE: ABX-PF1 DIV3

; CURRENT APPLICATION NUMBER: US/11/128,900

; PRIOR FILING DATE: 2005-05-12

; PRIOR APPLICATION NUMBER: US 10/776649

; PRIOR FILING DATE: 2004-02-10

; PRIOR APPLICATION NUMBER: US 10/612497

; PRIOR APPLICATION NUMBER: 2003-07-01

; PRIOR FILING DATE: 1999-12-23

; PRIOR APPLICATION NUMBER: US 60/113647

; PRIOR FILING DATE: 1998-12-23

; NUMBER OF SEQ ID NOS: 147

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 121

; LENGTH: 20

; TYPE: PRT

; ORGANISM: Homo sapiens

US-11-128-900-121

Query Match  
Best Local Similarity 25.0%; Score 24; DB 7; Length 20;  
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;QY 11 TAAVSPGK 18  
|:|:|:|:|

DB 12 TSLSPGE 19

## RESULT 38

US-11-128-900-122

; Sequence 122, Application US/11128900  
; Publication No. US20050287136A1

## GENERAL INFORMATION:

; APPLICANT: HANSON, DOUGLAS C.

; APPLICANT: NEVEU, MARK J.

; APPLICANT: MUELLER, EILEEN E.

; APPLICANT: HANKE, JEFFREY H.

; APPLICANT: GILMAN, STEVEN C.

; APPLICANT: DAVIS, C. GEOFFREY

; APPLICANT: CORVALAN, JOSE R.

```
/ TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
/ FILE REFERENCE: ABX-PF1 DIV3
/ CURRENT APPLICATION NUMBER: US/11/128,900
/ CURRENT FILING DATE: 2005-05-12
/ PRIOR APPLICATION NUMBER: US 10/776649
/ PRIOR FILING DATE: 2004-02-10
/ PRIOR APPLICATION NUMBER: US 10/612497
/ PRIOR APPLICATION NUMBER: 2003-07-01
/ PRIOR APPLICATION NUMBER: US 09/472087
/ PRIOR FILING DATE: 1999-12-23
/ PRIOR APPLICATION NUMBER: US 60/113647
/ PRIOR FILING DATE: 1998-12-23
/ NUMBER OF SEQ ID NOS: 147
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 122
/ LENGTH: 20
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-128-900-122
```

```
Query Match          25.0%; Score 24; DB 7; Length 20;
Best Local Similarity 50.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      11 TAAVSPGK 18
        |::|||:
Db      10 TSLSPGK 17
```

```
RESULT 39
US-11-128-900-123
/ Sequence 123, Application US/11128900
/ Publication No. US20050287136A1
/ GENERAL INFORMATION:
/ APPLICANT: HANSON, DOUGLAS C.
/ APPLICANT: NEVEU, MARK J.
/ APPLICANT: MUELLER, EILEEN E.
/ APPLICANT: HANKS, JEFFREY H.
/ APPLICANT: GILMAN, STEVEN C.
/ APPLICANT: DAVIS, C. GEOFFREY
/ APPLICANT: CORVALAN, JOSE R.
/ TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
/ FILE REFERENCE: ABX-PF1 DIV3
/ CURRENT APPLICATION NUMBER: US/11/128,900
/ CURRENT FILING DATE: 2005-05-12
/ PRIOR APPLICATION NUMBER: US 10/776649
/ PRIOR FILING DATE: 2004-02-10
/ PRIOR APPLICATION NUMBER: US 10/612497
/ PRIOR APPLICATION NUMBER: 2003-07-01
/ PRIOR APPLICATION NUMBER: US 09/472087
/ PRIOR FILING DATE: 1999-12-23
/ PRIOR APPLICATION NUMBER: US 60/113647
/ PRIOR FILING DATE: 1998-12-23
/ NUMBER OF SEQ ID NOS: 147
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 123
/ LENGTH: 20
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-128-900-123
```

```
Query Match          25.0%; Score 24; DB 7; Length 20;
Best Local Similarity 50.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      11 TAAVSPGK 18
        |::|||:
Db      10 TSLSPGK 17
```

```
RESULT 40
US-11-128-900-124
/ Sequence 124, Application US/11128900
```

```
/ Publication No. US20050287136A1
/ GENERAL INFORMATION:
/ APPLICANT: HANSON, DOUGLAS C.
/ APPLICANT: NEVEU, MARK J.
/ APPLICANT: MUELLER, EILEEN E.
/ APPLICANT: HANKS, JEFFREY H.
/ APPLICANT: GILMAN, STEVEN C.
/ APPLICANT: DAVIS, C. GEOFFREY
/ APPLICANT: CORVALAN, JOSE R.
/ TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
/ FILE REFERENCE: ABX-PF1 DIV3
/ CURRENT APPLICATION NUMBER: US/11/128,900
/ CURRENT FILING DATE: 2005-05-12
/ PRIOR APPLICATION NUMBER: US 10/776649
/ PRIOR FILING DATE: 2004-02-10
/ PRIOR APPLICATION NUMBER: US 10/612497
/ PRIOR APPLICATION NUMBER: 2003-07-01
/ PRIOR APPLICATION NUMBER: US 09/472087
/ PRIOR FILING DATE: 1999-12-23
/ PRIOR APPLICATION NUMBER: US 60/113647
/ PRIOR FILING DATE: 1998-12-23
/ NUMBER OF SEQ ID NOS: 147
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 124
/ LENGTH: 20
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-128-900-124
```

```
Query Match          25.0%; Score 24; DB 7; Length 20;
Best Local Similarity 50.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      11 TAAVSPGK 18
        |::|||:
Db      10 TSLSPGK 17
```

```
RESULT 41
US-11-128-900-125
/ Sequence 125, Application US/11128900
/ Publication No. US20050287136A1
/ GENERAL INFORMATION:
/ APPLICANT: HANSON, DOUGLAS C.
/ APPLICANT: NEVEU, MARK J.
/ APPLICANT: MUELLER, EILEEN E.
/ APPLICANT: HANKS, JEFFREY H.
/ APPLICANT: GILMAN, STEVEN C.
/ APPLICANT: DAVIS, C. GEOFFREY
/ APPLICANT: CORVALAN, JOSE R.
/ TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
/ FILE REFERENCE: ABX-PF1 DIV3
/ CURRENT APPLICATION NUMBER: US/11/128,900
/ CURRENT FILING DATE: 2005-05-12
/ PRIOR APPLICATION NUMBER: US 10/776649
/ PRIOR FILING DATE: 2004-02-10
/ PRIOR APPLICATION NUMBER: US 10/612497
/ PRIOR APPLICATION NUMBER: 2003-07-01
/ PRIOR APPLICATION NUMBER: US 09/472087
/ PRIOR FILING DATE: 1999-12-23
/ PRIOR APPLICATION NUMBER: US 60/113647
/ PRIOR FILING DATE: 1998-12-23
/ NUMBER OF SEQ ID NOS: 147
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 125
/ LENGTH: 20
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-128-900-125
```

```
Query Match          25.0%; Score 24; DB 7; Length 20;
Best Local Similarity 50.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
```

QY 11 TAAVSRGX 18  
|:||||:  
Db 10 TSLSPGE 17

RESULT 42  
US-10-919-492-1  
; Sequence 1, Application US/10919492  
; Publication No. US20050282249A1  
; GENERAL INFORMATION:  
; APPLICANT: STOUGAR, PETER  
; APPLICANT: HANSEN, OLE CAI  
; TITLE OF INVENTION: RECOMBINANT HEXOSE OXIDASE, A METHOD OF PRODUCING  
; TITLE OF INVENTION: SAME AND USE OF SUCH ENZYME  
; FILE REFERENCE: 14923.0014  
; CURRENT APPLICATION NUMBER: US/10/919,492  
; CURRENT FILING DATE: 2004-08-17  
; PRIOR APPLICATION NUMBER: 09/824,053  
; PRIOR FILING DATE: 2001-04-03  
; PRIOR APPLICATION NUMBER: 08/669,304  
; PRIOR FILING DATE: 1996-07-12  
; PRIOR APPLICATION NUMBER: PCT/DK96/00238  
; PRIOR FILING DATE: 1996-06-04  
; PRIOR APPLICATION NUMBER: 08/476,910  
; PRIOR FILING DATE: 1995-06-07  
; NUMBER OF SEQ ID NOS: 37  
; SOFTWARE: Patentin Ver. 3.2  
; SEQ ID NO 1  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-10-919-492-1

Query Match 24.0%; Score 23; DB 6; Length 8;  
Best Local Similarity 60.0%; Pred. No. 5.5e+04;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 PEPHG 7  
:||||:  
Db 1 YEPYG 5

RESULT 43  
US-10-859-643-31  
; Sequence 31, Application US/10859643  
; Publication No. US20060002993A1  
; GENERAL INFORMATION:  
; APPLICANT: Chaillita-Bid, Pia M.  
; APPLICANT: Raitano, Arthur B.  
; APPLICANT: Paris, Mary  
; APPLICANT: Hubert, Rene S.  
; APPLICANT: Morrison, Karen Jane Meyrick  
; APPLICANT: Jakobovits, Aya  
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein  
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of  
; FILE REFERENCE: 511582006203  
; CURRENT APPLICATION NUMBER: US/10/859,643  
; CURRENT FILING DATE: 2004-06-02  
; PRIOR APPLICATION NUMBER: US 10/005,480  
; PRIOR FILING DATE: 2001-11-07  
; NUMBER OF SEQ ID NOS: 765  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 31  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-859-643-31

Query Match 24.0%; Score 23; DB 6; Length 9;  
Best Local Similarity 66.7%; Pred. No. 5.5e+04;  
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 DAFEPH 6  
|:||||:  
Db 3 DCFCPH 8

RESULT 44  
US-10-859-643-115  
; Sequence 115, Application US/10859643  
; Publication No. US20060002993A1  
; GENERAL INFORMATION:  
; APPLICANT: Chaillita-Bid, Pia M.  
; APPLICANT: Raitano, Arthur B.  
; APPLICANT: Paris, Mary  
; APPLICANT: Hubert, Rene S.  
; APPLICANT: Morrison, Karen Jane Meyrick  
; APPLICANT: Jakobovits, Aya  
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein  
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of  
; FILE REFERENCE: 511582006203  
; CURRENT APPLICATION NUMBER: US/10/859,643  
; CURRENT FILING DATE: 2004-06-02  
; PRIOR APPLICATION NUMBER: US 10/005,480  
; PRIOR FILING DATE: 2001-11-07  
; NUMBER OF SEQ ID NOS: 765  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 115  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-859-643-115

Query Match 24.0%; Score 23; DB 6; Length 9;  
Best Local Similarity 66.7%; Pred. No. 5.5e+04;  
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 DAFEPH 6  
|:||||:  
Db 3 DCFCPH 8

RESULT 45  
US-10-859-643-698  
; Sequence 698, Application US/10859643  
; Publication No. US20060002993A1  
; GENERAL INFORMATION:  
; APPLICANT: Chaillita-Bid, Pia M.  
; APPLICANT: Raitano, Arthur B.  
; APPLICANT: Paris, Mary  
; APPLICANT: Hubert, Rene S.  
; APPLICANT: Morrison, Karen Jane Meyrick  
; APPLICANT: Jakobovits, Aya  
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein  
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of  
; FILE REFERENCE: 511582006203  
; CURRENT APPLICATION NUMBER: US/10/859,643  
; CURRENT FILING DATE: 2004-06-02  
; PRIOR APPLICATION NUMBER: US 10/005,480  
; PRIOR FILING DATE: 2001-11-07  
; NUMBER OF SEQ ID NOS: 765  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 698  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-859-643-698

Query Match 24.0%; Score 23; DB 6; Length 9;

Best Local Similarity 66.7%; Pred. No. 5.5e+04;  
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DAFEPH 6  
Db 3 DCFCPH 8

## RESULT 46

US-11-097-864-31  
Sequence 31, Application US/11097864  
Publication No. US20050265924A1  
GENERAL INFORMATION:  
APPLICANT: Challita-Bid, Pia M.  
APPLICANT: Raitano, Arthur B.  
APPLICANT: Farris, Mary  
APPLICANT: Hubert, Rene S.  
APPLICANT: Morrison, Karen Jane Meyrick  
APPLICANT: Jakobovits, Aya  
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 161P2F10B  
FILE REFERENCE: 511582006205  
CURRENT APPLICATION NUMBER: US/11/097,864  
PRIOR FILING DATE: 2005-04-01  
PRIOR APPLICATION NUMBER: US 10/062,109  
PRIOR FILING DATE: 2002-01-31  
PRIOR FILING DATE: 2001-11-07  
PRIOR APPLICATION NUMBER: US 10/005,480  
NUMBER OF SEQ ID NOS: 765  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 31  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Homo Saplen  
US-11-097-864-31

Query Match 24.0%; Score 23; DB 7; Length 9;  
Best Local Similarity 66.7%; Pred. No. 5.5e+04;  
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DAFEPH 6  
Db 3 DCFCPH 8

## RESULT 47

US-11-097-864-115  
Sequence 115, Application US/11097864  
Publication No. US20050265924A1  
GENERAL INFORMATION:  
APPLICANT: Challita-Bid, Pia M.  
APPLICANT: Raitano, Arthur B.  
APPLICANT: Farris, Mary  
APPLICANT: Hubert, Rene S.  
APPLICANT: Morrison, Karen Jane Meyrick  
APPLICANT: Jakobovits, Aya  
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 161P2F10B  
FILE REFERENCE: 511582006205  
CURRENT APPLICATION NUMBER: US/11/097,864  
PRIOR FILING DATE: 2005-04-01  
PRIOR APPLICATION NUMBER: US 10/062,109  
PRIOR FILING DATE: 2002-01-31  
PRIOR APPLICATION NUMBER: US 10/005,480  
PRIOR FILING DATE: 2001-11-07  
NUMBER OF SEQ ID NOS: 765  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 115  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Homo Saplen  
US-11-097-864-115

Query Match 24.0%; Score 23; DB 7; Length 9;  
Best Local Similarity 66.7%; Pred. No. 5.5e+04;  
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DAFEPH 6  
Db 3 DCFCPH 8

## RESULT 48

US-11-097-864-698  
Sequence 698, Application US/11097864  
Publication No. US20050265924A1  
GENERAL INFORMATION:  
APPLICANT: Challita-Bid, Pia M.  
APPLICANT: Raitano, Arthur B.  
APPLICANT: Farris, Mary  
APPLICANT: Hubert, Rene S.  
APPLICANT: Morrison, Karen Jane Meyrick  
APPLICANT: Jakobovits, Aya  
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 161P2F10B  
FILE REFERENCE: 511582006205  
CURRENT APPLICATION NUMBER: US/11/097,864  
PRIOR FILING DATE: 2005-04-01  
PRIOR APPLICATION NUMBER: US 10/062,109  
PRIOR FILING DATE: 2002-01-31  
PRIOR APPLICATION NUMBER: US 10/005,480  
PRIOR FILING DATE: 2001-11-07  
NUMBER OF SEQ ID NOS: 765  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 698  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Homo Saplen  
US-11-097-864-698

Query Match 24.0%; Score 23; DB 7; Length 9;  
Best Local Similarity 66.7%; Pred. No. 5.5e+04;  
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DAFEPH 6  
Db 3 DCFCPH 8

## RESULT 49

US-11-097-912-31  
Sequence 31, Application US/11097912  
Publication No. US20050265921A1  
GENERAL INFORMATION:  
APPLICANT: Challita-Bid, Pia M.  
APPLICANT: Raitano, Arthur B.  
APPLICANT: Farris, Mary  
APPLICANT: Hubert, Rene S.  
APPLICANT: Morrison, Karen Jane Meyrick  
APPLICANT: Jakobovits, Aya  
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 161P2F10B  
FILE REFERENCE: 511582006204  
CURRENT APPLICATION NUMBER: US/11/097,912  
PRIOR FILING DATE: 2005-04-01  
PRIOR APPLICATION NUMBER: US 10/062,109  
PRIOR FILING DATE: 2002-01-31  
PRIOR APPLICATION NUMBER: US 10/005,480  
PRIOR FILING DATE: 2001-11-07  
NUMBER OF SEQ ID NOS: 765  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 31  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Homo Saplen  
US-11-097-912-31

Query Match 24.0%; Score 23; DB 7; Length 9;  
Best Local Similarity 66.7%; Pred. No. 5.5e+04;  
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 DAFEPH 6  
| | | |  
Db 3 DCFCPH 8

## RESULT 50

US-11-097-912-115  
; Sequence 115, Application US/11097912  
; Publication No. US20050265921A1  
; GENERAL INFORMATION:  
; APPLICANT: Chaillita-Bid, Pia M.  
; APPLICANT: Raitano, Arthur B.  
; APPLICANT: Farris, Mary  
; APPLICANT: Hubert, Rene S.  
; APPLICANT: Morrison, Karen Jane Meyrick  
; APPLICANT: Jakobovits, Aya  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 161P2F10B  
; FILE REFERENCE: 511582006204  
; CURRENT APPLICATION NUMBER: US/11/097,912  
; PRIOR FILING DATE: 2005-04-01  
; PRIOR APPLICATION NUMBER: US 10/062,109  
; PRIOR FILING DATE: 2002-01-31  
; PRIOR APPLICATION NUMBER: US 10/005,480  
; PRIOR FILING DATE: 2001-11-07  
; NUMBER OF SEQ ID NOS: 765  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 115  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-11-097-912-115

Query Match 24.0%; Score 23; DB 7; Length 9;  
Best Local Similarity 66.7%; Pred. No. 5.5e+04;  
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 DAFEPH 6  
| | | |  
Db 3 DCFCPH 8

## RESULT 51

US-11-097-912-698  
; Sequence 698, Application US/11097912  
; Publication No. US20050265921A1  
; GENERAL INFORMATION:  
; APPLICANT: Chaillita-Bid, Pia M.  
; APPLICANT: Raitano, Arthur B.  
; APPLICANT: Farris, Mary  
; APPLICANT: Hubert, Rene S.  
; APPLICANT: Morrison, Karen Jane Meyrick  
; APPLICANT: Jakobovits, Aya  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 161P2F10B  
; FILE REFERENCE: 511582006204  
; CURRENT APPLICATION NUMBER: US/11/097,912  
; PRIOR FILING DATE: 2005-04-01  
; PRIOR APPLICATION NUMBER: US 10/062,109  
; PRIOR FILING DATE: 2002-01-31  
; PRIOR APPLICATION NUMBER: US 10/005,480  
; PRIOR FILING DATE: 2001-11-07  
; NUMBER OF SEQ ID NOS: 765  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 698  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo Sapien

US-11-097-912-698

Query Match 24.0%; Score 23; DB 7; Length 9;  
Best Local Similarity 66.7%; Pred. No. 5.5e+04;  
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 DAFEPH 6  
| | | |  
Db 3 DCFCPH 8

## RESULT 52

US-10-859-643-100  
; Sequence 100, Application US/10859643  
; Publication No. US2006000293A1  
; GENERAL INFORMATION:  
; APPLICANT: Chaillita-Bid, Pia M.  
; APPLICANT: Raitano, Arthur B.  
; APPLICANT: Farris, Mary  
; APPLICANT: Hubert, Rene S.  
; APPLICANT: Morrison, Karen Jane Meyrick  
; APPLICANT: Jakobovits, Aya  
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein  
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of  
; FILE REFERENCE: 511582006203  
; CURRENT APPLICATION NUMBER: US/10/859,643  
; CURRENT FILING DATE: 2004-06-02  
; PRIOR APPLICATION NUMBER: US 10/005,480  
; PRIOR FILING DATE: 2001-11-07  
; NUMBER OF SEQ ID NOS: 765  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 100  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-859-643-100

Query Match 24.0%; Score 23; DB 6; Length 10;  
Best Local Similarity 66.7%; Pred. No. 2.1e+02;  
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 DAFEPH 6  
| | | |  
Db 3 DCFCPH 8

## RESULT 53

US-10-859-643-433  
; Sequence 433, Application US/10859643  
; Publication No. US2006000293A1  
; GENERAL INFORMATION:  
; APPLICANT: Chaillita-Bid, Pia M.  
; APPLICANT: Raitano, Arthur B.  
; APPLICANT: Farris, Mary  
; APPLICANT: Hubert, Rene S.  
; APPLICANT: Morrison, Karen Jane Meyrick  
; APPLICANT: Jakobovits, Aya  
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein  
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of  
; FILE REFERENCE: 511582006203  
; CURRENT APPLICATION NUMBER: US/10/859,643  
; CURRENT FILING DATE: 2004-06-02  
; PRIOR APPLICATION NUMBER: US 10/005,480  
; PRIOR FILING DATE: 2001-11-07  
; NUMBER OF SEQ ID NOS: 765  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 433  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-859-643-433

Query Match 24.0%; Score 23; DB 6; Length 10;  
Best Local Similarity 66.7%; Pred. No. 2.1e+02;  
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 DAFEPH 6  
| | | |  
Db 4 DCRCPH 9

## RESULT 54

US-10-859-643-619  
; Sequence 619, Application US/10859643  
; Publication No. US20060029924A1  
; GENERAL INFORMATION:  
; APPLICANT: Chailita-Bld, Pia M.  
; APPLICANT: Raitano, Arthur B.  
; APPLICANT: Paris, Mary  
; APPLICANT: Hubert, Rene S.  
; APPLICANT: Morrison, Karen Jane Meyrick  
; APPLICANT: Jakobovits, Aya  
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein  
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of  
; FILE REFERENCE: 511582006205  
; CURRENT APPLICATION NUMBER: US/10/859,643  
; PRIOR FILING DATE: 2004-06-02  
; PRIOR APPLICATION NUMBER: US 10/005,480  
; PRIOR FILING DATE: 2001-11-07  
; NUMBER OF SEQ ID NOS: 765  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 619  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-859-643-619

Query Match 24.0%; Score 23; DB 6; Length 10;  
Best Local Similarity 66.7%; Pred. No. 2.1e+02;  
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 DAFEPH 6  
| | | |  
Db 4 DCRCPH 9

## RESULT 55

US-11-097-864-100  
; Sequence 100, Application US/11097864  
; Publication No. US20050265924A1  
; GENERAL INFORMATION:  
; APPLICANT: Chailita-Bld, Pia M.  
; APPLICANT: Raitano, Arthur B.  
; APPLICANT: Paris, Mary  
; APPLICANT: Hubert, Rene S.  
; APPLICANT: Morrison, Karen Jane Meyrick  
; APPLICANT: Jakobovits, Aya  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 161P2F10B  
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF CANCER  
; FILE REFERENCE: 511582006205  
; CURRENT APPLICATION NUMBER: US/11/097,864  
; PRIOR FILING DATE: 2005-04-01  
; PRIOR APPLICATION NUMBER: US 10/062,109  
; PRIOR FILING DATE: 2002-01-31  
; PRIOR APPLICATION NUMBER: US 10/005,480  
; PRIOR FILING DATE: 2001-11-07  
; NUMBER OF SEQ ID NOS: 765  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 100  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-11-097-864-100

Query Match 24.0%; Score 23; DB 7; Length 10;  
Best Local Similarity 66.7%; Pred. No. 2.1e+02;  
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 DAFEPH 6  
| | | |  
Db 3 DCRCPH 8

## RESULT 56

US-11-097-864-433  
; Sequence 433, Application US/11097864  
; Publication No. US20050265924A1  
; GENERAL INFORMATION:  
; APPLICANT: Chailita-Bld, Pia M.  
; APPLICANT: Raitano, Arthur B.  
; APPLICANT: Paris, Mary  
; APPLICANT: Hubert, Rene S.  
; APPLICANT: Morrison, Karen Jane Meyrick  
; APPLICANT: Jakobovits, Aya  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 161P2F10B  
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF CANCER  
; FILE REFERENCE: 511582006205  
; CURRENT APPLICATION NUMBER: US/11/097,864  
; PRIOR FILING DATE: 2005-04-01  
; PRIOR APPLICATION NUMBER: US 10/062,109  
; PRIOR FILING DATE: 2002-01-31  
; PRIOR APPLICATION NUMBER: US 10/005,480  
; PRIOR FILING DATE: 2001-11-07  
; NUMBER OF SEQ ID NOS: 765  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 433  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-11-097-864-433

Query Match 24.0%; Score 23; DB 7; Length 10;  
Best Local Similarity 66.7%; Pred. No. 2.1e+02;  
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 DAFEPH 6  
| | | |  
Db 4 DCRCPH 9

## RESULT 57

US-11-097-864-619  
; Sequence 619, Application US/11097864  
; Publication No. US20050265924A1  
; GENERAL INFORMATION:  
; APPLICANT: Chailita-Bld, Pia M.  
; APPLICANT: Raitano, Arthur B.  
; APPLICANT: Paris, Mary  
; APPLICANT: Hubert, Rene S.  
; APPLICANT: Morrison, Karen Jane Meyrick  
; APPLICANT: Jakobovits, Aya  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 161P2F10B  
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF CANCER  
; FILE REFERENCE: 511582006205  
; CURRENT APPLICATION NUMBER: US/11/097,864  
; PRIOR FILING DATE: 2005-04-01  
; PRIOR APPLICATION NUMBER: US 10/062,109  
; PRIOR FILING DATE: 2002-01-31  
; PRIOR APPLICATION NUMBER: US 10/005,480  
; PRIOR FILING DATE: 2001-11-07  
; NUMBER OF SEQ ID NOS: 765  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 619  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-11-097-864-619

US-11-097-864-619

Query Match 24.0%; Score 23; DB 7; Length 10;  
Best Local Similarity 66.7%; Pred. No. 2.1e+02;  
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 DAFEPH 6  
| | | |  
Db 4 DCFCPH 9

RESULT 58

US-11-097-912-100

; Sequence 100, Application US/11097912  
; Publication No. US20050265921A1  
; GENERAL INFORMATION:  
; APPLICANT: Chailita-Bid, Pia M.  
; APPLICANT: Raitano, Arthur B.  
; APPLICANT: Paris, Mary  
; APPLICANT: Hubert, Rene S.  
; APPLICANT: Morrison, Karen Jane Meyrick  
; APPLICANT: Jakobovits, Aya  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 161P2F10B  
; FILE REFERENCE: 511582006204  
; CURRENT APPLICATION NUMBER: US/11/097,912  
; PRIOR FILING DATE: 2005-04-01  
; PRIOR APPLICATION NUMBER: US 10/062,109  
; PRIOR FILING DATE: 2002-01-31  
; PRIOR APPLICATION NUMBER: US 10/005,480  
; PRIOR FILING DATE: 2001-11-07  
; NUMBER OF SEQ ID NOS: 765  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 100  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-11-097-912-100

Query Match 24.0%; Score 23; DB 7; Length 10;  
Best Local Similarity 66.7%; Pred. No. 2.1e+02;  
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 DAFEPH 6  
| | | |  
Db 3 DCFCPH 8

RESULT 59

US-11-097-912-433

; Sequence 433, Application US/11097912  
; Publication No. US20050265921A1  
; GENERAL INFORMATION:  
; APPLICANT: Chailita-Bid, Pia M.  
; APPLICANT: Raitano, Arthur B.  
; APPLICANT: Paris, Mary  
; APPLICANT: Hubert, Rene S.  
; APPLICANT: Morrison, Karen Jane Meyrick  
; APPLICANT: Jakobovits, Aya  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 161P2F10B  
; FILE REFERENCE: 511582006204  
; CURRENT APPLICATION NUMBER: US/11/097,912  
; PRIOR FILING DATE: 2005-04-01  
; PRIOR APPLICATION NUMBER: US 10/062,109  
; PRIOR FILING DATE: 2002-01-31  
; PRIOR APPLICATION NUMBER: US 10/005,480  
; PRIOR FILING DATE: 2001-11-07  
; NUMBER OF SEQ ID NOS: 765  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 433  
; LENGTH: 10  
; TYPE: PRT

; ORGANISM: Homo Sapien  
US-11-097-912-433

Query Match 24.0%; Score 23; DB 7; Length 10;  
Best Local Similarity 66.7%; Pred. No. 2.1e+02;  
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 DAFEPH 6  
| | | |  
Db 4 DCFCPH 9

RESULT 60

US-11-097-912-619

; Sequence 619, Application US/11097912  
; Publication No. US20050265921A1  
; GENERAL INFORMATION:  
; APPLICANT: Chailita-Bid, Pia M.  
; APPLICANT: Raitano, Arthur B.  
; APPLICANT: Paris, Mary  
; APPLICANT: Hubert, Rene S.  
; APPLICANT: Morrison, Karen Jane Meyrick  
; APPLICANT: Jakobovits, Aya  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 161P2F10B  
; FILE REFERENCE: 511582006204  
; CURRENT APPLICATION NUMBER: US/11/097,912  
; PRIOR FILING DATE: 2005-04-01  
; PRIOR APPLICATION NUMBER: US 10/062,109  
; PRIOR FILING DATE: 2002-01-31  
; PRIOR APPLICATION NUMBER: US 10/005,480  
; PRIOR FILING DATE: 2001-11-07  
; NUMBER OF SEQ ID NOS: 765  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 619  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-11-097-912-619

Query Match 24.0%; Score 23; DB 7; Length 10;  
Best Local Similarity 66.7%; Pred. No. 2.1e+02;  
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 DAFEPH 6  
| | | |  
Db 4 DCFCPH 9

RESULT 61

US-10-511-559-637

; Sequence 637, Application US/10511559  
; Publication No. US20050265304A1  
; GENERAL INFORMATION:  
; APPLICANT: JONES, Tim  
; APPLICANT: BAKER, Matthew  
; APPLICANT: CARR, Francis, J.  
; TITLE OF INVENTION: MODIFIED FACTOR VIII  
; FILE REFERENCE: MER-133  
; CURRENT APPLICATION NUMBER: US/10/511,559  
; PRIOR FILING DATE: 2004-10-15  
; PRIOR APPLICATION NUMBER: PCT/EP03/04063  
; PRIOR FILING DATE: 2003-04-17  
; PRIOR APPLICATION NUMBER: EP 02008712.8  
; PRIOR FILING DATE: 2002-04-18  
; PRIOR APPLICATION NUMBER: EP 03006554.4  
; PRIOR FILING DATE: 2003-03-24  
; NUMBER OF SEQ ID NOS: 1147  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 637  
; LENGTH: 13  
; TYPE: PRT  
; ORGANISM: Artificial Sequence



```

; FEATURE:
; OTHER INFORMATION: Potential Epitope of human Factor VIII
US-10-511-559-637

Query Match          24.0%; Score 23; DB 6; Length 13;
Best Local Similarity 44.4%; Pred. No. 2.8e+02;
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 8 YLTAVASP 16
   |||
   :||
Db 3 YACTTRISP 11

RESULT 62
US-10-966-371-14
; Sequence 14, Application US/10966371
; Publication No. US20050250692A1
; GENERAL INFORMATION:
; APPLICANT: Huang, Jung San
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INHIBITING CELL PROLIFERATION
; FILE REFERENCE: SLU 03-006 US
; CURRENT APPLICATION NUMBER: US/10/966,371
; PRIOR FILING DATE: 2004-10-15
; PRIOR APPLICATION NUMBER: US 60/512,516
; PRIOR FILING DATE: 2003-10-17
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-966-371-14

Query Match          24.0%; Score 23; DB 6; Length 14;
Best Local Similarity 66.7%; Pred. No. 3.1e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 PHGYLL 10
   |||
   :||
Db 4 PHGITL 9

RESULT 63
US-11-054-515-2916
; Sequence 2916, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunosepecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; PRIOR FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.

```

```

; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2916
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-2916

Query Match          24.0%; Score 23; DB 7; Length 14;
Best Local Similarity 57.1%; Pred. No. 3.1e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 FEHPGYL 9
   |||
   :||
Db 6 YESSGYL 12

RESULT 64
US-11-073-347-116
; Sequence 116, Application US/11073347
; Publication No. US20050260234A1
; GENERAL INFORMATION:
; APPLICANT: SIMARD, John J. L.
; TITLE OF INVENTION: ANTI-NEOVASCULATURE PREPARATIONS FOR
; FILE REFERENCE: MANK.015C1
; CURRENT APPLICATION NUMBER: US/11/073,347
; PRIOR FILING DATE: 2005-03-04
; PRIOR APPLICATION NUMBER: 10/094,699
; PRIOR FILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: 60/274,063
; PRIOR FILING DATE: 2001-03-07
; NUMBER OF SEQ ID NOS: 159
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 116
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapien
US-11-073-347-116

Query Match          24.0%; Score 23; DB 7; Length 14;
Best Local Similarity 66.7%; Pred. No. 3.1e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 APEPHG 7
   |||
   :||
Db 1 APEPHG 6

RESULT 65
US-11-022-562-35
; Sequence 35, Application US/11022562
; Publication No. US20050249742A1
; GENERAL INFORMATION:
; APPLICANT: Ruprecht, Ruth M.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING
; FILE REFERENCE: DEN-043CN
; CURRENT APPLICATION NUMBER: US/11/022,562
; PRIOR FILING DATE: 2004-12-22
; PRIOR APPLICATION NUMBER: PCT/US03/20322
; PRIOR FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: 60/392718
; PRIOR FILING DATE: 2002-06-27
; NUMBER OF SEQ ID NOS: 340
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Human Immunodeficiency Virus
US-11-022-562-35

```

Query Match	24.0%;	Score 23;	DB 7;	Length 15;
Best Local Similarity	40.0%;	Pred. No. 3.3e+02;		
Matches	4;	Conservative	3;	Mismatches 3;
				Indels 0;
				Gaps 0;

```
QY      7 GYLTLTAVSP 16
      | :: |||
Db      4 GQMVHQAI SP 13
```

```

RESULT 66 337-110
US-11-073-347-110
Sequence 110. Application US/11073347
Publication NO. US20050260234A1
GENERAL INFORMATION:
APPLICANT: SIMARD, John J. L.
APPLICANT: DIMOND, David C.
TITLE OF INVENTION: ANTI-NEOVASCULATURE PREPARATIONS FOR
TITLE OF INVENTION: CANCER
FILE REFERENCE: MANMK. 015C1
CURRENT APPLICATION NUMBER: US/11/073.347
CURRENT FILING DATE: 2005-03-04
PRIOR APPLICATION NUMBER: 10/094,699
PRIOR FILING DATE: 2002-03-07
PRIOR APPLICATION NUMBER: 60/274,063
PRIOR FILING DATE: 2001-03-07
NUMBER OF SEQ ID NOS: 159
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 110
LENGTH: 15
TYPE: PRT
ORGANISM: Homo sapien
US-11-073-347-110

```

Query Match	24.0%;	Score 23;	DB 7;	Length 15;
Best Local Similarity	66.7%;	Pred. No. 3.3e+02;		
Matches	4;	Conservative	0;	Mismatches 2;
			Indels	0;
			Gaps	0;

Oy	2	APEPHG	7
Db	1	AFSPQG	6

RESULT 67  
 US-11-045-024-13033  
 Sequence 13033, Application US/11045024  
 Publication No. US20050271676A1  
 GENERAL INFORMATION:  
 APPLICANT: Sette, Alessandro  
 APPLICANT: Sidney, John  
 APPLICANT: Southwood, Scott  
 APPLICANT: Livingston, Brian  
 APPLICANT: Chesnut, Robert  
 APPLICANT: Baker, Denise Marie  
 APPLICANT: Cells, Esteban  
 APPLICANT: Kubo, Ralph  
 APPLICANT: Grey, Howard M.  
 APPLICANT: Epimmune Inc.  
 TITLE OR INVENTION: Inducing Cellular Responses to Human Immunodeficiency  
 TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions  
 FILE REFERENCE: 2060\_0040007  
 CURRENT APPLICATION NUMBER: US/11/045\_024  
 CURRENT FILING DATE: 2005-01-28  
 PRIOR APPLICATION NUMBER: US 09/412,863  
 PRIOR FILING DATE: 1999-10-05  
 PRIOR APPLICATION NUMBER: US 08/027,146  
 PRIOR FILING DATE: 1993-03-05  
 PRIOR APPLICATION NUMBER: US 08/073,205  
 PRIOR FILING DATE: 1993-06-04  
 PRIOR APPLICATION NUMBER: US 08/103,396  
 PRIOR FILING DATE: 1993-08-06  
 PRIOR APPLICATION NUMBER: US 08/159,184  
 PRIOR FILING DATE: 1993-11-29  
 PRIOR APPLICATION NUMBER: US 08/159,339

```

: PRIOR FILING DATE: 1993-11-29
: PRIOR APPLICATION NUMBER: US 08/205,713
: PRIOR FILING DATE: 1994-03-04
: PRIOR APPLICATION NUMBER: US 08/347,610
: PRIOR FILING DATE: 1994-12-01
: NUMBER OF SEQ ID NOS: 14528
: SOFTWARE: FASTSEQ for Windows Version 4.0
: SEQ ID NO 13033
: LENGTH: 15
: TYPE: PRT
: ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-13033

```

Query Match	24.0%;	Score 23;	DB 7;	Length 15;
Best Local Similarity	40.0%;	Pred. No. 3.3e+02;		
Matches	4;	Conservative	3;	Mismatches 3;
				Indels 0;
				Gaps 0;

```
QY      7 GYLLTAVSP 16
        | : : | : |
Db      2 GQMVHQATSP 11
```

```

US-11-045-024-13034
RESULT 68
US-11-045-024-13034
Sequence 13034, Application US/11045024
Publication No. US20050271676A1
GENERAL INFORMATION:
APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
APPLICANT: Livingston, Brian
APPLICANT: Chesnut, Robert
APPLICANT: Baker, Denise Marie
APPLICANT: Cells, Eteban
APPLICANT: Kubo, Ralph
APPLICANT: Grey, Howard M.
APPLICANT: EpiImmune Inc.
TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
FILE REFERENCE: 2060.0040007
CURRENT APPLICATION NUMBER: US/11/045,024
CURRENT FILING DATE: 2005-01-28
PRIOR APPLICATION NUMBER: US 09/412,863
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: US 08/027,146
PRIOR FILING DATE: 1993-03-05
PRIOR APPLICATION NUMBER: US 08/073,205
PRIOR FILING DATE: 1993-06-04
PRIOR APPLICATION NUMBER: US 08/103,396
PRIOR FILING DATE: 1993-08-06
PRIOR APPLICATION NUMBER: US 08/159,184
PRIOR FILING DATE: 1993-11-29
PRIOR APPLICATION NUMBER: US 08/159,339
PRIOR FILING DATE: 1993-11-29
PRIOR APPLICATION NUMBER: US 08/205,713
PRIOR FILING DATE: 1994-03-04
PRIOR APPLICATION NUMBER: US 08/347,610
PRIOR FILING DATE: 1994-12-01
NUMBER OF SEQ ID NOS: 14528
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 13034
LENGTH: 15
TYPE: PRT
ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-13034

```

Query Match	24.0%	Score 23;	DB 7;	Length 15;
Best Local Similarity	40.0%	Pred. No. 3.3e+02;		
Matches 4/ Conservative	3/	Mismatches 3/	Indels 0/	Gaps 0/

QY 7 GYLTTAVSP 16  
| : : | : |  
Db 1 GQMVHQATSP 10

```
RESULT 69
US-11-045-024-13046
/ Sequence 13046, Application US/11045024
/ Publication No. US20050271676A1
/ GENERAL INFORMATION:
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Livingston, Brian
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Baker, Denise Marie
/ APPLICANT: Cella, Esteban
/ APPLICANT: Kubo, Ralph
/ APPLICANT: Grey, Howard M.
/ APPLICANT: Eptimmune Inc.
/ TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
/ FILE REFERENCE: 2060.0040007
/ CURRENT APPLICATION NUMBER: US/11/045,024
/ CURRENT FILING DATE: 2005-01-28
/ PRIOR APPLICATION NUMBER: US 09/412,863
/ PRIOR FILING DATE: 1999-10-05
/ PRIOR APPLICATION NUMBER: US 08/027,146
/ PRIOR FILING DATE: 1993-03-05
/ PRIOR APPLICATION NUMBER: US 08/073,205
/ PRIOR FILING DATE: 1993-06-04
/ PRIOR APPLICATION NUMBER: US 08/103,396
/ PRIOR FILING DATE: 1993-08-06
/ PRIOR APPLICATION NUMBER: US 08/159,184
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/159,339
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/205,713
/ PRIOR FILING DATE: 1994-03-04
/ PRIOR APPLICATION NUMBER: US 08/347,610
/ PRIOR FILING DATE: 1994-12-01
/ NUMBER OF SEQ ID NOS: 14528
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 13046
/ LENGTH: 15
/ TYPE: PRF
/ ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-13046

Query Match          24.0%; Score 23; DB 7; Length 15;
Best Local Similarity 40.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 7 GYLTTAAVSP 16
| : : | : |
Db 6 GQVWQAISP 15

RESULT 70
US-11-045-024-14210
/ Sequence 14210, Application US/11045024
/ Publication No. US20050271676A1
/ GENERAL INFORMATION:
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Livingston, Brian
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Baker, Denise Marie
/ APPLICANT: Cella, Esteban
/ APPLICANT: Kubo, Ralph
/ APPLICANT: Grey, Howard M.
/ APPLICANT: Eptimmune Inc.
/ TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
/ FILE REFERENCE: 2060.0040007
/ CURRENT APPLICATION NUMBER: US/11/045,024
/ CURRENT FILING DATE: 2005-01-28
/ PRIOR APPLICATION NUMBER: US 09/412,863
/ PRIOR FILING DATE: 1999-10-05
/ PRIOR APPLICATION NUMBER: US 08/027,146
/ PRIOR FILING DATE: 1993-03-05
/ PRIOR APPLICATION NUMBER: US 08/073,205
/ PRIOR FILING DATE: 1993-06-04
/ PRIOR APPLICATION NUMBER: US 08/103,396
/ PRIOR FILING DATE: 1993-08-06
/ PRIOR APPLICATION NUMBER: US 08/159,184
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/159,339
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/205,713
/ PRIOR FILING DATE: 1994-03-04
/ PRIOR APPLICATION NUMBER: US 08/347,610
/ PRIOR FILING DATE: 1994-12-01
/ NUMBER OF SEQ ID NOS: 14528
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 14210
/ LENGTH: 15
/ TYPE: PRF
/ ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-14210

Query Match          24.0%; Score 23; DB 7; Length 15;
Best Local Similarity 40.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 7 GYLTTAAVSP 16
| : : | : |
Db 2 GQVWQAISP 11
```

```
RESULT 71
US-11-045-024-14400
/ Sequence 14400, Application US/11045024
/ Publication No. US20050271676A1
/ GENERAL INFORMATION:
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Livingston, Brian
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Baker, Denise Marie
/ APPLICANT: Cella, Esteban
/ APPLICANT: Kubo, Ralph
/ APPLICANT: Grey, Howard M.
/ APPLICANT: Eptimmune Inc.
/ TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
/ FILE REFERENCE: 2060.0040007
/ CURRENT APPLICATION NUMBER: US/11/045,024
/ CURRENT FILING DATE: 2005-01-28
/ PRIOR APPLICATION NUMBER: US 09/412,863
/ PRIOR FILING DATE: 1999-10-05
/ PRIOR APPLICATION NUMBER: US 08/027,146
/ PRIOR FILING DATE: 1993-03-05
/ PRIOR APPLICATION NUMBER: US 08/073,205
/ PRIOR FILING DATE: 1993-06-04
/ PRIOR APPLICATION NUMBER: US 08/103,396
/ PRIOR FILING DATE: 1993-08-06
/ PRIOR APPLICATION NUMBER: US 08/159,184
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/159,339
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/205,713
/ PRIOR FILING DATE: 1994-03-04
/ PRIOR APPLICATION NUMBER: US 08/347,610
/ PRIOR FILING DATE: 1994-12-01
/ NUMBER OF SEQ ID NOS: 14528
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 14400
/ LENGTH: 15
/ TYPE: PRF
/ ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-14210

Query Match          24.0%; Score 23; DB 7; Length 15;
Best Local Similarity 40.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 7 GYLTTAAVSP 16
| : : | : |
Db 2 GQVWQAISP 11
```

SEQ ID NO 14400  
LENGTH: 15  
TYPE: PRT  
ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS  
US-11-045-024-14400

Query Match 24.0%; Score 23; DB 7; Length 15;  
Best Local Similarity 40.0%; Pred. No. 3.3e+02;  
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 7 GYLTRAASP 16  
| : : | : | : |  
Db 2 GQWVQAISP 11

RESULT 72  
US-11-045-024-14417  
Sequence 14417, Application US/11045024  
Publication No. US20050271676A1  
GENERAL INFORMATION:

APPLICANT: Sette, Alessandro  
APPLICANT: Sidney, John  
APPLICANT: Southwood, Scott  
APPLICANT: Livingston, Brian  
APPLICANT: Cheenut, Robert  
APPLICANT: Baker, Denise Marie  
APPLICANT: Cells, Estebean  
APPLICANT: Kubo, Ralph  
APPLICANT: Grey, Howard M.  
APPLICANT: Eplimmune Inc.  
TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency  
TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions  
FILE REFERENCE: 2060.0040007  
CURRENT APPLICATION NUMBER: US/11/045,024  
CURRENT FILING DATE: 2005-01-28  
PRIOR APPLICATION NUMBER: US 09/412,863  
PRIOR FILING DATE: 1999-10-05  
PRIOR APPLICATION NUMBER: US 08/027,146  
PRIOR FILING DATE: 1993-03-05  
PRIOR APPLICATION NUMBER: US 08/073,205  
PRIOR FILING DATE: 1993-06-04  
PRIOR APPLICATION NUMBER: US 08/103,396  
PRIOR FILING DATE: 1993-08-06  
PRIOR APPLICATION NUMBER: US 08/159,184  
PRIOR FILING DATE: 1993-11-29  
PRIOR APPLICATION NUMBER: US 08/159,339  
PRIOR FILING DATE: 1993-11-29  
PRIOR APPLICATION NUMBER: US 08/205,713  
PRIOR FILING DATE: 1994-03-04  
PRIOR APPLICATION NUMBER: US 08/347,610  
PRIOR FILING DATE: 1994-12-01  
NUMBER OF SEQ ID NOS: 14528  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 14417

LENGTH: 15  
TYPE: PRT  
ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS  
US-11-045-024-14417

Query Match 24.0%; Score 23; DB 7; Length 15;  
Best Local Similarity 40.0%; Pred. No. 3.3e+02;  
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 7 GYLTRAASP 16  
| : : | : | : |  
Db 2 GQWVQAISP 11

RESULT 73  
US-11-045-024-14477  
Sequence 14477, Application US/11045024  
Publication No. US20050271676A1  
GENERAL INFORMATION:

APPLICANT: Sette, Alessandro  
APPLICANT: Sidney, John  
APPLICANT: Southwood, Scott  
APPLICANT: Livingston, Brian  
APPLICANT: Cheenut, Robert  
APPLICANT: Baker, Denise Marie  
APPLICANT: Cells, Estebean  
APPLICANT: Kubo, Ralph  
APPLICANT: Grey, Howard M.  
APPLICANT: Eplimmune Inc.  
TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency  
TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions  
FILE REFERENCE: 2060.0040007  
CURRENT APPLICATION NUMBER: US/11/045,024  
CURRENT FILING DATE: 2005-01-28  
PRIOR APPLICATION NUMBER: US 09/412,863  
PRIOR FILING DATE: 1999-10-05  
PRIOR APPLICATION NUMBER: US 08/027,146  
PRIOR FILING DATE: 1993-03-05  
PRIOR APPLICATION NUMBER: US 08/073,205  
PRIOR FILING DATE: 1993-06-04  
PRIOR APPLICATION NUMBER: US 08/103,396  
PRIOR FILING DATE: 1993-08-06  
PRIOR APPLICATION NUMBER: US 08/159,184  
PRIOR FILING DATE: 1993-11-29  
PRIOR APPLICATION NUMBER: US 08/159,339  
PRIOR FILING DATE: 1993-11-29  
PRIOR APPLICATION NUMBER: US 08/205,713  
PRIOR FILING DATE: 1994-03-04  
PRIOR APPLICATION NUMBER: US 08/347,610  
PRIOR FILING DATE: 1994-12-01  
NUMBER OF SEQ ID NOS: 14528  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 14477  
LENGTH: 15  
TYPE: PRT  
ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS  
US-11-045-024-14477

Query Match 24.0%; Score 23; DB 7; Length 15;  
Best Local Similarity 40.0%; Pred. No. 3.3e+02;  
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 7 GYLTRAASP 16  
| : : | : | : |  
Db 2 GQWVQAISP 11

RESULT 74  
US-11-033-039-581  
Sequence 581, Application US/11033039  
Publication No. US20060002947A1  
GENERAL INFORMATION:

APPLICANT: HUMPHREYS, ROBERT  
APPLICANT: XU, MINZHEN  
TITLE OF INVENTION: LI-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES  
FILE REFERENCE: REH-2017US01  
CURRENT APPLICATION NUMBER: US/11/033,039  
CURRENT FILING DATE: 2005-01-11  
PRIOR APPLICATION NUMBER: 10/245,871  
PRIOR FILING DATE: 2002-09-17  
PRIOR APPLICATION NUMBER: 10/197,000  
PRIOR FILING DATE: 2002-07-17  
PRIOR APPLICATION NUMBER: 09/396,813  
PRIOR FILING DATE: 1999-09-14  
NUMBER OF SEQ ID NOS: 1452  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 581  
LENGTH: 15  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-11-033-039-581

US-11-033-039-581

Query Match 24.0%; Score 23; DB 7; Length 15;  
Best Local Similarity 80.0%; Pred. No. 3.3e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 14 VSPGK 18  
| : : : :  
DB 8 LSPGK 12

## RESULT 75

US-11-041-893-176  
; Sequence 176, Application US/11041893  
; Publication No. US2006002941A1  
; GENERAL INFORMATION:  
; APPLICANT: Mahaitas, Gregory G.  
; TITLE OF INVENTION: COMPOSITIONS COMPRISING IMMUNE RESPONSE  
; FILE REFERENCE: 100123.401  
; CURRENT FILING DATE: 2005-01-24  
; PRIOR FILING DATE: 2004-10-06  
; PRIOR APPLICATION NUMBER: US 60/616,855  
; PRIOR FILING DATE: 2004-01-23  
; NUMBER OF SEQ ID NOS: 295  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 176  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Trypanosoma cruzi  
US-11-041-893-176

Query Match 24.0%; Score 23; DB 7; Length 15;  
Best Local Similarity 44.4%; Pred. No. 3.3e+02;  
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 6 HGYLTAAY 14  
| : : : :  
DB 2 HNPFLVASV 10

## RESULT 76

US-11-033-039-839  
; Sequence 839, Application US/11033039  
; Publication No. US2006002947A1  
; GENERAL INFORMATION:  
; APPLICANT: HUMPHREYS, ROBERT  
; APPLICANT: XU, MINZHEN  
; TITLE OF INVENTION: LI-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES  
; FILE REFERENCE: REH-2017US01  
; CURRENT FILING DATE: 2005-01-11  
; PRIOR FILING DATE: 2002-09-17  
; PRIOR APPLICATION NUMBER: 10/245,871  
; PRIOR FILING DATE: 2002-07-17  
; PRIOR APPLICATION NUMBER: 10/197,000  
; PRIOR FILING DATE: 2002-07-17  
; PRIOR APPLICATION NUMBER: 09/396,813  
; PRIOR FILING DATE: 1999-09-14  
; NUMBER OF SEQ ID NOS: 1452  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 839  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-033-039-839

Query Match 24.0%; Score 23; DB 7; Length 16;  
Best Local Similarity 60.0%; Pred. No. 3.6e+02;  
Matches 6; Conservative 1; Mismatches 1; Indels 2; Gaps 1;

QY 6 HG--YLLTAA 13  
| : : : :  
DB 5 HGSXYLATAS 14

## RESULT 77

US-11-073-347-118  
; Sequence 118, Application US/11073347  
; Publication No. US20050260234A1  
; GENERAL INFORMATION:  
; APPLICANT: SIMARD, John J. L.  
; APPLICANT: DIAMOND, David C.  
; TITLE OF INVENTION: ANTI-NEOVASCULATURE PREPARATIONS FOR  
; FILE REFERENCE: MANKR.015C1  
; CURRENT FILING DATE: 2005-03-04  
; PRIOR FILING DATE: 2002-03-07  
; PRIOR APPLICATION NUMBER: 60/274,063  
; PRIOR FILING DATE: 2001-03-07  
; NUMBER OF SEQ ID NOS: 159  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 118  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-11-073-347-118

Query Match 24.0%; Score 23; DB 7; Length 17;  
Best Local Similarity 66.7%; Pred. No. 3.8e+02;  
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 APEPHG 7  
| : : : :  
DB 1 APEPG 6

## RESULT 78

US-11-033-039-993  
; Sequence 993, Application US/11033039  
; Publication No. US2006002947A1  
; GENERAL INFORMATION:  
; APPLICANT: HUMPHREYS, ROBERT  
; APPLICANT: XU, MINZHEN  
; TITLE OF INVENTION: LI-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES  
; FILE REFERENCE: REH-2017US01  
; CURRENT FILING DATE: 2005-01-11  
; PRIOR FILING DATE: 2002-09-17  
; PRIOR APPLICATION NUMBER: 10/245,871  
; PRIOR FILING DATE: 2002-07-17  
; PRIOR APPLICATION NUMBER: 10/197,000  
; PRIOR FILING DATE: 2002-07-17  
; PRIOR APPLICATION NUMBER: 09/396,813  
; PRIOR FILING DATE: 1999-09-14  
; NUMBER OF SEQ ID NOS: 1452  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 993  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: hybrid peptide  
; FEATURE:  
; NAME/KEY: MOD\_RES  
; LOCATION: (5)..(5)  
; OTHER INFORMATION: Ava  
US-11-033-039-993

Query Match 24.0%; Score 23; DB 7; Length 18;  
Best Local Similarity 40.0%; Pred. No. 4.1e+02;  
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 7 GYLTAAYSP 16  
| : : : :  
DB 7 GYLTAAYSP 16

Db 8 GQMHQAISP 17

RESULT 79

US-11-033-039-1048

/ Sequence 1048, Application US/11033039

/ Publication No. US2006002947A1

/ GENERAL INFORMATION:

/ APPLICANT: HUMPHREYS, ROBERT

/ TITLE OF INVENTION: LI-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES

/ FILE REFERENCE: REH-2017US01

/ CURRENT FILING DATE: 2005-01-11

/ PRIOR APPLICATION NUMBER: 10/245,871

/ PRIOR FILING DATE: 2002-09-17

/ PRIOR APPLICATION NUMBER: 10/197,000

/ PRIOR FILING DATE: 2002-07-17

/ PRIOR APPLICATION NUMBER: 09/396,813

/ PRIOR FILING DATE: 1999-09-14

/ NUMBER OF SEQ ID NOS: 1452

/ SOFTWARE: PatentIn version 3.3

/ SEQ ID NO 1048

/ LENGTH: 18

/ TYPE: PRT

/ ORGANISM: Artificial Sequence

/ FEATURE:

/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic

/ FEATURE:

/ NAME/KEY: MOD\_RES

/ LOCATION: (5)..(5)

/ OTHER INFORMATION: Ava

US-11-033-039-1048

Query Match 24.0%; Score 23; DB 7; Length 18;

Best Local Similarity 44.4%; Pred. No. 4.1e+02;

Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 7 GYLTPAVS 15

Db 10 GPILTGSPS 18

RESULT 80

US-11-054-515-3036

/ Sequence 3036, Application US/11054515

/ Publication No. US2005025532A1

/ GENERAL INFORMATION:

/ APPLICANT: Ruben et al.

/ TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys

/ FILE REFERENCE: PFS23P3

/ CURRENT APPLICATION NUMBER: US/11/054,515

/ CURRENT FILING DATE: 2005-02-10

/ PRIOR APPLICATION NUMBER: 60/543,296

/ PRIOR FILING DATE: 2004-02-11

/ PRIOR APPLICATION NUMBER: 60/580,347

/ PRIOR FILING DATE: 2004-06-18

/ PRIOR APPLICATION NUMBER: 10/293,418

/ PRIOR FILING DATE: 2002-11-14

/ PRIOR APPLICATION NUMBER: 60/331,469

/ PRIOR FILING DATE: 2001-11-16

/ PRIOR APPLICATION NUMBER: 60/340,817

/ PRIOR FILING DATE: 2001-12-19

/ PRIOR APPLICATION NUMBER: 09/880,748

/ PRIOR FILING DATE: 2001-06-15

/ PRIOR APPLICATION NUMBER: 60/293,499

/ PRIOR FILING DATE: 2001-05-25

/ PRIOR APPLICATION NUMBER: 60/277,379

/ PRIOR FILING DATE: 2001-03-21

/ PRIOR APPLICATION NUMBER: 60/276,248

/ PRIOR FILING DATE: 2001-03-16

/ PRIOR APPLICATION NUMBER: 60/240,816

/ PRIOR FILING DATE: 2000-10-17

/ Remaining Prior Application data removed - See File Wrapper or PAM.

/ NUMBER OF SEQ ID NOS: 3247

/ SEQ ID NO 3036

/ LENGTH: 19

/ TYPE: PRT

/ ORGANISM: Homo sapiens

US-11-054-515-3036

Query Match 24.0%; Score 23; DB 7; Length 19;

Best Local Similarity 66.7%; Pred. No. 4.4e+02;

Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 PEPHG 8

Db 11 FYPSGI 16

RESULT 81

US-11-022-562-286

/ Sequence 286, Application US/11022562

/ Publication No. US20050249742A1

/ GENERAL INFORMATION:

/ APPLICANT: Ruprecht, Ruth M.

/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING

/ FILE REFERENCE: DFN-043CN

/ CURRENT APPLICATION NUMBER: US/11/022,562

/ CURRENT FILING DATE: 2004-12-22

/ PRIOR APPLICATION NUMBER: PCT/US03/20322

/ PRIOR FILING DATE: 2003-06-27

/ PRIOR APPLICATION NUMBER: 60/392718

/ PRIOR FILING DATE: 2002-06-27

/ NUMBER OF SEQ ID NOS: 340

/ SOFTWARE: FastSeq for Windows Version 4.0

/ SEQ ID NO 286

/ LENGTH: 20

/ TYPE: PRT

/ ORGANISM: Human Immunodeficiency Virus

US-11-022-562-286

Query Match 24.0%; Score 23; DB 7; Length 20;

Best Local Similarity 40.0%; Pred. No. 4.6e+02;

Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 7 GYLTPAVS 16

Db 10 GQMHQAISP 19

RESULT 82

US-11-022-562-287

/ Sequence 287, Application US/11022562

/ Publication No. US20050249742A1

/ GENERAL INFORMATION:

/ APPLICANT: Ruprecht, Ruth M.

/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING

/ FILE REFERENCE: DFN-043CN

/ CURRENT APPLICATION NUMBER: US/11/022,562

/ CURRENT FILING DATE: 2004-12-22

/ PRIOR APPLICATION NUMBER: PCT/US03/20322

/ PRIOR FILING DATE: 2003-06-27

/ PRIOR APPLICATION NUMBER: 60/392718

/ PRIOR FILING DATE: 2002-06-27

/ NUMBER OF SEQ ID NOS: 340

/ SOFTWARE: FastSeq for Windows Version 4.0

/ SEQ ID NO 287

/ LENGTH: 20

/ TYPE: PRT

/ ORGANISM: Human Immunodeficiency Virus

US-11-022-562-287

Query Match 24.0%; Score 23; DB 7; Length 20;  
Best Local Similarity 40.0%; Pred. No. 4.6e+02;  
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 7 YL-TAAVSP 16  
DB 10 GCMVHQALSP 19

RESULT 83

US-11-045-024-3558  
; Sequence 3558, Application US/11045024  
; Publication No. US20050271676A1  
; GENERAL INFORMATION:  
; APPLICANT: Sette, Alessandro  
; APPLICANT: Sidney, John  
; APPLICANT: Southwood, Scott  
; APPLICANT: Livingston, Brian  
; APPLICANT: Chesnut, Robert  
; APPLICANT: Baker, Denise Marie  
; APPLICANT: Kubo, Ralph  
; APPLICANT: Grey, Howard M.  
; APPLICANT: EpiImmune Inc.  
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency  
; TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions  
; FILE REFERENCE: 2060.0040007  
; CURRENT APPLICATION NUMBER: US/11/045,024  
; PRIOR FILING DATE: 2005-01-28  
; PRIOR APPLICATION NUMBER: US 09/412,863  
; PRIOR FILING DATE: 1999-10-05  
; PRIOR APPLICATION NUMBER: US 08/027,146  
; PRIOR FILING DATE: 1993-03-05  
; PRIOR APPLICATION NUMBER: US 08/073,205  
; PRIOR FILING DATE: 1993-06-04  
; PRIOR APPLICATION NUMBER: US 08/103,396  
; PRIOR FILING DATE: 1993-08-06  
; PRIOR APPLICATION NUMBER: US 08/159,184  
; PRIOR FILING DATE: 1993-11-29  
; PRIOR APPLICATION NUMBER: US 08/159,339  
; PRIOR FILING DATE: 1993-11-29  
; PRIOR APPLICATION NUMBER: US 08/205,713  
; PRIOR FILING DATE: 1994-03-04  
; PRIOR APPLICATION NUMBER: US 08/347,610  
; PRIOR FILING DATE: 1994-12-01  
; NUMBER OF SEQ ID NOS: 14528  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3558  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS  
US-11-045-024-3558

Query Match 23.4%; Score 22.5; DB 7; Length 11;  
Best Local Similarity 60.0%; Pred. No. 2.9e+02;  
Matches 6; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

QY 8 YL-TAAVSP 16  
DB 1 YLALTLALKP 10

RESULT 84

US-11-045-024-10541  
; Sequence 10541, Application US/11045024  
; Publication No. US20050271676A1  
; GENERAL INFORMATION:  
; APPLICANT: Sette, Alessandro  
; APPLICANT: Sidney, John  
; APPLICANT: Southwood, Scott  
; APPLICANT: Livingston, Brian

APPLICANT: Chesnut, Robert  
APPLICANT: Baker, Denise Marie  
APPLICANT: Kubo, Ralph  
APPLICANT: Grey, Howard M.  
APPLICANT: EpiImmune Inc.

; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency  
; TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions  
; FILE REFERENCE: 2060.0040007  
; CURRENT APPLICATION NUMBER: US/11/045,024  
; PRIOR FILING DATE: 2005-01-28  
; PRIOR APPLICATION NUMBER: US 09/412,863  
; PRIOR FILING DATE: 1999-10-05  
; PRIOR APPLICATION NUMBER: US 08/027,146  
; PRIOR FILING DATE: 1993-03-05  
; PRIOR APPLICATION NUMBER: US 08/073,205  
; PRIOR FILING DATE: 1993-06-04  
; PRIOR APPLICATION NUMBER: US 08/103,396  
; PRIOR FILING DATE: 1993-08-06  
; PRIOR APPLICATION NUMBER: US 08/159,184  
; PRIOR FILING DATE: 1993-11-29  
; PRIOR APPLICATION NUMBER: US 08/159,339  
; PRIOR FILING DATE: 1993-11-29  
; PRIOR APPLICATION NUMBER: US 08/205,713  
; PRIOR FILING DATE: 1994-03-04  
; PRIOR APPLICATION NUMBER: US 08/347,610  
; PRIOR FILING DATE: 1994-12-01  
; NUMBER OF SEQ ID NOS: 14528  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 10541  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS  
US-11-045-024-10541

Query Match 23.4%; Score 22.5; DB 7; Length 11;  
Best Local Similarity 60.0%; Pred. No. 2.9e+02;  
Matches 6; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

QY 8 YL-TAAVSP 16  
DB 1 YLALTLALKP 10

RESULT 85  
US-11-045-024-12349  
; Sequence 12349, Application US/11045024  
; Publication No. US20050271676A1  
; GENERAL INFORMATION:  
; APPLICANT: Sette, Alessandro  
; APPLICANT: Sidney, John  
; APPLICANT: Southwood, Scott  
; APPLICANT: Livingston, Brian  
; APPLICANT: Chesnut, Robert  
; APPLICANT: Baker, Denise Marie  
; APPLICANT: Kubo, Ralph  
; APPLICANT: Grey, Howard M.  
; APPLICANT: EpiImmune Inc.  
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency  
; TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions  
; FILE REFERENCE: 2060.0040007  
; CURRENT APPLICATION NUMBER: US/11/045,024  
; PRIOR FILING DATE: 2005-01-28  
; PRIOR APPLICATION NUMBER: US 09/412,863  
; PRIOR FILING DATE: 1999-10-05  
; PRIOR APPLICATION NUMBER: US 08/027,146  
; PRIOR FILING DATE: 1993-03-05  
; PRIOR APPLICATION NUMBER: US 08/073,205  
; PRIOR FILING DATE: 1993-06-04  
; PRIOR APPLICATION NUMBER: US 08/103,396  
; PRIOR FILING DATE: 1993-08-06  
; PRIOR APPLICATION NUMBER: US 08/159,184

```

; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 12349
; LENGTH: 11
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-12349
```

```
Query Match      23.4%; Score 22.5; DB 7; Length 11;
Best Local Similarity 60.0%; Pred. No. 2.9e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 1; Gaps 1;
```

```
QY      8 YL-LTRAAVSP 16
      |||||:|
Db      1 YLALTRALIKP 10
```

```
RESULT 86
US-11-045-024-13314
; Sequence 13314, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: EpiImmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 13314
; LENGTH: 15
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-13314
```

```
Query Match      23.4%; Score 22.5; DB 7; Length 15;
Best Local Similarity 60.0%; Pred. No. 4.1e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 1; Gaps 1;
```

```
QY      8 YL-LTRAAVSP 16
```

```
Db      6 YLALTRALIKP 15
      |||||:|
```

```
RESULT 87
US-10-503-575-197
; Sequence 197, Application US/10503575
; Publication No. US20050244823A1
; GENERAL INFORMATION:
; APPLICANT: Drijfhout, Jan Router
; APPLICANT: van Veele, Petrus Antonius
; APPLICANT: Koning, Frits
; TITLE OF INVENTION: NOVEL EPITOPES FOR CELIAC DISEASE AND AUTOIMMUNE DISEASES, METHOD
; TITLE OF INVENTION: DETECTING THOSE AND NOVEL NON-ANTIGENIC FOOD COMPOUNDS
; FILE REFERENCE: 2799/72843-PCT-US
; CURRENT APPLICATION NUMBER: US/10/503,575
; CURRENT FILING DATE: 2004-08-04
; PRIOR APPLICATION NUMBER: PCT/NL03/00077
; PRIOR FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: EP 02075456.0
; PRIOR FILING DATE: 2002-02-04
; NUMBER OF SEQ ID NOS: 340
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 197
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-503-575-197
```

```
Query Match      23.4%; Score 22.5; DB 6; Length 19;
Best Local Similarity 58.3%; Pred. No. 5.3e+02;
Matches 7; Conservative 1; Mismatches 3; Indels 1; Gaps 1;
```

```
QY      7 GYLTA-AVSPG 17
      |||||:|
Db      2 GWLGAQAQEPG 13
```

```
RESULT 88
US-11-045-024-1025
; Sequence 1025, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: EpiImmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
```



```
/ PRIOR FILING DATE: 1994-12-01
/ NUMBER OF SEQ ID NOS: 14528
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 1025
/ LENGTH: 8
/ TYPE: PRT
/ ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-1025

Query Match      22.9%; Score 22; DB 7; Length 8;
Best Local Similarity 80.0%; Pred. No. 5.5e+04;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      13 AVSPG 17
        ||:|
Db      2 AVNPG 6

RESULT 89
US-11-045-024-3518
/ Sequence 3518, Application US/11045024
/ Publication No. US20050271676A1
/ GENERAL INFORMATION:
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Livingston, Brian
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Baker, Denise Marie
/ APPLICANT: Celis, Bsteban
/ APPLICANT: Kubo, Ralph
/ APPLICANT: Grey, Howard M.
/ APPLICANT: Bpimmune Inc.
/ TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
/ FILE REFERENCE: 2060.0040007
/ CURRENT APPLICATION NUMBER: US/11/045,024
/ PRIOR FILING DATE: 2005-01-28
/ PRIOR APPLICATION NUMBER: US 09/412,863
/ PRIOR FILING DATE: 1999-10-05
/ PRIOR APPLICATION NUMBER: US 08/027,146
/ PRIOR FILING DATE: 1993-03-05
/ PRIOR APPLICATION NUMBER: US 08/073,205
/ PRIOR FILING DATE: 1993-06-04
/ PRIOR APPLICATION NUMBER: US 08/103,396
/ PRIOR FILING DATE: 1993-08-06
/ PRIOR APPLICATION NUMBER: US 08/159,184
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/159,339
/ PRIOR FILING DATE: 1994-03-04
/ PRIOR APPLICATION NUMBER: US 08/347,610
/ PRIOR FILING DATE: 1994-12-01
/ NUMBER OF SEQ ID NOS: 14528
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 3518
/ LENGTH: 8
/ TYPE: PRT
/ ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-3518

Query Match      22.9%; Score 22; DB 7; Length 8;
Best Local Similarity 57.1%; Pred. No. 5.5e+04;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
/ Sequence 4007, Application US/11045024
/ Publication No. US20050271676A1
/ GENERAL INFORMATION:
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Livingston, Brian
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Baker, Denise Marie
/ APPLICANT: Celis, Bsteban
/ APPLICANT: Kubo, Ralph
/ APPLICANT: Grey, Howard M.
/ APPLICANT: Bpimmune Inc.
/ TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
/ FILE REFERENCE: 2060.0040007
/ CURRENT APPLICATION NUMBER: US/11/045,024
/ PRIOR FILING DATE: 2005-01-28
/ PRIOR APPLICATION NUMBER: US 09/412,863
/ PRIOR FILING DATE: 1999-10-05
/ PRIOR APPLICATION NUMBER: US 08/027,146
/ PRIOR FILING DATE: 1993-03-05
/ PRIOR APPLICATION NUMBER: US 08/073,205
/ PRIOR FILING DATE: 1993-06-04
/ PRIOR APPLICATION NUMBER: US 08/103,396
/ PRIOR FILING DATE: 1993-08-06
/ PRIOR APPLICATION NUMBER: US 08/159,184
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/159,339
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/205,713
/ PRIOR FILING DATE: 1994-03-04
/ PRIOR APPLICATION NUMBER: US 08/347,610
/ PRIOR FILING DATE: 1994-12-01
/ NUMBER OF SEQ ID NOS: 14528
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 4007
/ LENGTH: 8
/ TYPE: PRT
/ ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-4007

Query Match      22.9%; Score 22; DB 7; Length 8;
Best Local Similarity 80.0%; Pred. No. 5.5e+04;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      13 AVSPG 17
        ||:|
Db      3 AVNPG 7

RESULT 91
US-11-045-024-6362
/ Sequence 6362, Application US/11045024
/ Publication No. US20050271676A1
/ GENERAL INFORMATION:
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Livingston, Brian
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Baker, Denise Marie
/ APPLICANT: Celis, Bsteban
/ APPLICANT: Kubo, Ralph
/ APPLICANT: Grey, Howard M.
/ APPLICANT: Bpimmune Inc.
/ TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
/ FILE REFERENCE: 2060.0040007
/ CURRENT APPLICATION NUMBER: US/11/045,024
/ PRIOR FILING DATE: 2005-01-28
/ PRIOR APPLICATION NUMBER: US 09/412,863
/ PRIOR FILING DATE: 1999-10-05
```

```
/ PRIOR APPLICATION NUMBER: US 08/027,146
/ PRIOR FILING DATE: 1993-03-05
/ PRIOR APPLICATION NUMBER: US 08/073,205
/ PRIOR FILING DATE: 1993-06-04
/ PRIOR APPLICATION NUMBER: US 08/103,396
/ PRIOR FILING DATE: 1993-08-06
/ PRIOR APPLICATION NUMBER: US 08/159,184
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/159,339
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/205,713
/ PRIOR FILING DATE: 1994-03-04
/ PRIOR APPLICATION NUMBER: US 08/347,610
/ PRIOR FILING DATE: 1994-12-01
/ NUMBER OF SEQ ID NOS: 14528
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 6362
/ LENGTH: 8
/ TYPE: PRT
/ ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-6362
```

```
Query Match          22.9%; Score 22; DB 7; Length 8;
Best Local Similarity 80.0%; Pred. No. 5.5e+04;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      13 AVSPG 17
        |||:|
DB       2 AVNPG 6
```

```
RESULT 92
US-11-045-024-10522
```

```
/ Sequence 10522, Application US/11045024
/ Publication No. US20050271676A1
/ GENERAL INFORMATION:
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Livingston, Brian
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Baker, Denise Marie
/ APPLICANT: Cells, Esteban
/ APPLICANT: Kubo, Ralph
/ APPLICANT: Grey, Howard M.
/ APPLICANT: Eptimmune Inc.
/ TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
/ FILE REFERENCE: 2060.0040007
/ CURRENT APPLICATION NUMBER: US/11/045,024
/ PRIOR FILING DATE: 2005-01-28
/ PRIOR APPLICATION NUMBER: US 09/412,863
/ PRIOR FILING DATE: 1999-10-05
/ PRIOR APPLICATION NUMBER: US 08/027,146
/ PRIOR FILING DATE: 1993-03-05
/ PRIOR APPLICATION NUMBER: US 08/073,205
/ PRIOR FILING DATE: 1993-06-04
/ PRIOR APPLICATION NUMBER: US 08/103,396
/ PRIOR FILING DATE: 1993-08-06
/ PRIOR APPLICATION NUMBER: US 08/159,184
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/159,339
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/205,713
/ PRIOR FILING DATE: 1994-03-04
/ PRIOR APPLICATION NUMBER: US 08/347,610
/ PRIOR FILING DATE: 1994-12-01
/ NUMBER OF SEQ ID NOS: 14528
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 10522
```

```
LENGTH: 8
TYPE: PRT
ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
```

```
US-11-045-024-10522
```

```
Query Match          22.9%; Score 22; DB 7; Length 8;
Best Local Similarity 57.1%; Pred. No. 5.5e+04;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      10 LTAASP 16
        |||:|
DB       1 LTAALPK 7
```

```
RESULT 93
```

```
US-11-045-024-12335
/ Sequence 12335, Application US/11045024
/ Publication No. US20050271676A1
/ GENERAL INFORMATION:
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Livingston, Brian
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Baker, Denise Marie
/ APPLICANT: Cells, Esteban
/ APPLICANT: Kubo, Ralph
/ APPLICANT: Grey, Howard M.
/ APPLICANT: Eptimmune Inc.
/ TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
/ FILE REFERENCE: 2060.0040007
/ CURRENT APPLICATION NUMBER: US/11/045,024
/ PRIOR FILING DATE: 2005-01-28
/ PRIOR APPLICATION NUMBER: US 09/412,863
/ PRIOR FILING DATE: 1999-10-05
/ PRIOR APPLICATION NUMBER: US 08/027,146
/ PRIOR FILING DATE: 1993-03-05
/ PRIOR APPLICATION NUMBER: US 08/073,205
/ PRIOR FILING DATE: 1993-06-04
/ PRIOR APPLICATION NUMBER: US 08/103,396
/ PRIOR FILING DATE: 1993-08-06
/ PRIOR APPLICATION NUMBER: US 08/159,184
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/159,339
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/205,713
/ PRIOR FILING DATE: 1994-03-04
/ PRIOR APPLICATION NUMBER: US 08/347,610
/ PRIOR FILING DATE: 1994-12-01
/ NUMBER OF SEQ ID NOS: 14528
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 12335
```

```
LENGTH: 8
TYPE: PRT
ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
```

```
US-11-045-024-12335
```

```
Query Match          22.9%; Score 22; DB 7; Length 8;
Best Local Similarity 57.1%; Pred. No. 5.5e+04;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      10 LTAASP 16
        |||:|
DB       1 LTAALPK 7
```

```
RESULT 94
```

```
US-11-045-024-12616
/ Sequence 12616, Application US/11045024
/ Publication No. US20050271676A1
/ GENERAL INFORMATION:
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Livingston, Brian
```

APPLICANT: Chesnut, Robert  
APPLICANT: Baker, Denise Marie  
APPLICANT: Celis, Bateban  
APPLICANT: Kubo, Ralph  
APPLICANT: Grey, Howard M.  
APPLICANT: EpiImmune Inc.  
TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency  
FILE REFERENCE: 2060.0040007  
CURRENT APPLICATION NUMBER: US/11/045,024  
CURRENT FILING DATE: 2005-01-28  
PRIOR APPLICATION NUMBER: US 09/412,863  
PRIOR FILING DATE: 1999-10-05  
PRIOR APPLICATION NUMBER: US 08/027,146  
PRIOR FILING DATE: 1993-03-05  
PRIOR APPLICATION NUMBER: US 08/073,205  
PRIOR FILING DATE: 1993-06-04  
PRIOR APPLICATION NUMBER: US 08/103,396  
PRIOR FILING DATE: 1993-08-06  
PRIOR APPLICATION NUMBER: US 08/159,184  
PRIOR FILING DATE: 1993-11-29  
PRIOR APPLICATION NUMBER: US 08/159,339  
PRIOR FILING DATE: 1993-11-29  
PRIOR APPLICATION NUMBER: US 08/205,713  
PRIOR FILING DATE: 1994-03-04  
PRIOR APPLICATION NUMBER: US 08/347,610  
PRIOR FILING DATE: 1994-12-01  
NUMBER OF SEQ ID NOS: 14528  
SOFTWARE: FASTSEQ for Windows Version 4.0  
SEQ ID NO 12616  
LENGTH: 8  
TYPE: PRT  
ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS  
US-11-045-024-12616

Query Match 22.9%; Score 22; DB 7; Length 8;  
Best Local Similarity 80.0%; Pred. No. 5.5e+04;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 13 AVSPG 17  
DB 3 AVMPG 7

RESULT 95  
US-11-116-144-73  
Sequence 73, Application US/11116144  
Publication No. US20050277181A1  
GENERAL INFORMATION:  
APPLICANT: BERTHET, FRANCOIS XAVIER  
APPLICANT: CASADEVAL, FRANCESC VAYREDA  
APPLICANT: SANZ MARIA, MARIA CRUZ  
APPLICANT: GARCIA, TERESA LLOP  
APPLICANT: OLE, ANGELS MOR  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETECTING PATHOGEN  
FILE REFERENCE: INL-084  
CURRENT APPLICATION NUMBER: US/11/116,144  
CURRENT FILING DATE: 2005-04-27  
PRIOR APPLICATION NUMBER: PCT/ES04/000581  
PRIOR FILING DATE: 2004-12-23  
PRIOR APPLICATION NUMBER: EP 03380307.3  
PRIOR FILING DATE: 2003-12-23  
NUMBER OF SEQ ID NOS: 301  
SOFTWARE: PatentIn Ver. 3.3  
SEQ ID NO 73  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Bos taurus Immunodeficiency virus  
US-11-116-144-73

Query Match 22.9%; Score 22; DB 7; Length 8;  
Best Local Similarity 75.0%; Pred. No. 5.5e+04;

Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 4 EPHG 7  
DB 2 KPHG 5

RESULT 96  
US-10-999-866-60  
Sequence 60, Application US/10999866  
Publication No. US20050266004A1  
GENERAL INFORMATION:  
APPLICANT: GILES-KOMAR, Jill; SCALLON, Bernard J.; CAI, Ann  
TITLE OF INVENTION: ANTI-HUMAN LYMPHOTOXIN ALPHA ANTIBODIES, COMPOSITIONS, METHODS  
FILE REFERENCE: CEN5042NP  
CURRENT APPLICATION NUMBER: US/10/999,866  
CURRENT FILING DATE: 2004-11-30  
PRIOR APPLICATION NUMBER: 60/527,794  
PRIOR FILING DATE: 2003-12-08  
NUMBER OF SEQ ID NOS: 61  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 60  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE: MISC FEATURE  
NAME/KEY: LOCATION: (1)-(9)  
OTHER INFORMATION: HC CDR 3  
US-10-999-866-60

Query Match 22.9%; Score 22; DB 6; Length 9;  
Best Local Similarity 50.0%; Pred. No. 5.5e+04;  
Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 DAFEPHGY 8  
DB 2 DVNNPFGY 9

RESULT 97  
US-11-045-024-1138  
Sequence 1138, Application US/11045024  
Publication No. US20050271676A1  
GENERAL INFORMATION:  
APPLICANT: Sette, Alessandro  
APPLICANT: Sidney, John  
APPLICANT: Southwood, Scott  
APPLICANT: Livingston, Brian  
APPLICANT: Chesnut, Robert  
APPLICANT: Baker, Denise Marie  
APPLICANT: Celis, Bateban  
APPLICANT: Kubo, Ralph  
APPLICANT: Grey, Howard M.  
TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency  
FILE REFERENCE: 2060.0040007  
CURRENT APPLICATION NUMBER: US/11/045,024  
CURRENT FILING DATE: 2005-01-28  
PRIOR APPLICATION NUMBER: US 09/412,863  
PRIOR FILING DATE: 1999-10-05  
PRIOR APPLICATION NUMBER: US 08/027,146  
PRIOR FILING DATE: 1993-03-05  
PRIOR APPLICATION NUMBER: US 08/073,205  
PRIOR FILING DATE: 1993-06-04  
PRIOR APPLICATION NUMBER: US 08/103,396  
PRIOR FILING DATE: 1993-08-06  
PRIOR APPLICATION NUMBER: US 08/159,184  
PRIOR FILING DATE: 1993-11-29  
PRIOR APPLICATION NUMBER: US 08/347,610  
PRIOR FILING DATE: 1993-11-29  
PRIOR APPLICATION NUMBER: US 08/205,713

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; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1138
; LENGTH: 9
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-1138
```

```
Query Match      22.9%; Score 22; DB 7; Length 9;
Best Local Similarity 80.0%; Pred. No. 5.5e+04;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      13 AVSPG 17
      |||:|
DB      1 AVNPG 5
```

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RESULT 98
US-11-045-024-3530
; Sequence 3530, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Cells, Esteban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: EpiImmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3530
; LENGTH: 9
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-3530
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Query Match      22.9%; Score 22; DB 7; Length 9;
Best Local Similarity 57.1%; Pred. No. 5.5e+04;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
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```
QY      10 LTRAVSP 16
      |||:|
DB      2 LTRALINP 8
```

```
RESULT 99
US-11-045-024-4061
; Sequence 4061, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Cells, Esteban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: EpiImmune Inc.
```

```
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4061
; LENGTH: 9
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-4061
```

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Query Match      22.9%; Score 22; DB 7; Length 9;
Best Local Similarity 80.0%; Pred. No. 5.5e+04;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      13 AVSPG 17
      |||:|
DB      3 AVNPG 7
```

```
RESULT 100
US-11-045-024-5639
; Sequence 5639, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Cells, Esteban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: EpiImmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; CURRENT FILING DATE: 2005-01-28
```

/ PRIOR APPLICATION NUMBER: US 09/412,863  
 / PRIOR FILING DATE: 1999-10-05  
 / PRIOR APPLICATION NUMBER: US 08/027,146  
 / PRIOR FILING DATE: 1993-03-05  
 / PRIOR APPLICATION NUMBER: US 08/073,205  
 / PRIOR FILING DATE: 1993-06-04  
 / PRIOR APPLICATION NUMBER: US 08/103,396  
 / PRIOR FILING DATE: 1993-08-06  
 / PRIOR APPLICATION NUMBER: US 08/159,184  
 / PRIOR FILING DATE: 1993-11-29  
 / PRIOR APPLICATION NUMBER: US 08/159,339  
 / PRIOR FILING DATE: 1993-11-29  
 / PRIOR APPLICATION NUMBER: US 08/205,713  
 / PRIOR FILING DATE: 1994-03-04  
 / PRIOR APPLICATION NUMBER: US 08/347,610  
 / PRIOR FILING DATE: 1994-12-01  
 / NUMBER OF SEQ ID NOS: 14528  
 / SOFTWARE: FastSeq for Windows Version 4.0  
 / SEQ ID NO 5639  
 / LENGTH: 9  
 / TYPE: PRT  
 / ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS  
 US-11-045-024-5639

Query Match 22.9%, Score 22, DB 7, Length 9,  
 Best Local Similarity 80.0%, Pred. No. 5.5e+04,  
 Matches 4, Conservative 1, Mismatches 0, Indels 0, Gaps 0,  
 QY 13 AVSPG 17  
 ||:|  
 Db 4 AVNPG 8

Search completed: January 20, 2006, 19:46:32  
 Job time : 8.26923 secs

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GenCore version 5.1.6  
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OM protein - protein search, using SW model

Run on: January 20, 2006, 18:55:50 ; Search time 10.2115 Seconds

(without alignments)  
169,602 Million cell updates/sec

Title: US-09-662-293-6

Perfect score: 96

Sequence: 1 DAEPHGYLTAVSPRK 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 3886

Minimum DB seq length: 0

Maximum DB seq length: 20

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

1: PIR 80:\*

2: p1r1:\*

3: p1r2:\*

4: p1r3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	29	30.2	15	2	B56046	urinary tract ston
2	28	29.2	20	2	B39419	collagen alpha 5(I
3	28	29.2	20	2	A61264	MHC class I histoc
4	27	28.1	9	2	863491	diseasimulatory sulf
5	27	28.1	20	2	868028	iodochronine 5'-mo
6	27	28.1	20	2	A36016	granulocyte inhibi
7	25	26.0	10	2	PT0213	T-cell receptor al
8	25	26.0	13	2	863492	diseasimulatory sulf
9	25	26.0	14	2	B38222	exonuclease ABC c
10	25	26.0	16	2	H35141	T-cell receptor de
11	25	26.0	16	4	A33171	hypothetical prote
12	25	26.0	20	2	823981	outer layer protei
13	24	25.0	13	2	B47415	mannose-1-phosphat
14	24	25.0	14	2	PH1305	Ig heavy chain DJ
15	24	25.0	14	4	S00843	hypothetical prote
16	24	25.0	15	2	S10741	phosphoglucosylase
17	24	25.0	16	2	866613	protein p128 - Frl
18	23.5	24.5	16	2	A59155	multicystatin - Frl
19	23	24.0	11	1	GMROL	leucosulfakinin -
20	23	24.0	16	2	PH1604	Ig H chain V-D-J r
21	23	24.0	16	2	B36300	T-cell receptor de
22	23	24.0	18	2	T78841	chromoprotein rec
23	23	24.0	20	2	H28949	ribosomal protein
24	22	22.9	13	2	PH1772	T-cell receptor al
25	22	22.9	17	2	859512	probable integrin
26	22	22.9	20	2	A61276	superoxide dismuta
27	22	22.9	20	2	846479	retinoid-X-recepto
28	21	21.9	8	2	PH1618	Ig H chain V-D-J r
29	21	21.9	9	4	S15594	orf 1 para 5'-regi

30	21	21.9	10	2	A59173	nuclease Bn1 (RC 3
31	21	21.9	12	2	F84132	hypothetical prote
32	21	21.9	13	2	PC1008	40K extracellular
33	21	21.9	14	2	S00150	ovostatin - duck (
34	21	21.9	16	2	A11488	taurocyamine kinase
35	21	21.9	18	2	B32473	histidine-rich pro
36	21	21.9	18	2	S34121	lectin - spurge (E
37	21	21.9	18	2	S27141	hypothetical prote
38	21	21.9	19	2	G49048	T-cell receptor be
39	21	21.9	19	2	PT0332	Ig heavy chain CRD
40	20.5	21.4	20	2	A20999	fructose-bisphosph
41	20	20.8	6	2	PT0715	T-cell receptor be
42	20	20.8	10	2	PT0243	Ig heavy chain CRD
43	20	20.8	10	2	PH0944	T-cell receptor be
44	20	20.8	10	2	A46030	gonadolibetin I -
45	20	20.8	10	2	S77990	cytochrome-c oxida
46	20	20.8	11	2	A60656	perisulfakinin - A
47	20	20.8	12	2	S70344	amine oxidase (cop
48	20	20.8	13	2	A46463	preabsorbing anti
49	20	20.8	14	1	LFEBWT	trp operon leader
50	20	20.8	14	2	A56632	neousulfakinin-II -
51	20	20.8	14	2	S27140	hypothetical prote
52	20	20.8	15	2	PH1342	Ig heavy chain DJ
53	20	20.8	15	2	PH1310	Ig heavy chain DJ
54	20	20.8	16	2	A44413	proteaseome endope
55	20	20.8	16	2	PH1637	Ig H chain V-D-J r
56	20	20.8	16	2	PH0773	T-cell receptor be
57	20	20.8	17	2	A44799	pyrogenic exotoxin
58	20	20.8	18	2	S45373	translational elonga
59	20	20.8	18	2	I59649	human leukocyte an
60	20	20.8	18	2	S48862	murine cyclin H -
61	20	20.8	18	2	I51427	hemoglobin alpha c
62	20	20.8	19	2	A34467	36K microfilibril-as
63	20	20.8	20	2	A60801	acrosome stabiliz
64	20.3	20.3	20	2	A48367	glutaryl-CoA dehyd
65	19.5	19.8	5	2	PT0714	T-cell receptor be
66	19	19.8	9	2	PD0027	pev-tachykinin - p
67	19	19.8	12	2	S67528	napin - rape (frag
68	19	19.8	13	2	PH1190	T-cell receptor al
69	19	19.8	13	2	PT0263	Ig heavy chain CRD
70	19	19.8	14	1	LFEBWC	trp operon leader
71	19	19.8	14	2	PH1347	Ig heavy chain DJ
72	19	19.8	15	2	S24159	leukocyte elastase
73	19	19.8	15	2	S26535	T-cell receptor al
74	19	19.8	15	2	S29485	GRP-binding protei
75	19	19.8	15	2	A36315	recycling receptor
76	19	19.8	15	2	PA0006	lectin A3 - Paopho
77	19	19.8	16	2	A60551	leukocyte elastase
78	19	19.8	16	2	PT0282	Ig heavy chain CDR
79	19	19.8	16	2	S16376	L-septine dehydrata
80	19	19.8	17	2	S57991	hydroxyproline-ric
81	19	19.8	17	2	S09085	proteasome chain 4
82	19	19.8	17	2	B31435	adherence lectin 1
83	19	19.8	18	2	PH1323	Ig heavy chain DJ
84	19	19.8	18	2	S28408	placental-derived g
85	19	19.8	18	2	S20322	gluten - wheat
86	19	19.8	19	2	PH1339	Ig heavy chain DJ
87	19	19.8	19	2	A34233	trehalase inhibito
88	19	19.8	19	2	A56800	chymotrypsin I (EC
89	19	19.8	20	2	B34817	collagenolytic pro
90	19	19.8	20	2	C34817	collagenolytic pro
91	19	19.8	20	2	S07232	pollen allergen Po
92	19	19.8	20	2	A60372	Ig heavy chain DJ
93	19	19.8	20	2	PH1326	kalikrein (PK-120
94	19	19.8	20	2	S50175	oxidoreductase - P
95	19	19.8	20	2	S29637	jacalin beta-1 cha
96	19	19.8	20	2	S29636	serine proteinase
97	19	19.8	20	2	S71593	metalloproteinase
98	19	19.8	20	2	A58903	30K allergen - rye
99	18.5	18.8	16	2	S38292	24K exoantigen -
100	18	18.8	7	2	A33098	

## ALIGNMENTS

## RESULT 1

B56046  
urinary tract stone matrix protein 2, 21K - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 12-Apr-1995 #sequence\_revision 12-Apr-1995 #text\_change 12-Apr-1995

C/Accession: B56046

R/Binette, J.P.; Binette, M.B.; Gawinowicz, M.A.; Kendrick, N.

submitted to the Protein Sequence Database, February 1995.

A/Description: Isolation, characterization and sequence of stone proteins.

A/Reference number: A56046

A/Accession: B56046

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-15 <BIN>

A/Cross-references: UNIPARC:UPI000017C408

Query Match

Best Local Similarity 45.5%; Pred. No. 2e+02;

Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 8 YLTAAVSPG 18

DB 1 YLTAAVSPG 11

## RESULT 2

E39419  
collagen alpha 5(IV) chain - bovine (fragment)

C/Species: Bos primigenius taurus (cattle)

C/Date: 03-Apr-1992 #sequence\_revision 03-Apr-1992 #text\_change 09-Jul-2004

C/Accession: E39419

R/Gunwar, S.; Ballester, F.; Kalluri, R.; Timoneda, J.; Chonko, A.M.; Edwards, S.J.; Noe

J. Biol. Chem. 266, 15318-15324, 1991

A/Title: Glomerular basement membrane. Identification of dimeric subunits of the noncoll

A/Reference number: A39419; PMID:1869555

A/Accession: E39419

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-20 <GDN>

A/Cross-references: UNIPROT:Q7M2X3; UNIPARC:UPI00001773C8

C/Suprafamily: collagen alpha 1(IV) chain

C/Keywords: coiled coil; extracellular matrix; glycoprotein; trimer; triple helix

Query Match

Best Local Similarity 66.7%; Pred. No. 4e+02;

Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 6 HGVLIT 11

DB 10 HGVLIT 15

## RESULT 3

A61264  
MHC class I histocompatibility antigen B-P15 alpha chain - chicken (fragment)

C/Species: Gallus gallus (chicken)

C/Date: 09-Sep-1994 #sequence\_revision 09-Sep-1994 #text\_change 31-Dec-2004

C/Accession: A61264

R/Moller, L.B.; Kautman, J.; Verland, S.; Salomonsen, J.; Avila, D.; Lambrie, J.D.; Skjod

Immunogenetics 34, 110-120, 1991

A/Title: Variations in the cytoplasmic region account for the heterogeneity of the chick

A/Reference number: A61264; PMID:1869304

A/Accession: A61264

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-20 <MOL>

A/Cross-references: UNIPROT:Q95593; UNIPROT:Q31412; UNIPROT:Q9G1P6; UNIPARC:UPI0000176F9

C/Suprafamily: immunoglobulin homology

Query Match

Best Local Similarity 29.2%; Score 28; DB 2; Length 20;

Best Local Similarity 50.0%; Pred. No. 4e+02;

Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 8 YLTAAVSPG 17

DB 7 YLTAAVSPG 16

## RESULT 4

S63491  
disulfide isomerase beta chain, membrane-bound - Desulfobrevibrio desulfuricans

C/Species: Desulfobrevibrio desulfuricans

C/Date: 28-Oct-1996 #sequence\_revision 13-Mar-1997 #text\_change 17-Mar-1999

C/Accession: S63491

R/Staub, J.; Arendsen, A.F.; Hagen, W.R.; Kroneck, P.M.H.

Eur. J. Biochem. 233, 873-879, 1995

A/Title: Molecular properties of the disulfide isomerase from Desulfobrevibrio

A/Reference number: S63489; PMID:96085152; PMID:5521853

A/Accession: S63491

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-9 <STR>

A/Cross-references: UNIPARC:UPI000017AB65

Query Match

Best Local Similarity 71.4%; Pred. No. 2.8e+05;

Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 AEPHGY 8

DB 1 AEPHGY 7

## RESULT 5

S68028  
iodochromone 5'-monodeiodinase - rat (fragment)

C/Species: Rattus norvegicus (Norway rat)

C/Date: 15-Feb-1997 #sequence\_revision 13-Mar-1997 #text\_change 17-Mar-1999

C/Accession: S68028

R/Zhou, L.X.; Dehal, S.S.; Knäuper, D.; Morrell, S.; McKenzie, B.A.; Eccleston Jr., E.D.,

Arch. Biochem. Biophys. 322, 390-394, 1995

A/Title: Cytochrome P450 catalyzed covalent binding of methoxychlor to rat hepatic, micr

A/Reference number: S68028; PMID:96032659; PMID:7574712

A/Accession: S68028

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-20 <ZHO>

A/Cross-references: UNIPARC:UPI00001761A4

C/Suprafamily: protein disulfide-isomerase; thioredoxin homology

Query Match

Best Local Similarity 50.0%; Pred. No. 5.8e+02;

Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 DAFPHGYL 10

DB 11 DAFPHGYL 20

## RESULT 6

A36016  
granulocyte inhibitory protein - human

C/Species: Homo sapiens (man)

C/Date: 11-Jan-1991 #sequence\_revision 11-Jan-1991 #text\_change 09-Jul-2004

C/Accession: A36016

R/Hoerl, W.H.; Haag-Weber, M.; Georgopoulos, A.; Block, L.H.

Proc. Natl. Acad. Sci. U.S.A. 87, 6353-6357, 1990

A/Title: Physicochemical characterization of a polypeptide present in uremic serum that

A/Reference number: A36016; PMID:90349614; PMID:2385596

A/Accession: A36016

A/Status: preliminary

A/Molecule type: protein



A/Residues: 1-20 <HOB>  
A/Cross-references: UNIPROT:Q7M4S4; UNIPARC:UPI000020CD0  
C/Superfamily: immunoglobulin V region; immunoglobulin homology

Query Match 28.1%; Score 27; DB 2; Length 20;  
Best Local Similarity 62.5%; Pred. No. 5.8e+02;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 11 TAAVSPGK 18  
|:|||||:  
DB 10 TLVSVPGR 17

## RESULT 7

PT0213  
T-cell receptor alpha chain V-J region (7-10-D-3) - mouse (fragment)

C/Species: Mus musculus (house mouse)  
C/Date: 31-Dec-1991 #sequence\_revision 31-Dec-1991 #text\_change 30-May-1997  
C/Accession: PT0213

R/Nakano, N.; Kikuchi, H.; Nishimoto, H.; Kishimoto, T.

J. Exp. Med. 173, 1091-1097, 1991

A/Title: T cell receptor V gene usage of islet beta cell-reactive T cells is not restricted

A/Reference number: PT0209; PMID:91217621; PMID:1902501

A/Accession: PT0213

A/Molecule type: mRNA

A/Residues: 1-10 <NAK>

A/Cross-references: UNIPARC:UPI000017C790

C/Keywords: T-cell receptor

Query Match 26.0%; Score 25; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 6.1e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 AVSPG 17  
|:|||||:  
DB 2 AVSPG 6

## RESULT 8

S63492

dissimilatory sulfite reductase beta chain, soluble - Desulfovibrio desulfuricans (fragm

C/Species: Desulfovibrio desulfuricans

C/Date: 28-Oct-1996 #sequence\_revision 13-Mar-1997 #text\_change 17-Mar-1999

C/Accession: S63492

R/Stecher, U.; Arendsen, A.F.; Hagen, W.R.; Kroneck, P.M.H.

Eur. J. Biochem. 233, 873-879, 1995

A/Title: Molecular properties of the dissimilatory sulfite reductase from Desulfovibrio

A/Reference number: S63489; PMID:96085152; PMID:8521853

A/Accession: S63492

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-13 <STR>

A/Cross-references: UNIPARC:UPI000017AB66

Query Match 26.0%; Score 25; DB 2; Length 13;  
Best Local Similarity 71.4%; Pred. No. 8e+02;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 APEPHGY 8  
|:|||||:  
DB 1 APEPTGY 7

## RESULT 9

B36222

excinuclease ABC chain C (uvrC) [imported] - Pseudomonas fluorescens (fragment)

C/Species: Pseudomonas fluorescens

C/Date: 04-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change 20-Jun-2000

C/Accession: B36222

R/Laville, J.; Voisard, C.; Keel, C.; Maurhofer, M.; Defago, G.; Haas, D.

Proc. Natl. Acad. Sci. U.S.A. 89, 1562-1566, 1992

A/Title: Global control in Pseudomonas fluorescens mediating antibiotic synthesis and su

A/Contents: CHAO  
A/Accession: B36222  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-14 <LAV>  
A/Cross-references: UNIPARC:UPI000017A97D  
A/Note: sequence extracted from NCBI backbone (NCBIN:85369, NCBIPI:94242)

Query Match 26.0%; Score 25; DB 2; Length 14;  
Best Local Similarity 36.4%; Pred. No. 8.6e+02;  
Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 DAFPHGYLT 11  
|:|:|:|:|:  
DB 3 BQFDSAPLST 13

## RESULT 10

H35141

T-cell receptor delta chain V region (105.23) - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 31-Aug-1990 #sequence\_revision 31-Aug-1990 #text\_change 30-May-1997

C/Accession: H35141

R/Sim, G.K.; Augustin, A.

Cell 61, 397-405, 1990

A/Title: Dominantly inherited expression of BID, an invariant undiversified T cell rece

A/Reference number: A35141; PMID:90242386; PMID:2110506

A/Accession: H35141

A/Status: preliminary; not compared with conceptual translation

A/Molecule type: mRNA

A/Residues: 1-16 <SIM>

A/Cross-references: UNIPARC:UPI000017C859

C/Keywords: T-cell receptor

Query Match 26.0%; Score 25; DB 2; Length 16;  
Best Local Similarity 41.7%; Pred. No. 9.9e+02;  
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 7 GYLTAAVSPGK 18  
|:|:|:|:|:  
DB 4 GYLTGIRAPDK 15

## RESULT 11

A33171

hypothetical protein lpxA 3'-region - Escherichia coli (fragment)

C/Species: Escherichia coli

C/Date: 22-Oct-1999 #sequence\_revision 22-Oct-1999 #text\_change 22-Oct-1999

C/Accession: A33171

R/Coleman, U.; Raetz, C.R.H.

J. Bacteriol. 170, 1268-1274, 1988

A/Title: First committed step of lipid A biosynthesis in Escherichia coli: sequence of

A/Reference number: A33171; PMID:88339188; PMID:3277952

A/Accession: A33171

A/Molecule type: DNA

A/Residues: 1-16 <COL>

A/Cross-references: UNIPARC:UPI000017C8E5; GB:M19334; GB:M18265; GB:M18266; NID:G450760

C/Comment: This is the hypothetical translation of a sequence that was not reported as ;

Query Match 26.0%; Score 25; DB 4; Length 16;  
Best Local Similarity 62.5%; Pred. No. 9.9e+02;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 8 YLTTAAVS 15  
|:|:|:|:|:  
DB 9 YLITGRYS 16

## RESULT 12

S23981

outer layer protein - chicken (fragment)

C/Species: Gallus gallus (chicken)

C/Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 09-Jul-2004

C/Accession: S23981  
 R.Kido, S.; Morimoto, A.; Kim, F.; Doi, Y.  
 Biochem. J. 286, 17-22, 1992  
 A/Title: Isolation of a novel protein from the outer layer of the vitelline membrane.  
 A/Reference number: S23981; MUID:92392273; PMID:1520265  
 A/Accession: S23981  
 A/Status: preliminary  
 A/Molecule type: protein  
 A/Residues: 1-20 <KID>  
 A/Cross-references: UNIPROT:Q9PS49; UNIPARC:UPI00001389A5

Query Match 26.0%; Score 25; DB 2; Length 20;  
 Best Local Similarity 44.4%; Pred. No. 1.3e+03;  
 Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 6 HGYLTAAPV 14  
 ||| : |  
 DB 12 HGXYIRSKV 20

RESULT 13  
 B47415  
 mannose-1-phosphate guanylyltransferase (EC 2.7.7.13) 43K alpha chain - pig (fragment)  
 N/Alternate names: GDP-mannose pyrophosphorylase 43K alpha chain  
 C/Species: Sus scrofa domestica (domestic pig)  
 C/Date: 25-Feb-1994 #sequence\_revision 12-Aug-1996 #text\_change 12-Aug-1996  
 C/Accession: B47415  
 R.Szumilo, T.; Drake, R.R.; York, J.L.; Elbein, A.D.  
 J. Biol. Chem. 268, 17943-17950, 1993  
 A/Title: GDP-mannose pyrophosphorylase. Purification to homogeneity, properties, and use  
 A/Reference number: A47415; MUID:93352609; PMID:7688733  
 A/Accession: B47415  
 A/Molecule type: protein  
 A/Residues: 1-13 <SDU>  
 A/Cross-references: UNIPARC:UPI000017C470  
 C/Experimental source: liver  
 C/Complex: The enzyme appears to be a heterodimer of alpha and beta chains.  
 C/Function:  
 A/Description: generates GDP-mannose and pyrophosphate from mannose-1-phosphate and GTP  
 A/Note: also catalyzes synthesis of GDP-glucose from glucose-1-phosphate (EC 2.7.7.34 ac  
 C/Keywords: blocked amino end; nucleotidyltransferase

Query Match 25.0%; Score 24; DB 2; Length 13;  
 Best Local Similarity 66.7%; Pred. No. 1.2e+03;  
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 PHGYLL 10  
 ||| : |  
 DB 8 PHPFL 13

RESULT 14  
 PH1305  
 Ig heavy chain DJ region (clone C85-1B) - human (fragment)  
 C/Species: Homo sapiens (man)  
 C/Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999  
 C/Accession: PH1305  
 R.Masserman, R.; Gailit, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.  
 J. Exp. Med. 176, 1577-1581, 1992  
 A/Title: Predominance of fetal type DJH joining in young children with B precursor lymph  
 A/Reference number: PH1302; MUID:93094761; PMID:1460419  
 A/Accession: PH1305  
 A/Molecule type: DNA  
 A/Residues: 1-14 <MAS>  
 A/Cross-references: UNIPARC:UPI000017C252  
 C/Keywords: heterotrimer; immunoglobulin

Query Match 25.0%; Score 24; DB 2; Length 14;  
 Best Local Similarity 50.0%; Pred. No. 1.3e+03;  
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 7 GYLTAASP 16  
 ||| : |

DB 5 GYTTGARP 14

RESULT 15  
 S00843  
 hypothetical protein kgsa 5'-region - Escherichia coli  
 C/Species: Escherichia coli  
 C/Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
 C/Accession: S00843  
 R.van Gemen, B.; Koets, H.J.; Plooy, C.A.M.; Bodlaender, J.; van Knippenberg, P.H.  
 Biochimie 69, 841-848, 1987  
 A/Title: Characterization of the kgsa gene of Escherichia coli determining kasugamycin s  
 A/Reference number: S00843; MUID:86107880; PMID:3122846  
 A/Accession: S00843  
 A/Molecule type: DNA  
 A/Residues: 1-14 <VAN>  
 A/Cross-references: UNIPROT:Q47335; UNIPARC:UPI00000B9024; EMBL:X06536; NID:941884; PIDN  
 C/Comment: This is the hypothetical translation of a sequence that was not reported as a

Query Match 25.0%; Score 24; DB 4; Length 14;  
 Best Local Similarity 50.0%; Pred. No. 1.3e+03;  
 Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 9 LTTAASPK 18  
 ||| : |  
 DB 5 LTRRLSPK 14

RESULT 16  
 S10741  
 phosphoglucomutase (EC 5.4.2.2) - rabbit (fragment)  
 C/Species: Oryctolagus cuniculus (domestic rabbit)  
 C/Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 03-Jul-2004  
 C/Accession: S10741  
 R.Marchase, R.B.; Richardson, K.L.; Srisomsap, C.; Drake, R.R.; Haley, B.E.  
 Arch. Biochem. Biophys. 280, 122-129, 1990  
 A/Title: Resolution of phosphoglucomutase and the 62-kDa acceptor for the glucosylphosph  
 A/Reference number: S10741; MUID:90282481; PMID:161250  
 A/Accession: S10741  
 A/Molecule type: protein  
 A/Residues: 1-15 <MAR>  
 A/Cross-references: UNIPROT:Q7M2K5; UNIPARC:UPI000017C5D3  
 C/Keywords: intramolecular transferase; isomerase; phosphoprotein

Query Match 25.0%; Score 24; DB 2; Length 15;  
 Best Local Similarity 50.0%; Pred. No. 1.4e+03;  
 Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 7 GYLTAASP 16  
 ||| : |  
 DB 4 GILTRSHMP 13

RESULT 17  
 S66613  
 protein p12E - Friend murine leukemia virus (fragments)  
 C/Species: Friend murine leukemia virus  
 C/Date: 15-Feb-1997 #sequence\_revision 13-Mar-1997 #text\_change 13-Mar-1997  
 C/Accession: S66613  
 J.Hensel, J.J.; Hntz, M.; Karas, M.; Linder, D.; Stahl, B.; Geyer, R.  
 Eur. J. Biochem. 232, 373-380, 1995  
 A/Title: Localization of the palmitoylation site in the transmembrane protein p12E of F.  
 A/Reference number: S66613; MUID:96035869; PMID:7556184  
 A/Accession: S66613  
 A/Molecule type: protein  
 A/Status: preliminary  
 A/Molecule type: protein  
 A/Residues: 1-9,10-16 <HEN>  
 A/Cross-references: UNIPARC:UPI000017A87F; UNIPARC:UPI000017A880

Query Match 25.0%; Score 24; DB 2; Length 16;  
 Best Local Similarity 71.4%; Pred. No. 1.5e+03;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 10 LTAAVSP 16  
|||  
Db 5 LTLALSP 11

## RESULT 18

A59155  
multicyclicatin - tomato (fragment)  
C/Species: Lycopersicon esculentum (tomato)  
C/Date: 07-Dec-1999 #sequence\_revision 07-Dec-1999 #text\_change 09-Jul-2004  
C/Accession: A59155  
R/Jacinto, T./Fernandes, K.V.S./Machado, O.L.T./Silveira-Junior, C.L.  
Plant Sci. 138, 35-42, 1998  
A/Title: Leaves of transgenic tomato plants overexpressing prosystemin accumulate high 1  
A/Reference number: A59155  
A/Accession: A59155  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-16 <MAC>  
A/Cross-references: UNIPROT:Q7M1V9; UNIPARC:UPI000017B08D  
A/Note: 37 kDa CNBR fragment  
C/Keywords: cysteine proteinase inhibitor

Query Match 24.0%; Score 23.5; DB 2; Length 16;  
Best Local Similarity 50.0%; Pred. No. 1.8e+03;  
Matches 6; Conservative 2; Mismatches 3; Indels 1; Gaps 1;  
OY 8 YLLT-AAVSPCK 18  
|||  
Db 1 YITFAATDAGK 12

## RESULT 19

GMROL  
leucobulfaflakinin - Madeira cockroach  
N/Alternate names: LSK  
C/Species: Leucophaea maderae (Madeira cockroach)  
C/Date: 17-Mar-1987 #sequence\_revision 17-Mar-1987 #text\_change 09-Jul-2004  
C/Accession: A01622  
R/Nachman, R.J./Holman, G.M./Haddon, W.F./Lang, N.  
Science 234, 71-73, 1986  
A/Title: Leucobulfaflakinin, a sulfated insect neuropeptide with homology to gastrin and ch  
A/Reference number: A01622; MUID:66315858; PMID:3745893  
A/Accession: A01622  
A/Molecule type: protein  
A/Residues: 1-11 <MAC>  
A/Cross-references: UNIPROT:P04428; UNIPARC:UPI000012B960  
C/Suprafamily: gastrin  
C/Keywords: amidated carboxyl end; hormone; sulfoprotein  
P/6/Binding site: sulfate (Tyr) (covalent) #status experimental  
P/11/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 24.0%; Score 23; DB 1; Length 11;  
Best Local Similarity 33.3%; Pred. No. 1.4e+03;  
Matches 3; Conservative 4; Mismatches 2; Indels 0; Gaps 0;  
OY 1 DAFEPHGYL 9  
|||  
Db 1 EQFEDYGHM 9

## RESULT 20

PH1604  
Ig H chain V-D-J region (wild-type clone 327) - mouse (fragment)  
C/Species: Mus musculus (house mouse)  
C/Date: 02-Jun-1994 #sequence\_revision 02-Jun-1994 #text\_change 17-Mar-1999  
C/Accession: PH1604  
R/Levinson, D.A./Campos-Torres, J./Leder, P.  
J. Exp. Med. 178, 317-329, 1993  
A/Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice  
A/Reference number: PH1580; MUID:93301609; PMID:8315387  
A/Accession: PH1604  
A/Molecule type: DNA

A/Residues: 1-16 <LBY>  
A/Cross-references: UNIPARC:UPI000017C6C0  
A/Experimental source: bone marrow pre-B lymphocyte  
C/Keywords: immunoglobulin

Query Match 24.0%; Score 23; DB 2; Length 16;  
Best Local Similarity 66.7%; Pred. No. 2.1e+03;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
OY 5 PHGYLL 10  
|||  
Db 4 PHRWLL 9

## RESULT 21

B36300  
T-cell receptor delta chain V-J region - mouse (fragment)  
C/Species: Mus musculus (house mouse)  
C/Date: 28-Mar-1991 #sequence\_revision 28-Mar-1991 #text\_change 30-May-1997  
C/Accession: B36300  
R/Matis, L.A./Fry, A.M./Cron, R.Q./Cotterman, M.M./Dick, R.F./Bluestone, J.A.  
Science 245, 746-749, 1989  
A/Title: Structure and specificity of a class II MHC alloreactive gammadelta T cell rec  
A/Reference number: A36300; MUID:89368895; PMID:2528206  
A/Accession: B36300  
A/Status: preliminary; not compared with conceptual translation  
A/Molecule type: mRNA  
A/Residues: 1-16 <MAT>  
A/Cross-references: UNIPARC:UPI000017C861  
C/Keywords: T-cell receptor

Query Match 24.0%; Score 23; DB 2; Length 16;  
Best Local Similarity 33.3%; Pred. No. 2.1e+03;  
Matches 4; Conservative 2; Mismatches 6; Indels 0; Gaps 0;  
OY 7 GYLLTAAVSRCK 18  
|||  
Db 3 GYIPGIGIRGK 14

## RESULT 22

I78841  
thrombopoietin receptor - mouse (fragment)  
C/Species: Mus sp. (mouse)  
C/Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 05-Nov-1999  
C/Accession: I78841  
R/Alexander, W.S./Dunn, A.R.  
Oncogene 10, 795-803, 1995  
A/Title: Structure and transcription of the genomic locus encoding murine c-Mpl, a rece  
A/Reference number: I58350; MUID:95166571; PMID:7662460  
A/Accession: I78841  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: mRNA  
A/Residues: 118 <RSS>  
A/Cross-references: UNIPARC:UPI0000004PB; GB:S76842; NID:9912990; PIDN:AA83462.1; PID  
C/Genetics: A/Gene: c-mpl1

Query Match 24.0%; Score 23; DB 2; Length 18;  
Best Local Similarity 75.0%; Pred. No. 2.4e+03;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
OY 4 EPHG 7  
|||  
Db 1 QPHG 4

## RESULT 23

H28949  
ribosomal protein H2C12 [validated] - Haloarcula marismortui (fragment)  
C/Species: Haloarcula marismortui  
C/Date: 30-Jun-1989 #sequence\_revision 30-Jun-1989 #text\_change 09-Jul-2004  
C/Accession: H28949

R/Walsh, M.J.; McDougall, J.; Wittmann-Liebold, B.  
Biochemistry 27, 6867-6876, 1988  
A/Title: Extended N-terminal sequencing of proteins of archaebacterial ribosomes blotted  
A/Reference number: A28926; PMID:89062418; PMID:3196689  
A/Accession: H28949  
A/Molecule type: protein  
A/Residues: 1-20 <MAL>  
A/Cross-references: UNIPROT:P12740; UNIPARC:UPI0000134270  
A/Note: the protein is designated as ribosomal protein LCI2  
C/Keywords: protein biosynthesis

Query Match 24.0%; Score 23; DB 2; Length 20;  
Best Local Similarity 33.3%; Pred. No. 2.7e+03;  
Matches 4; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 6 HGYLITAVNSPG 17  
| | | | |  
DB 5 YSYRDATKXPG 16

## RESULT 24

PH1772  
T cell receptor alpha chain V region (clone 2V alpha 23-3) - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 16-Jul-1999  
C/Accession: PH1772  
R/Portelli, S.; Yockey, C.E.; Brenner, M.B.; Balx, S.P.  
J. Exp. Med. 178, 1-16, 1993  
A/Title: Analysis of T cell antigen receptor (TCR) expression by human peripheral blood  
A/Reference number: PH1754; PMID:93301585; PMID:8391057  
A/Accession: PH1772  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-13 <POR>  
A/Cross-references: UNIPARC:UPI000017C37C

Query Match 22.9%; Score 22; DB 2; Length 13;  
Best Local Similarity 62.5%; Pred. No. 2.5e+03;  
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 AEPHNGYL 9  
| | | | |  
DB 3 AVEPAGQL 10

## RESULT 25

S59512  
probable integrin alpha3 beta1 - mouse (fragment)  
C/Species: Mus musculus (house mouse)  
C/Date: 19-Mar-1997 #sequence\_revision 25-Apr-1997 #text\_change 09-Jul-2004  
C/Accession: S59512  
R/McCormick, J.T.; Johnstone, R.M.  
Biochem. J. 311, 743-751, 1995  
A/Title: Identification of the integrin alpha(3)beta(1) as a component of a partially pu  
A/Reference number: S59512; PMID:96067588; PMID:7487928  
A/Accession: S59512  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-17 <MCC>  
A/Cross-references: UNIPROT:Q7M0D8; UNIPARC:UPI000005353C

Query Match 22.9%; Score 22; DB 2; Length 17;  
Best Local Similarity 80.0%; Pred. No. 3.3e+03;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 13 AVSPG 17  
| | | | |  
DB 13 AVNPG 17

## RESULT 26

A61276

superoxide dismutase (EC 1.15.1.1) (Fe/Mn) homolog - chicken (fragment)  
N/Alternate names: osteoclast membrane glycoprotein  
C/Species: Gallus gallus (chicken)  
C/Date: 12-May-1994 #sequence\_revision 12-May-1994 #text\_change 05-Mar-1999  
C/Accession: A61276  
R/Dursaler, M.J.; Li, L.; Osoby, P.  
J. Cell. Biochem. 46, 219-233, 1991  
A/Title: Purification and characterization of an osteoclast membrane glycoprotein with h  
A/Reference number: A61276; PMID:92129474; PMID:1723067  
A/Accession: A61276  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-20 <OUR>  
A/Cross-references: UNIPARC:UPI000017C038  
C/Function: catalyzes the dismutation of 2 molecules of peroxide radical to dioxygen  
A/Description: metalloprotein; oxidoreductase  
C/Keywords: metalloprotein; oxidoreductase

Query Match 22.9%; Score 22; DB 2; Length 20;  
Best Local Similarity 80.0%; Pred. No. 3.9e+03;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DAFEP 5  
| | | | |  
DB 12 DALRP 16

## RESULT 27

S46479  
retinoid-X-receptor-gamma - chicken  
C/Species: Gallus gallus (chicken)  
C/Date: 15-Jul-1995 #sequence\_revision 10-Nov-1995 #text\_change 09-Jul-2004  
C/Accession: S46479  
R/Seleiro, E.A.P.; Darling, D.; Brickell, P.M.  
Biochem. J. 301, 283-288, 1994  
A/Title: The chicken retinoid-X-receptor-gamma gene gives rise to two distinct species c  
A/Reference number: S46478; PMID:94311845; PMID:8037682  
A/Accession: S46479  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-20 <SEL>  
A/Cross-references: UNIPROT:Q91380; UNIPARC:UPI000017C033; GB:S72435; NID:G619294; PIDN

Query Match 22.9%; Score 22; DB 2; Length 20;  
Best Local Similarity 75.0%; Pred. No. 3.9e+03;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 PHGY 8  
| | | | |  
DB 17 PHSY 20

## RESULT 28

PH1618  
Ig H chain V-D-J region (clone B-lees 33) - mouse (fragment)  
C/Species: Mus musculus (house mouse)  
C/Date: 02-Jun-1994 #sequence\_revision 02-Jun-1994 #text\_change 17-Mar-1999  
C/Accession: PH1618  
R/Levinson, D.A.; Campos-Torres, J.; Leder, P.  
J. Exp. Med. 178, 317-329, 1993  
A/Title: Molecular characterization of transgene-induced immunodeficiency in B-lees mice  
A/Reference number: PH1618; PMID:93301609; PMID:8315387  
A/Accession: PH1618  
A/Molecule type: DNA  
A/Residues: 1-8 <LEV>  
A/Cross-references: UNIPARC:UPI000017C6A7  
A/Experimental source: bone marrow pre-B lymphocyte  
C/Keywords: immunoglobulin

Query Match 21.9%; Score 21; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 HGY 8  
|||  
Db 4 HGY 6

## RESULT 29

orf 1 para 5'-region - human  
S15594  
C/Species: Homo sapiens (man)  
C/Date: 04-Jun-1999 #sequence\_revision 04-Jun-1999 #text\_change 28-Jun-1999  
C/Accession: S15594  
R/Brand: N.J.; Petkovich, M.; Chambon, P.  
Nucleic Acids Res. 18, 6799-6806, 1990  
A/Title: Characterization of a functional promoter for the human retinolic acid receptor-  
A/Reference number: S15594; MUID:91088249; PMID:2175878  
A/Accession: S15594  
A/Molecule type: DNA  
A/Residues: 1-9 <BRA>  
A/Cross-references: UNIPARC:UPI000017CEBB; EMBL:X56057; NID:935875  
C/Date: this ORF from Fig. 2 is not annotated in GenBank entry HSRARAL, release 111.0  
C/Comment: This sequence is not thought to be translated.  
A/Genetic: GDB:RARA  
A/Cross-references: GDB:120337; OMIM:180240  
A/Map position: 17q12-17q12

Query Match 21.9%; Score 21; DB 4; Length 9;  
Best Local Similarity 42.9%; Pred. No. 2.8e+05;  
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 10 LTAAVSP 16  
: |||:  
Db 1 MAALAP 7

## RESULT 30

A59173  
nuclease Bn1 (EC 3.1.-.-) - *Basidiobolus haplosporius* (fragment)  
C/Species: *Basidiobolus haplosporius*  
C/Date: 18-Feb-2000 #sequence\_revision 18-Feb-2000 #text\_change 09-Jul-2004  
C/Accession: A59173  
R/Brand: N.; Shankar, V.  
submitted to the Protein Sequence Database, February 2000  
A/Description: Single-strand-specific, guanylic acid preferential nuclease from *Basidiobolus*  
A/Reference number: A59173  
A/Accession: A59173  
A/Status: Preliminary  
A/Molecule type: Protein  
A/Residues: 1-10 <DSS>  
A/Cross-references: UNIPROT:Q7M4X1; UNIPARC:UPI000017CAF9  
A/Note: extracellular, single-strand-specific nuclease  
C/Keyword: hydrolase

Query Match 21.9%; Score 21; DB 2; Length 10;  
Best Local Similarity 80.0%; Pred. No. 2.8e+03;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 GYLTT 11  
: |||:  
Db 5 GHLLT 9

## RESULT 31

P84132  
hypothetical protein BH3862 [Imported] - *Bacillus halodurans* (strain C-125)  
C/Species: *Bacillus halodurans*  
C/Date: 01-Dec-2000 #sequence\_revision 01-Dec-2000 #text\_change 09-Jul-2004  
C/Accession: P84132  
R/Takam, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira  
Nucleic Acids Res. 28, 4317-4331, 2000  
A/Title: Complete genome sequence of the alkaliphilic bacterium *Bacillus halodurans* and  
A/Reference number: A83650; MUID:20512582; PMID:11058132  
A/Accession: P84132

A/Status: Preliminary  
A/Molecule type: DNA  
A/Residues: 1-12 <STO>  
A/Cross-references: UNIPROT:Q9K670; UNIPARC:UPI00000C4307; GB:AP001520; GB:BA000004; NI  
C/Genetics:  
A/Experimental source: strain C-125  
A/Genetic: BH3862

Query Match 21.9%; Score 21; DB 2; Length 12;  
Best Local Similarity 57.1%; Pred. No. 3.4e+03;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 8 YLTAAY 14  
: |||:  
Db 3 YLTKIT 9

## RESULT 32

PC1008  
40K extracellular proteinase - *Dichelobacter nodosus* (fragment)  
C/Species: *Dichelobacter nodosus*  
C/Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 09-Jul-2004  
C/Accession: PC1008  
R/Gong, Y.H.; Moses, B.  
Acta Microbiol. Sin. 31, 433-437, 1991  
A/Title: Overexpression of an extracellular bacteroides nodosus protease in *E.coli* and  
A/Reference number: PC1008  
A/Accession: PC1008  
A/Molecule type: Protein  
A/Residues: 1-13 <GON>  
A/Cross-references: UNIPROT:Q7M1A2; UNIPARC:UPI000017AB53  
A/Note: article in Chinese with English abstract  
C/Comment: This protease is involved in the pathogenesis of footrot.

Query Match 21.9%; Score 21; DB 2; Length 13;  
Best Local Similarity 41.7%; Pred. No. 3.7e+03;  
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 2 AEPHGYLTAA 13  
: |||:  
Db 1 AFINRHLLSLIA 12

## RESULT 33

S00150  
ovostatin - duck (fragment)  
N/Alternate names: ovomacroglobulin  
C/Species: *Anas platyrhynchos* (domestic duck)  
C/Date: 19-Mar-1997 #sequence\_revision 01-Aug-1997 #text\_change 09-Jul-2004  
C/Accession: S00150  
R/Nagase, H.; Harris Jr., B.D.; Brew, K.  
J. Biol. Chem. 261, 1421-1426, 1986  
A/Title: Evidence for a thiol ester in duck ovostatin (ovomacroglobulin).  
A/Reference number: S00150; MUID:86111792; PMID:3511043  
A/Accession: S00150  
A/Status: Preliminary  
A/Molecule type: Protein  
A/Residues: 1-14 <NAG>  
A/Cross-references: UNIPROT:Q7LZ22; UNIPARC:UPI000017BD01  
A/Note: part of this sequence, including the amino end of the mature chicken and duck p.

Query Match 21.9%; Score 21; DB 2; Length 14;  
Best Local Similarity 45.5%; Pred. No. 4e+03;  
Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 4 EPHGYLTAAV 14  
: |||:  
Db 4 EPGYLTMPAV 14

## RESULT 34

A11488  
taurocyamine kinase (EC 2.7.3.4) - lugworm (fragment)

C/Species: *Arenicola marina* (lugworm, rock worm)  
 C/Date: 05-Jun-1987 #sequence\_rev1sion 05-Jun-1987 #text\_change 09-Jul-2004  
 C/Accession: A11488  
 R/Breuer, A.; Zeitoun, Y.; Pradel, L.A.  
 Biochim. Biophys. Acta 393, 1-9, 1975  
 A/Title: Comparative structural studies of the active site of ATP:guanidine phosphotrans  
 A/Reference number: A11488; MUID:75184095; PMID:166684  
 C/Accession: A11488  
 A/Molecule type: protein  
 A/Residues: 1-16 <BR>  
 A/Cross-references: UNIPROT:P11917; UNIPARC:UPI0000128121  
 C/Keywords: phosphotransferase

Query Match 21.9%; Score 21; DB 2; Length 16;  
 Best Local Similarity 45.5%; Pred. No. 4.6e+03;  
 Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 7 GYLLTRAVSPG 17  
 DB 2 GYLGTCTPTNIG 12

RESULT 35  
 B32473  
 histidine-rich protein C, peptide P-5 - liver fluke (fragment)  
 C/Species: *Fasciola hepatica* (liver fluke)  
 C/Date: 25-Sep-1989 #sequence\_rev1sion 03-May-1994 #text\_change 09-Jul-2004  
 C/Accession: B32473  
 R/Walke, J.H.; Rice-Ficht, A.C.  
 Biochemistry 28, 6104-6110, 1989  
 A/Title: A histidine-rich protein from the vitellaria of the liver fluke *Fasciola hepatica*  
 A/Reference number: A32473; MUID:89375343; PMID:2775756  
 C/Accession: B32473  
 A/Molecule type: protein  
 A/Residues: 1-18 <MAL>  
 A/Cross-references: UNIPROT:Q7M3X9; UNIPARC:UPI0000177DAS  
 A/Note: 18-Gly and 18-His were also found  
 C/Suprafamily: period clock protein; EGF homology  
 C/Keywords: egg yolk  
 P1,5/Modified site: 3',4'-dihydroxyphenylalanine (Tyr) #status experimental

Query Match 21.9%; Score 21; DB 2; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 5.2e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 HG Y 8  
 DB 3 HG Y 5

RESULT 36  
 S36121  
 lectin - spurge (*Euphorbia characias*)  
 C/Species: *Euphorbia characias*  
 C/Date: 09-Dec-1993 #sequence\_rev1sion 27-Feb-1997 #text\_change 09-Jul-2004  
 C/Accession: S36121  
 R/Stiipe, F.; Ilicastro, F.; Morini, M.C.; Parente, A.; Savino, G.; Abbondanza, A.; Bolog  
 Biochim. Biophys. Acta 1158, 33-39, 1993  
 A/Title: Purification and partial characterization of a mitogenic lectin from the latex  
 A/Reference number: S36120; MUID:93357266; PMID:8353129  
 A/Accession: S36121  
 A/Status: preliminary  
 A/Molecule type: protein  
 A/Residues: 1-18 <SNI>  
 A/Cross-references: UNIPROT:P33886; UNIPARC:UPI00001256C0

Query Match 21.9%; Score 21; DB 2; Length 18;  
 Best Local Similarity 75.0%; Pred. No. 5.2e+03;  
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 PHGY 8  
 DB 10 PNGY 13

RESULT 37  
 S27141  
 hypothetical protein 2 estrogen receptor 5'-region - human  
 C/Species: *Homo sapiens* (man)  
 C/Date: 05-Mar-1994 #sequence\_rev1sion 12-May-1995 #text\_change 16-Aug-2004  
 C/Accession: S27141  
 R/Keaveney, M.; Klug, J.; Gannon, F.  
 DNA Seq. 2, 347-358, 1992  
 A/Title: Sequence analysis of the 5' flanking region of the human estrogen receptor gene  
 A/Reference number: S27140; MUID:93075998; PMID:1476547  
 C/Accession: S27141  
 A/Status: translation not shown  
 A/Molecule type: DNA  
 A/Residues: 1-18 <KBA>  
 A/Cross-references: UNIPARC:UPI000011DP56; EMBL:X62462; NID:g31201; PIDN:CAA44320.1; PIC  
 C/Genetics: 13/2  
 A/introns: 13/2

Query Match 21.9%; Score 21; DB 2; Length 18;  
 Best Local Similarity 37.5%; Pred. No. 5.2e+03;  
 Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 DAFEPHGY 8  
 DB 7 DVLDPAGW 14

RESULT 38  
 G49048  
 T-cell receptor beta chain V region (CDR3 junction, clone Vbeta20.1) - human (fragment)  
 C/Species: *Homo sapiens* (man)  
 C/Date: 21-Jan-1994 #sequence\_rev1sion 18-Nov-1994 #text\_change 30-May-1997  
 C/Accession: G49048  
 R/Siod, M.; Kjeldsen-Kragh, J.; Suleyman, S.; Vinje, O.; Natvig, J.B.; Forre, O.  
 Eur. J. Immunol. 22, 2413-2418, 1992  
 A/Title: Limited heterogeneity of T cell receptor variable region gene usage in juvenile  
 A/Reference number: A49048; MUID:9287250; PMID:1387614  
 C/Accession: G49048  
 A/Status: preliminary; not compared with conceptual translation  
 A/Molecule type: mRNA  
 A/Residues: 1-19 <SIO>  
 A/Cross-references: UNIPARC:UPI0000176DED  
 A/Experimental source: patient SS, IL-2R+ synovial T-cells  
 A/Note: sequence extracted from NCBI backbone (NCBIP:113269)  
 C/Suprafamily: immunoglobulin V region; immunoglobulin homology  
 C/Keywords: T-cell receptor

Query Match 21.9%; Score 21; DB 2; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 5.5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 HG Y 8  
 DB 14 HG Y 16

RESULT 39  
 PT0332  
 Ig heavy chain CRD3 region (clone U2-139) - human (fragment)  
 C/Species: *Homo sapiens* (man)  
 C/Date: 30-Sep-1993 #sequence\_rev1sion 30-Sep-1993 #text\_change 16-Aug-1996  
 C/Accession: PT0332  
 R/Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.  
 J. Exp. Med. 173, 395-407, 1991  
 A/Title: Preferential utilization of specific immunoglobulin heavy chain diversity and j  
 A/Reference number: PT0222; MUID:91108337; PMID:1899102  
 C/Accession: PT0332  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-19 <YAM>  
 A/Cross-references: UNIPARC:UPI000017C21A  
 A/Experimental source: B lymphocyte

C/Keywords: heterotetramer; immunoglobulin

Query Match 21.9%; Score 21; DB 2; Length 19;

Best Local Similarity 50.0%; Pred. No. 5.5e+03;

Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 DAPPHGY 8  
| | | |  
| | | |

DB 1 DAPPPYY 8

RESULT 40

A20999

Fructose-bisphosphate aldolase (BC 4.1.2.13) - chicken (fragment)

C/Species: Gallus gallus (chicken)

C/Date: 21-May-1988 #sequence\_revision 21-May-1988 #text\_change 09-Jul-2004

C/Accession: A20999

R/Leibherz, H.G.; Bates, O.J.; Bradehaw, R.A.

J. Biol. Chem. 259, 1132-1135, 1984

A/Title: Cellular fructose-P2 aldolase has a derivatized (blocked) NH2 terminus.

A/Reference number: A20999; MUID:84111506; PMID:6693379

A/Accession: A20999

A/Molecule type: protein

A/Residues: 1-20 <LBB>

A/Cross-references: UNIPROT:Q7LZB6; UNIPARC:UPI0000175PFS

C/Superfamily: fructose-bisphosphate aldolase

C/Keywords: aldehyde-lyase, carbon-carbon lyase, gluconeogenesis, glycolysis, pentose ph

Query Match 21.4%; Score 20.5; DB 2; Length 20;

Best Local Similarity 41.7%; Pred. No. 7e+03;

Matches 5; Conservative 2; Mismatches 2; Indels 3; Gaps 1;

QY 5 PHGYLTNAVSP 16  
| | | | | | | |  
| | | | | | | |

DB 1 PHGY--PALTP 9

RESULT 41

PT0715

T-cell receptor beta chain V-D-J region (165-3A) - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997

C/Accession: PT0715

R/Peeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A/Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.

A/Reference number: PT0509; MUID:9127601; PMID:1711558

A/Accession: PT0715

A/Status: translation not shown

A/Molecule type: DNA

A/Residues: 1-6 <PBB>

A/Cross-references: UNIPARC:UPI000017C847

A/Experimental source: newborn thymus, strain BALB/c

C/Keywords: T-cell receptor

Query Match 20.8%; Score 20; DB 2; Length 6;

Best Local Similarity 66.7%; Pred. No. 2.8e+05;

Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 13 AVSPGK 18  
| | | | | | | |  
| | | | | | | |

DB 1 ASSPGQ 6

RESULT 42

PT0243

Ig heavy chain CDR3 region (clone 2-103A) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996

C/Accession: PT0243

R/Yamada, M.; Maeserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.

J. Exp. Med. 173, 395-407, 1991

A/Title: Preferential utilization of specific immunoglobulin heavy chain diversity and

A/Reference number: PT0222; MUID:91108337; PMID:1899102

A/Accession: PT0243

A/Molecule type: DNA

A/Residues: 1-10 <YAM>

A/Cross-references: UNIPARC:UPI000017C1B3

A/Experimental source: B lymphocyte

C/Keywords: heterotetramer; immunoglobulin

Query Match 20.8%; Score 20; DB 2; Length 10;

Best Local Similarity 42.9%; Pred. No. 4.1e+03;

Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 FBPHGYL 9  
| | | | |  
| | | | |

DB 4 YDSSGYL 10

RESULT 43

PH0944

T-cell receptor beta chain V-D-J region (clone 15) - rat (fragment)

C/Species: Rattus norvegicus (Norway rat)

C/Date: 09-Oct-1992 #sequence\_revision 09-Oct-1992 #text\_change 30-May-1997

C/Accession: PH0944

R/Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.

J. Exp. Med. 174, 1467-1476, 1991

A/Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergy

A/Reference number: PH0941; MUID:92078857; PMID:1836012

A/Accession: PH0944

A/Residues: 1-10 <GOL>

A/Cross-references: UNIPARC:UPI000017C9B1

A/Experimental source: complete Freund's adjuvant-immunized lymph node

A/Note: the authors translated the codon GAC for residue 9 as Glu

C/Keywords: T-cell receptor

Query Match 20.8%; Score 20; DB 2; Length 10;

Best Local Similarity 57.1%; Pred. No. 4.1e+03;

Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 AFPHGY 8  
| | | | |  
| | | | |

DB 2 ASSPGY 8

RESULT 44

A46030

Gonadoliberin I - spiny dogfish

N/Alternate names: gonadotropin-releasing hormone

C/Species: Squalus acanthias (spiny dogfish)

C/Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 09-Jul-2004

C/Accession: A46030

R/Lovejoy, D.A.; Fischer, W.H.; Ngamwongchon, S.; Craig, A.G.; Nahorniak, C.S.; Peter,

Proc. Natl. Acad. Sci. U.S.A. 89, 6373-6377, 1992

A/Title: Distinct sequence of gonadotropin-releasing hormone (GnRH) in dogfish brain pr

A/Reference number: A46030; MUID:92335300; PMID:1631133

A/Accession: A46030

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-10 <LOV>

A/Cross-references: UNIPROT:P27429; UNIPARC:UPI000012B910

C/Keywords: hormone; pyroglutamic acid

F/1/Modified site: pyroglutamic acid (Glu) #status experimental

Query Match 20.8%; Score 20; DB 2; Length 10;

Best Local Similarity 75.0%; Pred. No. 4.1e+03;

Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 HGVL 9  
| | | | |  
| | | | |

DB 5 HGWL 8

RESULT 45

S77990  
cytochrome-c oxidase (EC 1.9.3.1) chain VIIc - bigeye tuna (fragment)  
C/Species: Thunnus obesus (bigeye tuna)  
C/Date: 17-Sep-1997 #sequence\_revision 17-Sep-1997 #text\_change 09-Jul-2004  
C/Accession: S77990  
R/Arnold, S.; Lee, J.; Kim, M.; Song, E.; Linder, D.; Lottspeich, F.; Kadenbach, B.  
submitted to the Protein Sequence Database, June 1997  
A/Reference number: S77980  
A/Accession: S77990  
A/Molecule type: protein  
A/Residues: 1-10 <ARN>  
A/Cross-references: UNIPROT:P80982; UNIPARC:UPI0000128169  
A/Experimental source: heart; liver  
C/Genetics:  
A/Genome: nuclear  
C/Function:  
A/Pathway: oxidative phosphorylation; respiratory chain  
C/Keywords: electron transfer; membrane-associated complex; mitochondrial inner membrane

Query Match 20.8%; Score 20; DB 2; Length 10;  
Best Local Similarity 66.7%; Pred. No. 4.1e+03; Indels 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 13 AVSPGK 18  
| | | |  
Db 4 AEGPGK 9

RESULT 46  
A60656  
perisulfakinin - American cockroach  
C/Species: Periplaneta americana (American cockroach)  
C/Date: 14-May-1993 #sequence\_revision 14-May-1993 #text\_change 09-Jul-2004  
C/Accession: A60656  
R/Venestra, J.A.  
Neuropeptides 14, 145-149, 1989  
A/Title: Isolation and structure of two gastrin/CKK-like neuropeptides from the American  
A/Reference number: A60656; MUID:90137190; PMID:2615921  
A/Accession: A60656  
A/Molecule type: protein  
A/Residues: 1-11 <VEE>  
A/Cross-references: UNIPROT:P36885; UNIPARC:UPI0000128962  
C/Comment: This neuropeptide stimulates hindgut contractions.  
C/Keyword: amidated carboxyl end; neuropeptide; sulfoprotein  
F/Binding site: sulfate (Tyr) (covalent) #status experimental  
F/11/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 20.8%; Score 20; DB 2; Length 11;  
Best Local Similarity 22.2%; Pred. No. 4.5e+03; Indels 0; Gaps 0;  
Matches 2; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 DAFPHGYL 9  
| | | |  
Db 1 EOPDDYGHM 9

RESULT 47  
S70344  
amine oxidase (copper-containing) (EC 1.4.3.6) I - Aspergillus niger (fragments)  
C/Species: Aspergillus niger  
C/Date: 19-Mar-1998 #sequence\_revision 17-Apr-1998 #text\_change 17-Apr-1998  
C/Accession: S70344  
R/Frederick, I.; Pec, P.; Luhnova, L.; Toyama, H.; Matsushita, K.; Hirota, S.; Kitagawa, T.  
Biochim. Biophys. Acta 1295, 59-72, 1996  
A/Title: Two amine oxidases from Aspergillus niger AKU 3102 contain topa quinone as the  
A/Reference number: S70344; MUID:96283794; PMID:8679675  
A/Accession: S70344  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-7;8-12 <FRB>  
A/Cross-references: UNIPROT:UPI000017B3B5; UNIPARC:UPI000017B3B6  
C/Keywords: oxidoreductase

Query Match 20.8%; Score 20; DB 2; Length 12;  
Best Local Similarity 75.0%; Pred. No. 5e+03; Indels 0; Gaps 0;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 EPHG 7  
| | | |  
Db 4 EPHG 7

RESULT 48  
A46463  
preabsorbing antigen (PA-Ag) - Streptococcus sp. (fragment)  
C/Species: Streptococcus sp.  
C/Date: 18-Jun-1993 #sequence\_revision 25-Apr-1997 #text\_change 20-Sep-1999  
C/Accession: A46463  
R/Toshizawa, N.; Oshima, S.; Segel, I.; Shitizu, J.; Treiser, G.  
J. Immunol. 148, 3110-3116, 1992  
A/Title: Role of a streptococcal antigen in the pathogenesis of acute poststreptococcal  
A/Reference number: A46463; MUID:92251171; PMID:1578137  
A/Accession: A46463  
A/Molecule type: protein  
A/Residues: 1-13 <YOS>  
A/Cross-references: UNIPARC:UPI00000866E6; PIDN:AAB22148.1; PID:G249161  
A/Note: sequence extracted from NCBI backbone (NCBIP:100561)

Query Match 20.8%; Score 20; DB 2; Length 13;  
Best Local Similarity 66.7%; Pred. No. 5.4e+03; Indels 0; Gaps 0;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 12 AAVSPG 17  
| | | |  
Db 5 AASAPG 10

RESULT 49  
LFBMT  
trp operon leader peptide - Salmonella typhimurium  
C/Species: Salmonella typhimurium  
C/Date: 02-Apr-1982 #sequence\_revision 02-Apr-1982 #text\_change 03-Jul-2004  
C/Accession: A03590  
R/Lee, F.; Bertrand, K.; Bennett, G.; Yanofsky, C.  
J. Mol. Biol. 121, 193-217, 1978  
A/Title: Comparison of the nucleotide sequences of the initial transcribed regions of trp  
A/Reference number: A02850; MUID:78196931; PMID:351195  
A/Accession: A03590  
A/Molecule type: DNA  
A/Residues: 1-14 <LEB>  
A/Cross-references: UNIPROT:P03054; UNIPARC:UPI000012892E  
C/Genetics:  
A/Gene: trpL; trpE  
C/Function:  
A/Description: involved in control of tryptophan operon transcription by attenuation  
C/Superfamily: trp leader peptide

Query Match 20.8%; Score 20; DB 1; Length 14;  
Best Local Similarity 40.0%; Pred. No. 5.8e+03; Indels 0; Gaps 0;  
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 3 EEPHGYLTA 12  
| | | |  
Db 5 FALHGMWRTS 14

RESULT 50  
A56632  
neosalafakinin-II - flesh fly (Sarcophaga bullata)  
N/Alternate names: Neb-SK-II  
N/Contains: neosalafakinin-I (Neb-SK-I)  
C/Species: Sarcophaga bullata  
C/Date: 21-Jul-1995 #sequence\_revision 21-Jul-1995 #text\_change 09-Jul-2004  
C/Accession: A56632  
R/Fonagy, A.; Schoofs, L.; Proost, P.; Van Damme, J.; De Loof, A.  
Comp. Biochem. Physiol. C 103, 135-142, 1992



A/Title: Isolation and primary structure of two sulfakinin-like peptides from the flesh  
A/Reference number: A56532; MUID:93083101; PMID:1360367  
A/Accession: A56532  
A/Molecule type: protein  
A/Residues: 1-14 <F0N>  
A/Cross-references: UNIPROT:P41493; UNIPARC:UPI000013054D  
A/Experimental source: head  
A/Note: sequence extracted from NCBI backbone (NCBIP:120391)  
C/Keywords: amidated carboxyl end; neuropeptide; sulfoprotein  
F/1-14/Product: neosulfakinin-I #status experimental <NSK2>  
F/6-14/Product: neosulfakinin-I #status experimental <NSK1>  
F/9/Binding site: sulfate (Tyr) (covalent) #status predicted  
F/14/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 20.8%; Score 20; DB 2; Length 14;  
Best Local Similarity 22.2%; Pred. No. 5.8e+03;  
Matches 2; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 DAFPHGYL 9  
| | | | |  
DB 4 EGFDDYGHM 12

RESULT 51  
S27140  
hypothetical protein 1 estrogen receptor 5'-region - human  
C/Species: Homo sapiens (man)  
C/Date: 05-Mar-1994 #sequence\_revision 12-May-1995 #text\_change 16-Aug-2004  
C/Accession: S27140  
R/Keaveney, M.; Klug, J.; Gannon, F.  
DNA Seq. 2, 347-358, 1992  
A/Title: Sequence analysis of the 5' flanking region of the human estrogen receptor gene  
A/Reference number: S27140; MUID:93075998; PMID:1476547  
A/Accession: S27140  
A/Status: translation not shown  
A/Molecule type: DNA  
A/Residues: 1-14 <KEA>  
A/Cross-references: UNIPARC:UPI000011DF55; EMBL:X62462; NID:931201; PIND:CAA4319.1; PII

Query Match 20.8%; Score 20; DB 2; Length 14;  
Best Local Similarity 27.3%; Pred. No. 5.8e+03;  
Matches 3; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 6 HGULTAAVSP 16  
| | | | |  
DB 4 HSFPLSHSLGP 14

RESULT 52  
PH1342  
Ig heavy chain DJ region (clone C507-95) - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999  
C/Accession: PH1342  
R/Messerman, R.; Gallili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.  
J. Exp. Med. 176, 1577-1581, 1992  
A/Title: Predominance of fetal type DJH joining in young children with B precursor lymph  
A/Reference number: PH1302; MUID:93094761; PMID:1460419  
A/Accession: PH1342  
A/Molecule type: DNA  
A/Residues: 1-15 <MAS>  
A/Cross-references: UNIPARC:UPI000017C240  
C/Keywords: heterotetramer; immunoglobulin

Query Match 20.8%; Score 20; DB 2; Length 15;  
Best Local Similarity 75.0%; Pred. No. 6.3e+03;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 PHGY 8  
| | | | |  
DB 4 PRGY 7

RESULT 53  
PH110  
Ig heavy chain DJ region (clone C770-107) - human (fragment)

C/Species: Homo sapiens (man)  
C/Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999  
C/Accession: PH110  
R/Messerman, R.; Gallili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.  
J. Exp. Med. 176, 1577-1581, 1992  
A/Title: Predominance of fetal type DJH joining in young children with B precursor lymph  
A/Reference number: PH1302; MUID:93094761; PMID:1460419  
A/Accession: PH110  
A/Molecule type: DNA  
A/Residues: 1-15 <MAS>  
A/Cross-references: UNIPARC:UPI000017C24P  
C/Keywords: heterotetramer; immunoglobulin

Query Match 20.8%; Score 20; DB 2; Length 15;  
Best Local Similarity 50.0%; Pred. No. 6.3e+03;  
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 7 GULTAAVSP 16  
| | | | |  
DB 6 GALTGARBP 15

RESULT 54  
A44413  
proteasome endopeptidase complex (EC 3.4.25.1) 24K chain - bovine (fragment)  
N/Alternate names: multicatalytic proteinase complex 24K chain; proteasome  
N/Contents: multicatalytic proteinase complex 21K chain  
C/Species: Bos primigenius taurus (cattle)  
C/Date: 30-Apr-1993 #sequence\_revision 23-Mar-1995 #text\_change 09-Jul-2004  
C/Accession: A44413; B44413  
R/Yu, B.; Pereira, M.E.; Wilk, S.  
J. Biol. Chem. 268, 2029-2036, 1993  
A/Title: Changes in the structure and catalytic activities of the bovine pituitary mult  
A/Reference number: A44413; MUID:93131959; PMID:8420977  
A/Accession: A44413  
A/Molecule type: protein  
A/Residues: 1-16 <YU1>  
A/Cross-references: UNIPROT:Q9TRJ7; UNIPARC:UPI00000867F3  
A/Experimental source: pituitary  
A/Note: sequence extracted from NCBI backbone (NCBIP:123115)  
C/Suprafamily: multicatalytic endopeptidase complex chain C9  
C/Keywords: hydrolase

Query Match 20.8%; Score 20; DB 2; Length 16;  
Best Local Similarity 42.9%; Pred. No. 6.7e+03;  
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 6 HGULTAA 12  
| | | | |  
DB 10 HGIVVAA 16

RESULT 55  
PH1637  
Ig H chain V-D-J region (clone B-Jess 226) - mouse (fragment)  
C/Species: Mus musculus (house mouse)  
C/Date: 02-Jun-1994 #sequence\_revision 02-Jun-1994 #text\_change 17-Mar-1999  
C/Accession: PH1637  
R/Levinson, D.A.; Campos-Torres, J.; Leder, P.  
J. Exp. Med. 178, 317-329, 1993  
A/Title: Molecular characterization of transgene-induced immunodeficiency in B-Jess mic  
A/Reference number: PH1580; MUID:93101609; PMID:8315387  
A/Accession: PH1637  
A/Molecule type: DNA  
A/Residues: 1-16 <LEV>  
A/Cross-references: UNIPARC:UPI000017C6A0  
A/Experimental source: bone marrow pre-B lymphocyte  
C/Keywords: immunoglobulin

Query Match 20.8%; Score 20; DB 2; Length 16;

Best Local Similarity 50.0%; Pred. No. 6.7e+03;  
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 6 HGYLTT 11  
| : |  
| : |  
Db 4 HGAMVT 9

## RESULT 56

PH0773  
T-cell receptor beta chain (C7) - mouse (fragment)  
C/Species: Mus musculus (house mouse)  
C/Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 05-Nov-1999  
C/Accession: PH0773  
R/Casanova, J.L.; Romero, P.; Widmann, C.; Koutileky, P.; Maryanski, J.L.  
J. Exp. Med. 174, 1371-1383, 1991  
A/Title: T cell receptor genes in a series of class I major histocompatibility complex-I  
allelic exclusion and antigen-specific repertoire.  
A/Reference number: PH0746; MUID:92078846; PMID:1836010  
A/Accession: PH0773  
A/Molecule type: mRNA  
A/Residues: 1-16 <CNS>  
A/Cross-references: UNIPARC:UPI0000115FC0; EMBL:X60868; NID:950247; PIDD:CAA43257.1; PII  
A/Experimental sources: T lymphocyte  
C/Keywords: T-cell receptor

Query Match 20.8%; Score 20; DB 2; Length 16;  
Best Local Similarity 66.7%; Pred. No. 6.7e+03;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 13 AVSPGK 18  
| : | : |  
| : | : |  
Db 2 ASSFGQ 7

## RESULT 57

A44799  
pyrogenic exotoxin C - Streptococcus pyogenes (fragment)  
C/Species: Streptococcus pyogenes  
C/Date: 24-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change 31-Dec-2004  
C/Accession: A44799  
R/Kapur, V.; Nelson, K.; Schlievert, P.M.; Selander, R.K.; Musser, J.M.  
Infect. Immun. 60, 3513-3517, 1992  
A/Title: Molecular population genetic evidence of horizontal spread of two alleles of th  
A/Reference number: A44799; MUID:92363541; PMID:1500157  
A/Accession: A44799  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-17 <KAP>  
A/Cross-references: UNIPROT:P13380; UNIPROT:Q8MKX2; UNIPARC:UPI000017AC80  
A/Experimental sources: strain T18P, MGAS 1585  
A/Note: sequence inconsistent with the nucleotide translation  
A/Note: sequence extracted from NCBI backbone (NCBI:110912, NCBI:P110914)  
C/Superfamily: enterotoxin B  
C/Keywords: exotoxin

Query Match 20.8%; Score 20; DB 2; Length 17;  
Best Local Similarity 37.5%; Pred. No. 7.1e+03;  
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 9 LITRAVSP 16  
| : | : |  
| : | : |  
Db 2 ILISTISP 9

## RESULT 58

S45373  
translation elongation factor EF-1a - common tobacco  
C/Species: Nicotiana tabacum (common tobacco)  
C/Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 09-Jul-2004  
C/Accession: S45373  
R/Marty, I.; Brugidou, C.; Chartier, Y.; Meyer, Y.  
Plant J. 4, 265-278, 1993

A/Title: Growth-related gene expression in Nicotiana tabacum mesophyll protoplasts.  
A/Reference number: S45373; MUID:94035181; PMID:8220482

A/Accession: S45373  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-18 <MAR>  
A/Cross-references: UNIPROT:Q40499; UNIPARC:UPI000006A737; EMBL:Z14080; NID:9443955; PII

Query Match 20.8%; Score 20; DB 2; Length 18;  
Best Local Similarity 33.3%; Pred. No. 7.5e+03;  
Matches 5; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 4 BPHGYLTPAASPGK 18  
| : | : | : |  
| : | : | : |  
Db 3 DPHGKVTKAAQKK 17

## RESULT 59

I59649  
human leukocyte antigen alpha chain - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 09-Jul-2004  
C/Accession: I59649  
R/Fogdell, A.; Olerup, O.  
Tissue Antigens 44, 19-24, 1994  
A/Title: The DOA1\*0104 allele is carried by DRB1\*1001- and DRB1\*1401-positive haplotypes  
A/Reference number: I59649; MUID:95064785; PMID:7974465  
A/Accession: I59649  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-18 <RES>  
A/Cross-references: UNIPROT:Q30216; UNIPARC:UPI000008A43F; GB:S75685; NID:9913771; PIDD  
C/Genetics: GDB:HLA-DQA1  
A/Accession: GDB:HLA-DQA1  
A/Status: preliminary  
A/Reference number: I59649; MUID:95064785; PMID:7974465  
A/Accession: I59649  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-18 <RES>  
A/Cross-references: UNIPROT:Q30216; UNIPARC:UPI000008A43F; GB:S75685; NID:9913771; PIDD  
A/Map position: 6p21.3-6p21.3

Query Match 20.8%; Score 20; DB 2; Length 18;  
Best Local Similarity 57.1%; Pred. No. 7.5e+03;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 10 LITRAVSP 16  
| : | : |  
| : | : |  
Db 5 LITMNSP 11

## RESULT 60

S48862  
murine cyclin H - mouse  
C/Species: Mus musculus (house mouse)  
C/Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 09-Jul-2004  
C/Accession: S48862  
R/Hall, F.L.; Wu, L.  
submitted to the EMBL Data Library, October 1994  
A/Reference number: S48862  
A/Accession: S48862  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-18 <HNL>  
A/Cross-references: UNIPROT:Q61458; UNIPARC:UPI000016CCB5; EMBL:X82441; NID:9563899; PII

Query Match 20.8%; Score 20; DB 2; Length 18;  
Best Local Similarity 36.4%; Pred. No. 7.5e+03;  
Matches 4; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 3 FEPHGYLTPAA 13  
| : | : | : |  
| : | : | : |  
Db 8 YHPRIMLTCA 18

## RESULT 61

I51427  
hemoglobin alpha chain - African clawed frog (fragment)

C;Species: Xenopus laevis (African clawed frog)  
C;Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 09-Jul-2004  
C;Accession: I51427  
R;Patient: R.K.; Elington, J.A.; Kay, R.M.; Williams, J.G.  
Cell 21, 565-573, 1980  
A;Title: Internal organization of the major adult alpha- and beta-globin genes of X.laevis  
A;Reference number: I51427; PMID:81001900; PMID:6250724  
A;Accession: I51427  
A;Status: preliminary, translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-18 <PRT>  
A;Cross-references: UNIPROT:P67468; UNIPARC:UPI00001770CF; GB:J00975; NID:g214198; PID:g  
C;Keywords: blood; oxygen carrier

Query Match 20.8%; Score 20; DB 2; Length 18;  
Best Local Similarity 50.0%; Pred. No. 7.5e+03;  
Matches 6; Conservative 0; Mismatches 4; Indels 2; Gaps 1;

QY 6 HGVLTAAYSPG 17  
DB 7 HAYDL-RVDPG 16

RESULT 62  
A34467  
3K microfibril-associated protein - pig (fragment)  
C;Species: Sus scrofa domestica (domestic pig)  
C;Date: 08-Jun-1990 #sequence\_revision 08-Jun-1990 #text\_change 09-Jul-2004  
C;Accession: A34467  
R;Kobayashi, R.; Teshima, Y.; Masuda, H.; Shozawa, T.; Numata, Y.; Myauchi, K.; Hayakawa  
J. Biol. Chem. 264, 17437-17444, 1989  
A;Title: Isolation and characterization of a new 36-kDa microfibril-associated glycoprotein  
A;Reference number: A34467; PMID:90008913; PMID:2793866  
C;Accession: A34467  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-19 <KOB>  
A;Cross-references: UNIPROT:Q7M366; UNIPARC:UPI000017C450

Query Match 20.8%; Score 20; DB 2; Length 19;  
Best Local Similarity 60.0%; Pred. No. 8e+03;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DAFBP 5  
DB 10 DKFOP 14

RESULT 63  
A60801  
acrosome stabilizing factor large chain - rabbit (fragment)  
C;Species: Oryctolagus cuniculus (domestic rabbit)  
C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999  
C;Accession: A60801  
R;Wilson, W.L.; Oliphant, G.  
Biol. Reprod. 37, 159-169, 1987  
A;Title: Isolation and biochemical characterization of the subunits of the rabbit sperm  
A;Reference number: A60801; PMID:88000873; PMID:3651543  
C;Accession: A60801  
A;Molecule type: protein  
A;Residues: 1-20 <WIL>  
A;Cross-references: UNIPARC:UPI000017C5B3  
A;Comment: spermatozoa must undergo capacitation and the acrosome reaction to become cap  
C;Keywords: glycoprotein; semen

Query Match 20.8%; Score 20; DB 2; Length 20;  
Best Local Similarity 57.1%; Pred. No. 8.4e+03;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 BPHGYLL 10  
DB 12 BXPGL 18

RESULT 64  
A48367  
glutaryl-CoA dehydrogenase (BC 1.3.99.7) - Pseudomonas sp. (fragment)  
C;Species: Pseudomonas sp.  
C;Date: 01-Dec-1993 #sequence\_revision 29-Sep-1999 #text\_change 29-Sep-1999  
C;Accession: A48367  
R;Hartel, U.; Eckel, E.; Koch, J.; Fuchs, G.; Linder, D.; Buckel, W.  
Arch. Microbiol. 159, 174-181, 1993  
A;Title: Purification of glutaryl-CoA dehydrogenase from Pseudomonas sp., an enzyme inv.  
A;Reference number: A48367; PMID:93175988; PMID:8439237  
C;Accession: A48367  
A;Molecule type: protein  
A;Residues: 1-20 <HAR>  
A;Cross-references: UNIPARC:UPI00000BDFCE; PIDN:AA825430.1; PID:g265706  
A;Experimental source: strain KB 740  
A;Note: sequence extracted from NCBI backbone (NCBIP:125304)  
C;Keywords: oxidoreductase

Query Match 20.3%; Score 19.5; DB 2; Length 20;  
Best Local Similarity 55.6%; Pred. No. 1e+04;  
Matches 5; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

QY 1 DAFBPHGYL 9  
DB 8 DADPY-YL 15

RESULT 65  
PT0714  
T-cell receptor beta chain V-D-J region (165-31) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 09-Jul-2004  
C;Accession: PT0714  
R;Feeney, A.J.  
J. Exp. Med. 174, 115-124, 1991  
A;Title: Functional sequences of fetal T cell receptor beta chains have few N regions.  
A;Reference number: PT0509; PMID:91277601; PMID:1711558  
C;Accession: PT0714  
A;Status: translation not shown  
A;Molecule type: DNA  
A;Residues: 1-5 <FRB>  
A;Cross-references: UNIPROT:Q8BGR5; UNIPARC:UPI000017C849  
A;Experimental source: newborn thymus, strain BALB/c  
C;Keywords: T-cell receptor

Query Match 19.8%; Score 19; DB 2; Length 5;  
Best Local Similarity 80.0%; Pred. No. 2.8e+05;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 13 AVSPG 17  
DB 1 ASSPG 5

RESULT 66  
PD0027  
pev-tachykinin - penaeid shrimp (Penaeus vannamei) (fragment)  
C;Species: Penaeus vannamei  
C;Date: 21-Aug-1998 #sequence\_revision 21-Aug-1998 #text\_change 09-Jul-2004  
C;Accession: PD0027  
R;Nieto, J.; Veelaert, D.; Derna, R.; Waelkens, E.; Ceratliens, A.; Coact, G.; Devreese,  
Biochem. Biophys. Res. Commun. 248, 406-411, 1998  
A;Title: Identification of one tachykinin- and two kinin-related peptides in the brain c  
A;Reference number: PD0027; PMID:98342103; PMID:9675150  
C;Accession: PD0027  
A;Molecule type: protein  
A;Residues: 1-9 <NIB>  
A;Cross-references: UNIPROT:Q7M313; UNIPARC:UPI000017CB0C  
C;Comment: This peptide belongs to myotropic neuropeptides.

Query Match 19.8%; Score 19; DB 2; Length 9;  
Best Local Similarity 60.0%; Pred. No. 2.8e+05;

Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 5 PHGYL 9  
| | : |  
| | : |  
Db 2 PSGFL 6

RESULT 67  
S67528  
napin - rape (fragments)  
C/Species: Brassica napus (rape)  
C/Date: 14-Feb-1997 #sequence\_revision 13-Mar-1997 #text\_change 13-Mar-1997  
C/Accession: S67528  
R/Muren, E.; Ek, B.; Raak, L.  
Eur. J. Biochem. 227, 316-321, 1995  
A/Title: Processing of the 2S storage protein pronapin in Brassica napus and in transfor  
A/Reference number: S67528; MUID:95154306; PMID:7851402  
A/Accession: S67528  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-67-12 <MUR>  
A/Cross-references: UNIPARC:UPI000017B02B; UNIPARC:UPI000017B02C

Query Match 19.8%; Score 19; DB 2; Length 12;  
Best Local Similarity 60.0%; Pred. No. 7.3e+03;  
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 FEPHG 7  
| | | |  
| | | |  
Db 5 FRPG 9

RESULT 68  
PH190  
T-cell receptor alpha chain V region (Cw3/10.1) - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 16-Jul-1999  
C/Accession: PH190  
R/Casanova, J.L.; Cerotini, J.C.; Matthes, M.; Necker, A.; Gounnier, H.; Barra, C.; Wic  
J. Exp. Med. 176, 439-447, 1992  
A/Title: H-2-restricted cytolytic T lymphocytes specific for HLA display T cell receptor  
A/Reference number: S26512; MUID:92364546; PMID:1380061  
A/Accession: PH190  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-12 <CAS>  
A/Cross-references: UNIPARC:UPI000017C395

Query Match 19.8%; Score 19; DB 2; Length 12;  
Best Local Similarity 42.9%; Pred. No. 7.3e+03;  
Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 AEPHGY 8  
| | | |  
| | | |  
Db 2 AVSEHGF 8

RESULT 69  
PT0263  
Ig heavy chain CRD3 region (clone 2-121B) - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996  
C/Accession: PT0263  
R/Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.  
J. Exp. Med. 173, 395-407, 1991  
A/Title: Preferential utilization of specific immunoglobulin heavy chain diversity and J  
A/Reference number: PT0222; MUID:91108337; PMID:1899102  
A/Accession: PT0263  
A/Molecule type: DNA  
A/Residues: 1-13 <YAM>  
A/Cross-references: UNIPARC:UPI000017C1F0  
A/Experimental source: B lymphocyte  
A/Keywords: heterotetramer; immunoglobulin

Query Match 19.8%; Score 19; DB 2; Length 13;  
Best Local Similarity 75.0%; Pred. No. 7.9e+03;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 HGYL 9  
| | | |  
| | | |  
Db 7 YGYL 10

RESULT 70  
LFBWC  
trp operon leader peptide - Citrobacter freundii  
C/Species: Citrobacter freundii  
C/Date: 14-Nov-1983 #sequence\_revision 14-Nov-1983 #text\_change 09-Jul-2004  
C/Accession: A03592  
R/Blumenberg, M.; Yanofsky, C.  
J. Bacteriol. 152, 57-62, 1982  
A/Title: Evolutionary divergence of the Citrobacter freundii tryptophan operon regulator  
A/Reference number: A91792; MUID:83007061; PMID:6749821  
A/Accession: A03592  
A/Molecule type: DNA  
A/Residues: 1-14 <BLU>  
A/Cross-references: UNIPROT:P03056; UNIPARC:UPI000012B89A  
A/Genetics:  
A/Gene: trpL  
C/Function:  
A/Description: involved in control of tryptophan operon transcription by attenuation  
C/Superfamily: trp leader peptide

Query Match 19.8%; Score 19; DB 1; Length 14;  
Best Local Similarity 40.0%; Pred. No. 8.5e+03;  
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 3 FEPHGYLTA 12  
| | | | : |  
| | | | : |  
Db 5 FVLHGWRRTS 14

RESULT 71  
PH1347  
Ig heavy chain DJ region (clone C100-103A) - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999  
C/Accession: PH1347  
R/Wasserman, R.; Gallili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.  
J. Exp. Med. 176, 1577-1581, 1992  
A/Title: Predominance of fetal type DJH joining in young children with B precursor lymph  
A/Reference number: PH1302; MUID:93094761; PMID:1460419  
A/Accession: PH1347  
A/Molecule type: DNA  
A/Residues: 1-14 <WAS>  
A/Cross-references: UNIPARC:UPI000017C21C  
A/Keywords: heterotetramer; immunoglobulin

Query Match 19.8%; Score 19; DB 2; Length 14;  
Best Local Similarity 44.4%; Pred. No. 8.5e+03;  
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 8 YLTRA VAVSP 16  
| | | | | |  
| | | | | |  
Db 6 FLTTGAREP 14

RESULT 72  
S24159  
leukocyte elastase (EC 3.4.21.37) - sheep (fragment)  
N/Alternate names: neutrophil elastase  
C/Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)  
C/Date: 22-Nov-1993 #sequence\_revision 27-Feb-1997 #text\_change 09-Jul-2004  
C/Accession: S24159  
R/Junger, W.G.; Hallstrom, S.; Liu, F.C.; Redl, H.; Schlag, G.  
Biol. Chem. Hoppe-Seyler 373, 691-698, 1992

A/Title: The enzymatic and release characteristics of sheep neutrophil elastase: a compd  
 A/Reference number: 824159; PMID:93039751; PMID:1418684  
 A/Accession: 824159  
 A/Status: preliminary  
 A/Molecule type: protein  
 A/Residues: 1-15 <JUN>  
 A/Cross-references: UNIPROT:Q9TRL3; UNIPARC:UPI0000086F8A  
 A/Superfamily: trypsin; trypsin homology  
 C/Keywords: hydrolase, serine proteinase

Query Match 19.8%; Score 19; DB 2; Length 15;  
 Best Local Similarity 42.9%; Pred. No. 9.1e+03;  
 Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 AFBPHGY 8  
 DB 6 AAFPHAM 12

## RESULT 73

S25535  
 T-cell receptor alpha chain V region (clone Cw3/10.1) - mouse (fragment)  
 C/Species: Mus musculus (house mouse)  
 A/Variety: clone Cw3/10.1  
 C/Date: 11-Mar-1998 #sequence\_revision 17-Apr-1998 #text\_change 17-Mar-1999  
 C/Accession: S25535  
 R/Casanova, J.L.; Cerottini, J.C.; Matthes, M.; Necker, A.; Gournier, H.; Barra, C.; Wild  
 J. Exp. Med. 176, 439-447, 1992  
 A/Title: H-2-restricted cytolytic T lymphocytes specific for HLA display T cell receptor  
 A/Reference number: S25512; PMID:92364546; PMID:1380061  
 A/Accession: S25535  
 A/Molecule type: mRNA  
 A/Residues: 1-15 <CNS>  
 A/Cross-references: UNIPARC:UPI00001769C2; EMBL:X67986  
 A/Experimental source: cytolytic T lymphocyte, clone Cw3/10.1  
 C/Superfamily: immunoglobulin V region; immunoglobulin homology  
 C/Keywords: T-cell receptor

Query Match 19.8%; Score 19; DB 2; Length 15;  
 Best Local Similarity 42.9%; Pred. No. 9.1e+03;  
 Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 AFBPHGY 8  
 DB 2 AVSHGPF 8

## RESULT 74

S29485  
 GTP-binding protein o-ral - Pacific electric ray (fragment)  
 C/Species: Torpedo californica (Pacific electric ray)  
 C/Date: 22-Nov-1993 #sequence\_revision 27-Feb-1997 #text\_change 13-Mar-1997  
 C/Accession: S29485  
 R/Volkhardt, W.; Peyssner, J.; Elferink, L.A.; Scheller, R.H.  
 FEBS Lett. 317, 53-56, 1993  
 A/Title: Association of three small GTP-binding proteins with cholinergic synaptic vesic  
 A/Reference number: S29485; PMID:93154521; PMID:8428634  
 A/Accession: S29485  
 A/Status: preliminary  
 A/Molecule type: protein  
 A/Residues: 1-15 <VOL>  
 A/Cross-references: UNIPARC:UPI000017BPJ3

Query Match 19.8%; Score 19; DB 2; Length 15;  
 Best Local Similarity 60.0%; Pred. No. 9.1e+03;  
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 BPHG 7  
 DB 9 YBPTG 13

## RESULT 75

A36315  
 recycling receptor p180 - human (fragment)  
 C/Species: Homo sapiens (man)  
 C/Date: 25-Jan-1991 #sequence\_revision 25-Jan-1991 #text\_change 30-Sep-1993  
 C/Accession: A36315  
 R/Isacke, C.M.; van der Geer, P.; Hunter, T.; Trowbridge, I.S.  
 Mol. Cell. Biol. 10, 2606-2618, 1990  
 A/Title: p180, a novel recycling transmembrane glycoprotein with restricted cell type e  
 A/Reference number: A36315; PMID:90258846; PMID:2188094  
 A/Accession: A36315  
 A/Status: preliminary  
 A/Molecule type: protein  
 A/Residues: 1-15 <ISA>  
 A/Cross-references: UNIPARC:UPI000017C3J7

Query Match 19.8%; Score 19; DB 2; Length 15;  
 Best Local Similarity 42.9%; Pred. No. 9.1e+03;  
 Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 BPHGYL 10  
 DB 9 BPHVPLI 15

## RESULT 76

PA0006  
 lectin A3 - Psophocarpus scandens (fragment)  
 C/Species: Psophocarpus scandens  
 C/Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 09-Jul-2004  
 C/Accession: PA0006  
 R/Kort, A.A.  
 Phytochemistry 27, 2847-2855, 1988  
 A/Title: Isolation and characterization of the lectins from the seeds of Psophocarpus s  
 A/Reference number: PA0005  
 A/Accession: PA0006  
 A/Molecule type: protein  
 A/Residues: 1-15 <KOR>  
 A/Cross-references: UNIPROT:P22583; UNIPARC:UPI000012B3BR  
 A/Experimental source: seed  
 C/Comment: The seeds of Psophocarpus contain two distinct groups of lectins which can b  
 C/Keywords: lectin

Query Match 19.8%; Score 19; DB 2; Length 15;  
 Best Local Similarity 60.0%; Pred. No. 9.1e+03;  
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DAFBP 5  
 DB 9 NVFEP 13

## RESULT 77

A60551  
 leukocyte elastase (BC 3.4.21.37) - dog (fragment)  
 C/Species: Canis lupus familiaris (dog)  
 C/Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 09-Jul-2004  
 C/Accession: A60551  
 R/Axelsson, L.; Bergenfelt, M.; Björck, P.; Olsson, R.; Olsson, K.  
 Scand. J. Clin. Lab. Invest. 50, 35-42, 1990  
 A/Title: Release of immunoreactive canine leukocyte elastase normally and in endotoxin  
 A/Reference number: A60551; PMID:90193608; PMID:1690443  
 A/Accession: A60551  
 A/Molecule type: protein  
 A/Residues: 1-16 <AXE>  
 A/Cross-references: UNIPROT:O8MDJ1; UNIPARC:UPI0000175C1F  
 C/Superfamily: trypsin; trypsin homology  
 C/Keywords: hydrolase; leukocyte; lysosome; serine proteinase

Query Match 19.8%; Score 19; DB 2; Length 16;  
 Best Local Similarity 40.0%; Pred. No. 9.8e+03;  
 Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 BPHGY 8

Db 8 QPHAW 12

# RESULT 78

PT0282

Ig heavy chain CDR3 region (clone 4-94A) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996

C:Accession: PT0282

R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caron, A.J.; Rovera, G.

J. Exp. Med. 173, 395-407, 1991

A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and J

A:Reference number: PT0222; MUID:91108337; PMID:1899102

C:Accession: PT0282

A:Molecule type: DNA

A:Residues: 1-16 <YAM>

A:Cross-references: UNIPARC:UPI000017C1DA

A:Experimental source: B lymphocyte

C:Keywords: heterotrimer; immunoglobulin

Query Match 19.8%; Score 19; DB 2; Length 16;  
Best Local Similarity 60.0%; Pred. No. 9.8e+03;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 FEPHG 7  
| | |  
| | |  
Db 9 FDPWG 13

# RESULT 79

S16376

L-serine dehydratase beta chain - Peptostreptococcus asaccharolyticus

C:Species: Peptostreptococcus asaccharolyticus

C:Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 09-Jul-2004

C:Accession: S16376

R:Grabowski, R.; Buckel, W.

Eur. J. Biochem. 199, 89-94, 1991

A:Title: Purification and properties of an iron-sulfur-containing and pyridoxal-phosphat

A:Reference number: S16224; MUID:91293139; PMID:2065681

C:Accession: S16376

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-16 <EUR>

A:Cross-references: UNIPROT:P33074; UNIPARC:UPI000017ABR6

Query Match 19.8%; Score 19; DB 2; Length 16;  
Best Local Similarity 35.7%; Pred. No. 9.8e+03;  
Matches 5; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 2 AFEFGYLLTAVS 15  
| | | | |  
| | | | |  
Db 3 AFEVWGPIWGPSS 16

# RESULT 80

S57991

hydroxyproline-rich protein - Sebandia rostrata (fragment)

C:Species: Sebandia rostrata

C:Date: 13-Jan-1996 #sequence\_revision 01-Mar-1996 #text\_change 09-Jul-2004

C:Accession: S57991

R:Goormachtig, S.; Valerio-Lepintec, M.; Szczyglowski, K.; van Montagu, M.; Holsters, M.

submitted to the EMBL Data Library, March 1995

A:Description: Use of differential display to identify novel Sebandia rostrata genes ent

A:Reference number: S57991

A:Accession: S57991

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-17 <GOO>

A:Cross-references: UNIPROT:Q41400; UNIPARC:UPI000004ACD95; EMBL:Z48673; NID:G899484; PID

C:Superfamily: hydroxyproline-rich glycoprotein

Query Match 19.8%; Score 19; DB 2; Length 17;

Best Local Similarity 75.0%; Pred. No. 1e+04;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 PRGY 8  
| | |  
| | |  
Db 3 PHRY 6

# RESULT 81

S09085

proteasome chain 4 - rat (fragment)

N:Alternate names: multicatalytic proteinase chain 4

C:Species: Rattus norvegicus (Norway rat)

C:Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 18-Jun-1993

C:Accession: S09085

R:Lilley, K.S.; Davison, M.D.; Rivett, A.J.

FEBS Lett. 262, 327-329, 1990

A:Title: N-terminal sequence similarities between components of the multicatalytic prote

A:Reference number: S09082; MUID:90242957; PMID:2335214

C:Accession: S09085

A:Molecule type: protein

A:Residues: 1-17 <LIL>

A:Cross-references: UNIPARC:UPI000017C99F

Query Match 19.8%; Score 19; DB 2; Length 17;  
Best Local Similarity 28.6%; Pred. No. 1e+04;  
Matches 2; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 AFEFGY 8  
| | | | |  
| | | | |  
Db 1 SFSFYAF 7

# RESULT 82

B31435

adherence lectin light chain - Entamoeba histolytica (fragment)

C:Species: Entamoeba histolytica

C:Date: 31-Jul-1989 #sequence\_revision 31-Jul-1989 #text\_change 09-Jul-2004

C:Accession: B31435

R:Periti Jr., W.A.; Chapman, M.D.; Snodgrass, T.; Mann, B.J.; Broman, J.; Ravdin, J.I.

J. Biol. Chem. 264, 3007-3012, 1989

A:Title: Subunit structure of the galactose and N-acetyl-D-galactosamine-inhibitable adh

A:Reference number: A31435; MUID:89123408; PMID:2536731

C:Accession: B31435

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-17 <PER>

A:Cross-references: UNIPROT:Q24846; UNIPARC:UPI000017B5D4

Query Match 19.8%; Score 19; DB 2; Length 17;  
Best Local Similarity 50.0%; Pred. No. 1e+04;  
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DAFEPH 6  
| | | | |  
| | | | |  
Db 7 DQFSPN 12

# RESULT 83

PH1323

Ig heavy chain DJ region (clone C174-113) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999

C:Accession: PH1323

R:Wasserman, R.; Gallili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.

J. Exp. Med. 176, 1577-1581, 1992

A:Title: Predominance of fetal type DJH joining in young children with B precursor lymph

A:Reference number: PH1302; MUID:93094761; PMID:1460419

C:Accession: PH1323

A:Molecule type: DNA

A:Residues: 1-18 <WAS>

A:Cross-references: UNIPARC:UPI0000176937

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

Query Match 19.8%; Score 19; DB 2; Length 18;  
Best Local Similarity 60.0%; Pred. No. 1.1e+04;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 FEPHG 7  
| | | |  
DB 11 FDPWG 15

#### RESULT 84

S28408

platelet-derived growth factor receptor beta - pig (fragment)

C;Species: Sus scrofa domestica (domestic pig)

C;Date: 27-Jan-1995 #sequence\_revision 27-Jan-1995 #text\_change 07-May-1999

C;Accession: S28408

R;Reinhardt, L.; Mori, S.; Arridsson, A.K.; Eriksson, A.; Wernstedt, C.; Hellman, U.;

EMBO J. 11, 3911-3919, 1992

A;Title: Identification of two C-terminal autophosphorylation sites in the PDGF beta-rec

A;Reference number: S28408; PMID:1356585

A;Accession: S28408

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-4;5-18 <ROB>

A;Cross-references: UNIPARC:UPI000017C472; UNIPARC:UPI000017C473

A;Keywords: growth factor receptor

Query Match 19.8%; Score 19; DB 2; Length 18;  
Best Local Similarity 44.4%; Pred. No. 1.1e+04;  
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 10 LTAVSFGK 18  
| | | | |  
DB 3 LDXAVQPN 11

RESULT 85  
S20322  
gluten - wheat

C;Species: Triticum aestivum (common wheat)

C;Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 09-Jul-2004

C;Accession: S20322

R;Fukushima, S.; Yoshikawa, M.

FEBS Lett. 286, 107-111, 1992

A;Title: Oligod peptides derived from wheat gluten: their isolation and characterization

A;Reference number: S20322; PMID:1309704

A;Accession: S20322

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-18 <FUK>

A;Cross-references: UNIPROT:Q7M1G0; UNIPARC:UPI000017B139

Query Match 19.8%; Score 19; DB 2; Length 18;  
Best Local Similarity 50.0%; Pred. No. 1.1e+04;  
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 FEPHG 8  
| | | |  
DB 2 YPTGY 7

RESULT 86  
PH1339  
Ig heavy chain DJ region (clone C272-119) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999

C;Accession: PH1339

R;Maberman, R.; Gallili, N.; Ito, Y.; Ketchard, B.A.; Shane, S.; Rovera, G.

J. Exp. Med. 176, 1577-1581, 1992

A;Title: Predominance of fetal type DJH joining in young children with B precursor lymph

A;Molecule type: DNA

A;Residues: 1-19 <RAS>

A;Cross-references: UNIPARC:UPI000017C23A

C;Keywords: heterotetramer; immunoglobulin

Query Match 19.8%; Score 19; DB 2; Length 19;  
Best Local Similarity 60.0%; Pred. No. 1.2e+04;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 FEPHG 7  
| | | |  
DB 12 FDPWG 16

#### RESULT 87

A34233

trehalase inhibitor - American cockroach (fragment)

C;Species: Periplaneta americana (American cockroach)

C;Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 09-Jul-2004

C;Accession: A34233

R;Hayakawa, Y.; Jahagirdar, A.P.; Yaguchi, M.; Downer, R.G.H.

J. Biol. Chem. 264, 16165-16169, 1989

A;Title: Purification and characterization of trehalase inhibitor from hemolymph of the

A;Reference number: A34233; PMID:89380218; PMID:2777784

A;Accession: A34233

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-19 <HAY>

A;Cross-references: UNIPROT:P19986; UNIPARC:UPI000012DA2D

Query Match 19.8%; Score 19; DB 2; Length 19;  
Best Local Similarity 75.0%; Pred. No. 1.2e+04;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 PHGY 8  
| | | |  
DB 5 PHVY 8

RESULT 88  
A56900  
chymotrypsin I (EC 3.4.21.-) - penaeid shrimp (Penaeus vanamei) (fragment)

C;Species: Penaeus vanamei

C;Date: 11-Aug-1995 #sequence\_revision 11-Aug-1995 #text\_change 09-Jul-2004

C;Accession: A56900

R;Van Wormhout, A.; Le Chevalier, P.; Sello, D.

Comp. Biochem. Physiol. B 103, 675-680, 1992

A;Title: Purification, biochemical characterization and N-terminal sequence of a serine

apoda).

A;Reference number: A56900; PMID:93092601; PMID:1458841

A;Accession: A56900

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-20 <VAN>

A;Cross-references: UNIPROT:O18487; UNIPARC:UPI0000175C07

A;Note: sequence extracted from NCBI backbone (NCBIPI:120229)

A;Note: a second variant, designated chymotrypsin II, had an identical N-terminal sequ

C;Comment: This enzyme has chymotrypsin and collagenolytic activities.

C;Superfamily: trypsin; trypsin homology

C;Keywords: hydrolase; protein digestion; serine proteinase

Query Match 19.8%; Score 19; DB 2; Length 20;  
Best Local Similarity 40.0%; Pred. No. 1.2e+04;  
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 5 PHGYLTAV 14  
| | | | |  
DB 9 PHSWPHQAL 18

#### RESULT 89

B34817

collagenolytic proteinase (EC 3.4.21.-), 35K, chain A - red king crab (fragment)

C;Species: Paratithodes camtschatica (red king crab)

C/Date: 13-Jul-1990 #sequence\_revision 13-Jul-1990 #text\_change 09-Jul-2004  
 C/Accession: B34817  
 R/Klimova, O.A.; Borukhov, S.I.; Solovyeva, N.I.; Balaevskaya, T.O.; Strongin, A.Y.  
 Biochem. Biophys. Res. Commun. 166, 1411-1420, 1990  
 A/Title: The isolation and properties of collagenolytic proteases from crab hepatopancre  
 A/Reference number: A34817; PMID:90165951; PMID:2154979  
 A/Accession: B34817  
 A/Status: preliminary  
 A/Molecule type: protein  
 A/Residues: 1-20 <KLI>  
 A/Cross-references: UNIPROT:P20732; UNIPARC:UPI0000127E39  
 C/Superfamily: trypsin; trypsin homology  
 C/Keywords: hydrolase; serine proteinase

Query Match 19.8%; Score 19; DB 2; Length 20;  
 Best Local Similarity 60.0%; Pred. No. 1.2e+04;  
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 14 VSPGK 18  
 DB 7 VTPGE 11

RESULT 90  
 C34817  
 collagenolytic proteinase (EC 3.4.21.-), 36K, chain B - red king crab (fragment)  
 C/Species: Paratithodes camtschatica (red king crab)  
 C/Date: 13-Jul-1990 #sequence\_revision 13-Jul-1990 #text\_change 09-Jul-2004  
 C/Accession: C34817  
 R/Klimova, O.A.; Borukhov, S.I.; Solovyeva, N.I.; Balaevskaya, T.O.; Strongin, A.Y.  
 Biochem. Biophys. Res. Commun. 166, 1411-1420, 1990  
 A/Title: The isolation and properties of collagenolytic proteases from crab hepatopancre  
 A/Reference number: A34817; PMID:90165951; PMID:2154979  
 A/Accession: C34817  
 A/Status: preliminary  
 A/Molecule type: protein  
 A/Residues: 1-20 <KLI>  
 A/Cross-references: UNIPROT:P20733; UNIPARC:UPI0000127E37  
 C/Superfamily: trypsin; trypsin homology  
 C/Keywords: hydrolase; serine proteinase

Query Match 19.8%; Score 19; DB 2; Length 20;  
 Best Local Similarity 60.0%; Pred. No. 1.2e+04;  
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 14 VSPGK 18  
 DB 7 VTPGE 11

RESULT 91  
 S07232  
 ribulose-bisphosphate carboxylase subunit-binding protein alpha chain - garden pea (frag  
 N/Alternate names: rubisco subunit-binding protein alpha chain  
 C/Species: Pisum sativum (garden pea)  
 C/Date: 31-Mar-1991 #sequence\_revision 31-Mar-1991 #text\_change 09-Jul-2004  
 C/Accession: S07232  
 R/Mugrove, J.E.; Johnson, R.A.; Ellis, R.J.  
 Eur. J. Biochem. 163, 529-534, 1987  
 A/Title: Disassociation of the ribulosebisphosphate-carboxylase large-subunit binding prot  
 A/Reference number: S07232; PMID:87161853; PMID:3549295  
 A/Accession: S07232  
 A/Molecule type: protein  
 A/Residues: 1-20 <MDS>  
 A/Cross-references: UNIPROT:P08926; UNIPARC:UPI000017834B  
 C/Comment: This protein binds the newly synthesized large subunit and the newly imported  
 C/Superfamily: chaperonin groEL  
 C/Keywords: chaperonin; heterododecamer; molecular chaperone

Query Match 19.8%; Score 19; DB 2; Length 20;  
 Best Local Similarity 60.0%; Pred. No. 1.2e+04;  
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 AEPKH 6  
 DB 6 AFDQH 10

RESULT 92  
 A60372  
 pollen allergen Poa-pi - Kentucky bluegrasses (fragment)  
 C/Species: Poa pratensis (Kentucky bluegrasses)  
 C/Date: 11-Feb-1993 #sequence\_revision 11-Feb-1993 #text\_change 31-Dec-2004  
 C/Accession: A60372; A33086  
 R/Ekramoddoullah, A.K.M.  
 Int. Arch. Allergy Appl. Immunol. 93, 371-377, 1990  
 A/Title: Two-dimensional gel electrophoretic analyses of Kentucky bluegrasses and rye gras  
 A/Reference number: A60372; PMID:91317571; PMID:2101126  
 A/Accession: A60372  
 A/Molecule type: protein  
 A/Residues: 1-20 <EKR>  
 A/Cross-references: UNIPARC:UPI00001794BC  
 C/Superfamily: Major pollen allergen/expansion  
 C/Keywords: hydroxyproline; pollen  
 F/5,8/Modified site: hydroxyproline (Pro) #status experimental

Query Match 19.8%; Score 19; DB 2; Length 20;  
 Best Local Similarity 66.7%; Pred. No. 1.2e+04;  
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 12 AAVSPG 17  
 DB 2 AKVPPG 7

RESULT 93  
 PH1326  
 Ig heavy chain DJ region (clone C515-116) - human (fragment)  
 C/Species: Homo sapiens (man)  
 C/Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999  
 C/Accession: PH1326  
 R/Wasserman, R.; Galili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.  
 J. Exp. Med. 176, 1577-1581, 1992  
 A/Title: Predominance of fetal type DJH joining in young children with B precursor lymph  
 A/Reference number: PH1302; PMID:93094761; PMID:1460419  
 A/Accession: PH1326  
 A/Molecule type: DNA  
 A/Residues: 1-20 <MAS>  
 A/Cross-references: UNIPARC:UPI000017C242  
 C/Keywords: heterotrimer; immunoglobulin

Query Match 19.8%; Score 19; DB 2; Length 20;  
 Best Local Similarity 57.1%; Pred. No. 1.2e+04;  
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DAFEPHG 7  
 DB 11 DAFDIMG 17

RESULT 94  
 S50175  
 kallikrein (PK-120) - human  
 C/Species: Homo sapiens (man)  
 C/Date: 14-Jul-1995 #sequence\_revision 21-Jul-1995 #text\_change 21-Jul-1995  
 C/Accession: S50175  
 R/Pu, X.P.; Iwamoto, A.; Nishimura, H.; Nagasawa, S.  
 Biochim. Biophys. Acta 1208, 338-343, 1994  
 A/Title: Purification and characterization of a novel substrate for plasma kallikrein (F  
 A/Reference number: S50175; PMID:95035036; PMID:7947966  
 A/Accession: S50175  
 A/Status: preliminary  
 A/Molecule type: protein  
 A/Residues: 1-20 <PUX>



A/Cross-references: UNIPARC:UPI000017C287

Query Match 19.8%; Score 19; DB 2; Length 20;

Best Local Similarity 44.4%; Pred. No. 1.2e+04;

Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 8 YLTTAAVSP 16  
| | | | |  
DB 8 YSLDLALLP 16

RESULT 95

S45637

oxidoreductase - Proteus vulgaris (fragment)

C/Species: Proteus vulgaris

C/Date: 10-Dec-1994 #sequence\_revision 13-Mar-1997 #text\_change 09-Jul-2004

C/Accession: S45637

R/Trautwein, T.; Kraus, F.; Lottepeich, F.; Simon, H.

Eur. J. Biochem. 222, 1025-1032, 1994

A/Title: The (2R)-hydroxycarboxylate-viologen-oxidoreductase from Proteus vulgaris is a

A/Reference number: S45637; PMID:94298804; PMID:8026480

A/Accession: S45637

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-20 <TRA>

A/Cross-references: UNIPROT:Q9R4Y1; UNIPARC:UPI00000B9A19

Query Match

Best Local Similarity 19.8%; Score 19; DB 2; Length 20;

Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 LTTAAVS 15  
| | | | |  
DB 14 LTTGALS 20

RESULT 96

S29636

Jacalin beta-1 chain - Artocarpus champedon (fragment)

C/Species: Artocarpus champedon

C/Date: 19-Mar-1997 #sequence\_revision 17-Jul-1998 #text\_change 09-Jul-2004

C/Accession: S29636

R/Ngoc, L.D.; Brillard, M.; Hoebke, J.

Biochim. Biophys. Acta 1156, 219-222, 1993

A/Title: The alpha- and beta-subunits of the jacalins are cleavage products from a 17-kD

A/Reference number: S29635; PMID:93152601; PMID:8427879

A/Accession: S29636

A/Molecule type: protein

A/Residues: 1-20 <NGO>

A/Cross-references: UNIPROT:Q9S8T0; UNIPARC:UPI00000A4123

A/Experimental source: seed

C/Complex: heterotetramer; two alpha and two beta chains

C/Function:

A/Description: seed storage protein

A/Note: Jacalin for D-galactosyl-beta-1-3-N-acetylgalactosamine, a tumor-associated T-cell

A/Keyword: heterotetramer; Jacalin; seed; storage protein

Query Match 19.8%; Score 19; DB 2; Length 20;  
Best Local Similarity 38.5%; Pred. No. 1.2e+04;  
Matches 5; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 4 EPHGYLTTAAVSP 16  
| | | | |  
DB 2 EQSGISQTVIVGP 14

RESULT 97

S71593

Serine proteinase inhibitor, 33K - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 19-Mar-1998 #sequence\_revision 17-Apr-1998 #text\_change 09-Jul-2004

C/Accession: S71593

R/Rao, C.N.; Liu, Y.Y.; Peavey, C.L.; Woodley, D.T.

Arch. Biochem. Biophys. 317, 311-314, 1995

A/Title: Novel extracellular matrix-associated serine proteinase inhibitors from human

A/Reference number: S71592; PMID:95177668; PMID:7872799

A/Accession: S71593

A/Molecule type: protein

A/Residues: 1-20 <RAO>

A/Cross-references: UNIPROT:Q9UC66; UNIPARC:UPI00000727A3

C/Function:

A/Description: involved in turnover of connective tissues

A/Keyword: serine proteinase inhibitor

Query Match 19.8%; Score 19; DB 2; Length 20;  
Best Local Similarity 75.0%; Pred. No. 1.2e+04;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 EPHG 7  
| | | | |  
DB 5 EPHG 8

RESULT 98

A58903

metalloproteinase AP34 (EC 3.4.24.-) - Aeromonas caviae (fragment)

C/Species: Aeromonas caviae

C/Date: 31-Dec-2001 #sequence\_revision 31-Dec-2001 #text\_change 09-Jul-2004

C/Accession: A58903

R/Toma, C.

submitted to the Protein Sequence Database, November 1998

A/Description: Metalloproteinase AP34.

A/Reference number: A58903

A/Accession: A58903

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-20 <TOM>

A/Cross-references: UNIPROT:Q7M027; UNIPARC:UPI000017CB88

C/Keywords: hydrolase; metalloproteinase

Query Match 19.8%; Score 19; DB 2; Length 20;  
Best Local Similarity 45.5%; Pred. No. 1.2e+04;  
Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 DAEPPHGYLTT 11  
| | | | |  
DB 2 DMTGPGNVKT 12

RESULT 99

S38292

30K allergen - rye (fragment)

C/Species: Secale cereale (rye)

C/Date: 19-May-1994 #sequence\_revision 27-Feb-1997 #text\_change 09-Jul-2004

C/Accession: S38292

R/Petersen, A.; Schramm, G.; Becker, W.M.; Schlaak, M.

Biol. Chem. Hoppe-Seyler 374, 855-861, 1993

A/Title: Comparison of four grass pollen species concerning their allergens of grass gr

A/Reference number: S38288; PMID:94092339; PMID:7505588

A/Accession: S38292

A/Molecule type: protein

A/Residues: 1-16 <PET>

A/Cross-references: UNIPROT:Q7M263; UNIPARC:UPI000017B131

Query Match 19.3%; Score 18.5; DB 2; Length 16;  
Best Local Similarity 45.5%; Pred. No. 1.2e+04;  
Matches 5; Conservative 1; Mismatches 2; Indels 3; Gaps 1;

QY 7 GYLTTAAVSPG 17  
| | | | |  
DB 4 GY--APAPG 11

RESULT 100

A33098

244K exoantigen - malaria parasite (Plasmodium falciparum) (fragments)

C:Species: Plasmodium falciparum  
 C:Date: 24-Aug-1990 #sequence\_revision 24-Aug-1990 #text\_change 03-Jun-2000  
 C:Accession: A33098  
 R/Nichols, J.H.; Hager, L.P.  
 submitted to the Protein Sequence Database, May 1990  
 A:Reference number: A33098  
 A:Accession: A33098  
 A>Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-7 <NTC>  
 A/Cross-references: UNIPARC:UPI000017B5E9

Query Match 18.8%; Score 18; DB 2; Length 7;  
 Best Local Similarity 60.0%; Pred. No. 2.8e+05;  
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy	13 AVSPG 17	:
Db	1 ALGPG 5	

Search completed: January 20, 2006, 19:12:13  
 Job time : 11.2115 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 20, 2006, 18:54:54 ; Search time 59.8846 Seconds  
(without alignment)  
212.066 Million cell updates/sec

Title: US-09-662-293-6

Perfect score: 96  
Sequence: 1 DAFEPHGYLLTAASPRK 18

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 14590

Minimum DB seq length: 0  
Maximum DB seq length: 20

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : Uniprot\_05.80:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysts of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30	31.2	20	1	SODF PASPI
2	29	30.2	17	2	Q7T150_CHICK
3	28	29.2	15	2	Q86865_VIRU
4	28	29.2	20	2	Q7M2X3_BOVIN
5	27	28.1	16	2	Q21922_GCAUD
6	27	28.1	19	2	Q9UC80_HUMAN
7	27	28.1	20	2	Q7M4S4_HUMAN
8	26.5	27.6	19	2	Q47554_ECOLI
9	26	27.1	12	2	Q53183_RHOSO
10	26	27.1	15	2	Q86867_VIRU
11	26	27.1	15	2	Q86869_VIRU
12	25	26.0	15	1	UC16_MALIZ
13	25	26.0	15	2	Q71UK9_HAICO
14	25	26.0	16	2	Q9JHM3_RAT
15	25	26.0	17	2	Q9H8Q1_PARK
16	25	26.0	17	2	Q9H8Q2_AJBDS
17	25	26.0	17	2	Q9H8Q3_AJBDS
18	25	26.0	19	2	Q423U7_PLABR
19	25	26.0	20	1	VMO2_CHICK
20	25	26.0	20	2	Q8MWE1_HUMAN
21	25	26.0	20	2	Q9TWM3_BOVMO
22	25	26.0	20	2	Q9SVV2_MOUSE
23	24	25.0	10	2	Q6LCT8_RAT
24	24	25.0	12	2	Q05328_GSPFN
25	24	25.0	14	2	Q47335_ECOLI
26	24	25.0	15	2	Q7M2K5_BABIT
27	24	25.0	16	2	Q77489_TUPGL
28	24	25.0	16	2	Q56385_GCYAN
29	24	25.0	18	2	Q86WJ4_HUMAN
30	24	25.0	19	2	Q8TDB3_HUMAN
31	24	25.0	20	2	Q9PRY1_TORCA

32	23.5	24.5	16	2	Q7M1V9_LYCCE	Q7M1V9_Lycopersico
33	23.5	24.5	19	2	Q9UCG2_HUMAN	Q9UCG2_homo sapien
34	23	24.0	11	1	LSK1_LEOMA	P04428_Leucophaea
35	23	24.0	12	2	Q4YEX5_PLABR	Q4YEX5_plasmodium
36	23	24.0	13	1	ADPA_TENMO	P83109_tenebrio mo
37	23	24.0	13	2	Q9UDC6_HUMAN	Q9UDC6_homo sapien
38	23	24.0	16	2	Q4YXZ7_PLABR	Q4YXZ7_plasmodium
39	23	24.0	17	2	Q6R9U8_HUMAN	Q6R9U8_homo sapien
40	23	24.0	17	2	Q29395_CANPA	Q29395_canis famli
41	23	24.0	18	2	Q424N4_PLABR	Q424N4_plasmodium
42	23	24.0	18	2	Q6LD80_PMTRI	Q6LD80_mus sp. chr
43	23	24.0	18	2	Q7ZW73_9H1Y1	Q7ZW73_human immun
44	23	24.0	19	2	Q9SGI3_ABTAL	Q9SGI3_abies alba
45	23	24.0	20	1	PL1_LUFLU	P83363_lupinus lut
46	23	24.0	20	1	PL6_LUFLU	P83368_lupinus lut
47	23	24.0	20	2	Q9BRP3_HUMAN	Q9BRP3_homo sapien
48	23	24.0	20	2	Q9RAU5_STRSL	Q9RAU5_streptococ
49	22	22.9	9	2	Q81IS2_MOUSE	Q81IS2_mus musculu
50	22	22.9	10	2	Q9MJ05_PODCU	Q9MJ05_podospora c
51	22	22.9	10	2	Q9QY21_PMTRI	Q9QY21_rattus sp.
52	22	22.9	11	2	Q86D31_TRYCR	Q86D31_trypanosoma
53	22	22.9	14	2	Q9M0Q3_PODCU	Q9M0Q3_podospora c
54	22	22.9	14	2	Q5Q817_TRIMA	Q5Q817_trichechus
55	22	22.9	14	2	Q5Q8J5_TCYDI	Q5Q8J5_cyclopes d4
56	22	22.9	14	2	Q5Q8J7_SPAEH	Q5Q8J7_spalax leuc
57	22	22.9	15	1	GSTR1_ESERO	P82399_pseudomonas
58	22	22.9	15	2	Q05694_MOUSE	Q05694_mus musculu
59	22	22.9	15	2	Q69353_HNV2	Q69353_human herpe
60	22	22.9	16	2	Q9TRR1_RABIT	Q9TRR1_mus musculu
61	22	22.9	16	2	Q9QZY3_MOUSE	Q9QZY3_mus musculu
62	22	22.9	17	2	Q6ICD1_HUMAN	Q6ICD1_homo sapien
63	22	22.9	17	2	Q7MD8_MOUSE	Q7MD8_mus musculu
64	22	22.9	18	2	Q7SMF5_HUMAN	Q7SMF5_homo sapien
65	22	22.9	19	2	Q5C123_SCHJA	Q5C123_schistosoma
66	22	22.9	19	2	Q4YGN5_PLABR	Q4YGN5_plasmodium
67	22	22.9	19	2	Q4WZ87_9EUTR	Q4WZ87_mantis termi
68	22	22.9	19	2	Q7TBG5_ADE08	Q7TBG5_human adeno
69	22	22.9	20	1	PL3_LUFLU	P83365_lupinus lut
70	22	22.9	20	2	Q8NFW3_HUMAN	Q8NFW3_homo sapien
71	22	22.9	20	2	Q6ICN3_ECOLI	Q6ICN3_escherichia
72	21.5	22.4	16	2	Q9PRR9_GAVES	Q9PRR9_aanas (ducks
73	21.5	22.4	18	2	Q5GKS4_COXBL	Q5GKS4_coxella bu
74	21.5	22.4	20	2	Q84U84_SORBN	Q84U84_brahydanio
75	21	21.9	10	2	Q7M4X1_9ZYGO	Q7M4X1_glycine max
76	21	21.9	10	2	Q7KZ15_HELPY	Q7KZ15_homo sapien
77	21	21.9	10	2	Q9R7J8_HELPY	Q9R7J8_helicobacte
78	21	21.9	11	2	Q86D32_TRYCR	Q86D32_trypanosoma
79	21	21.9	11	2	Q9TRW5_BOVIN	Q9TRW5_bos taurus
80	21	21.9	11	2	Q9K670_BACHD	Q9K670_bacillus ha
81	21	21.9	12	2	Q88575_9PICO	Q88575_thellex's e
82	21	21.9	12	2	Q88576_9PICO	Q88576_thellex's e
83	21	21.9	12	2	Q88577_9PICO	Q88577_thellex's e
84	21	21.9	12	2	Q88578_9PICO	Q88578_thellex's e
85	21	21.9	12	2	Q88579_9PICO	Q88579_thellex's e
86	21	21.9	12	2	Q88580_9PICO	Q88580_thellex's e
87	21	21.9	12	2	Q88581_9PICO	Q88581_thellex's e
88	21	21.9	12	2	Q88582_9PICO	Q88582_thellex's e
89	21	21.9	13	2	Q18890_ATBBR	Q18890_ateles belz
90	21	21.9	13	2	Q18890_ATBBR	Q18890_ateles belz
91	21	21.9	13	2	Q6ZYT7_9CARY	Q6ZYT7_baceteroides
92	21	21.9	14	2	Q7L622_ANNBL	Q7L622_aanes platyr
93	21	21.9	14	2	Q6ZYT6_9CARY	Q6ZYT6_silene ural
94	21	21.9	15	2	Q9SGI6_ORZSA	Q9SGI6_oryza sativ
95	21	21.9	15	2	Q9QV62_9MTRI	Q9QV62_mus sp. dif
96	21	21.9	16	1	KTRC_AREMA	P11917_arenicola m
97	21	21.9	16	2	Q44543_ANAVA	Q44543_anabaena va
98	21	21.9	17	2	Q14316_HUMAN	Q14316_homo sapien
99	21	21.9	17	2	Q7RQV2_PLAYO	Q7RQV2_plasmodium
100	21	21.9	17	2		

## ALIGNMENTS

```

RESULT 1
SODF_PASPI
ID SODF_PASPI STANDARD; PRT; 20 AA.
AC P81527;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Superoxide dismutase [Fe] (BC 1.15.1.1) (Fragment).
GN NamesoB;
OS Pasteurella piscicida (Photobacterium damsela subsp. piscicida).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Photobacterium.
OX NCBI_TaxID=38294;
RN [1]
RP PROTEIN SEQUENCE.
RC STRAIN=MT1415;
RC MEDLINE=99173752; PubMed=10075430;
RA Barnes A.C., Balebona M.C., Horne M.T., Ellis A.E.;
RT "Superoxide dismutase and catalase in Photobacterium damsela subsp.
RT piscicida and their roles in resistance to reactive oxygen species.";
RT Microbiology 145:483-494(1999).
CC -1- FUNCTION: Destroys radicals which are normally produced within the
CC cells and which are toxic to biological systems.
CC -1- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
CC -1- COFACTOR: Binds 1 iron ion per subunit (By similarity).
CC -1- SUBUNIT: Homodimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Periplasmic.
CC -1- SIMILARITY: Belongs to the iron/manganese superoxide dismutase
CC family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC HSP: P09157; IISC.
CC InterPro: IPR001189; SODismutase.
CC DR PANTHER: PTHR11404; SODismutase; 1.
CC Pfam: PF00081; Sod_Fe_N; 1.
CC Direct protein sequencing; Iron; Metal-binding; Oxidoreductase;
CC Periplasmic.
CC KW NON_TER
CC FT SEQUENCE 20 AA; 2153 MW; AAD31FDA8553B6D CRC64;
SQ
Query Match 31.2%; Score 30; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.5e+03;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 DAFEPH 6
DB 12 DALEPH 17

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RA Paton I.R., Smith J., Burt D.W.;
RT "Mapping the ABCA4, IMPDH2 and TIMP3 genes in chicken.";
RL Anim. Genet. 34:395-396(2003).
DR EMBL; AY326267; AAF94880.1; -; Genomic_DNA.
DR GO; GO:0005578; C:extracellular matrix (sensu Metazoa); IEA.
DR GO; GO:0008191; F:metalloendopeptidase inhibitor activity; IEA.
DR InterPro; IPR001820; Prot_inh_TIMP.
DR PANTHER; PTHR1844; Prot_inh_TIMP; 1.
DR Pfam; PF00965; TIMP; 1.
FT NON_TER
FT NON_TER
SQ SEQUENCE 17 AA; 2030 MW; DABD6B493259F1F3 CRC64;
Query Match 30.2%; Score 29; DB 2; Length 17;
Best Local Similarity 54.5%; Pred. No. 1.9e+03;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 8 YLITPAVSPGK 18
DB 6 YLITGRVVEGK 16

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RESULT 3
Q86865_YVIRU
ID Q86865_YVIRU PRELIMINARY; PRT; 15 AA.
AC Q86865;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE LCMV viral protein protein (Fragment).
GN Name=LCMV viral protein;
OS Lymphocytic choriomeningitis virus.
OC Viruses; ssRNA negative-strand viruses; Arenaviridae; Arenaviruses;
OC Old world arenaviruses.
OX NCBI_TaxID=11623;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=95190990; PubMed=7533851;
RT Moskopidie D., Zinkernagel R.M.;
RT "Immunobiology of cytotoxic T-cell escape mutants of lymphocytic
RT choriomeningitis virus.";
RT J. Virol. 69:2187-2193(1995).
DR EMBL; S75741; AAB33667.1; -; mRNA.
FT NON_TER
FT SEQUENCE 15 AA; 1599 MW; 2D3720FAF776C1A7 CRC64;
SQ
Query Match 29.2%; Score 28; DB 2; Length 15;
Best Local Similarity 62.5%; Pred. No. 2.4e+03;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 4 EPHGYLIT 11
DB 6 DPGGYCLT 13

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RESULT 4
Q7M2X3_BOVIN
ID Q7M2X3_BOVIN PRELIMINARY; PRT; 20 AA.
AC Q7M2X3;
DT 01-MAR-2004 (TREMBLrel. 26, Created)
DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Collagen alpha 5(IV) chain (Fragment).
OS Bos taurus (Bovine).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP PROTEIN SEQUENCE.
RX PubMed=1869555;
RA Gunwar S., Ballesster F., Kalluri R., Timoneda J., Chonko A.M.,
RA Edwards S.J., Noelken M.E., Hudson B.G.;

```

RT "Glomerular basement membrane. Identification of dimeric subunits of  
RT the noncollagenous domain (hexamer) of collagen IV and the Goodpasture  
RT antigen."  
RL J Biol. Chem. 266:15318-15324 (1991).

DR PIR, E39419; E39419.  
FT NON\_TER 1  
FT NON\_TER 20  
SQ SEQUENCE 20 AA; 2050 MW; 3B4855916F8939C8 CRC64;

Query Match 29.2%; Score 28; DB 2; Length 20;  
Best Local Similarity 66.7%; Pred. No. 3.3e+03;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 6 HGVLIT 11  
DB 10 HGPLIT 15

RESULT 5  
021922\_9CAUD PRELIMINARY; PRT; 16 AA.

ID 021922\_021923;  
AC 021922; 021923;  
DT 01-JAN-1998 (TrEMBLrel. 05, Created)  
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)  
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)  
DE Integrase (Fragment).

GN NameInt;  
OS Streptococcus thermophilus bacteriophage Sf121.  
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.  
NCBI\_TaxID=64186;

RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=98008989; PubMed=9344917; DOI=10.1006/viro.1997.8769;  
RA Brutin A., Foley S., Brusow H.;  
RT "The site-specific integration system of the temperate Streptococcus  
RT thermophilus bacteriophage phfSf121.";  
RL Virology 237:148-158 (1997).

DR EMBL, AF013584; AAC48809.1; -; Genomic DNA.  
EMBL, AF013587; AAC48910.1; -; Genomic DNA.  
FT NON\_TER 1  
SQ SEQUENCE 16 AA; 1856 MW; 8FA82D3270B9A959 CRC64;

Query Match 28.1%; Score 27; DB 2; Length 16;  
Best Local Similarity 57.1%; Pred. No. 3.8e+03;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 DAFEPHG 7  
DB 10 NALKPHG 16

RESULT 6  
09UC80\_HUMAN PRELIMINARY; PRT; 19 AA.

ID 09UC80\_HUMAN PRELIMINARY;  
AC 09UC80;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
DE 21.5 kDa stone matrix protein (SC 1.15.1.1) (Superoxide dismutase  
DE [Mn/Fe]) (Fragment).  
OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;  
OC Homo.  
NCBI\_TaxID=9606;

RP PROTEIN SEQUENCE.  
RA Binette J.P., Binette M.B.;  
RT "Sequencing of proteins extracted from stones."  
RL Submitted (JUL-1995) to the EMBL/GenBank/DBD databases.

CC -1- FUNCTION: Destructs radicals which are normally produced within the  
CC cells and which are toxic to biological systems (By similarity).  
CC -1- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2O(2)).

CC -1- SIMILARITY: Belongs to the iron/manganese superoxide dismutase  
CC family.

DR HSP; P09223; 1D70.  
DR GO; GO:0046872; F:metal ion binding; IEA.  
DR GO; GO:0016491; F:oxidoreductase activity; IEA.  
DR GO; GO:0004784; F:superoxide dismutase activity; IEA.  
DR GO; GO:0006801; P:superoxide metabolism; IEA.  
DR InterPro: IPR001189; SODismutase.  
DR Pfam: PF00081; Sod\_Fe\_N; 1.  
KW Oxidoreductase.

SQ SEQUENCE 19 AA; 2116 MW; ADD0DAB848E87894 CRC64;

Query Match 28.1%; Score 27; DB 2; Length 19;  
Best Local Similarity 66.7%; Pred. No. 4.5e+03;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DAFEPH 6  
DB 12 DALQPH 17

RESULT 7  
07M4S4\_HUMAN PRELIMINARY; PRT; 20 AA.

ID 07M4S4\_HUMAN PRELIMINARY;  
AC 07M4S4;  
DT 01-MAR-2004 (TrEMBLrel. 26, Created)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Granulocyte inhibitory protein.

OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;  
OC Homo.  
NCBI\_TaxID=9606;

RP PROTEIN SEQUENCE.  
RX PubMed=2385596;  
RA Hoelzl W.H., Haeg-Weber M., Georgopoulos A., Block L.H.;  
RT "Physicochemical characterization of a polypeptide present in uremic  
RT serum that inhibits the biological activity of polymorphonuclear  
RT cells."

RL Proc. Natl. Acad. Sci. U.S.A. 87:6353-6357 (1990).  
RN [2]  
RP PROTEIN SEQUENCE.

RX PubMed=2385596;  
RA Hoelzl W.H., Haeg-Weber M., Georgopoulos A., Block L.H.;  
RT "Physicochemical characterization of a polypeptide present in uremic  
RT serum that inhibits the biological activity of polymorphonuclear  
RT cells."

RL Proc. Natl. Acad. Sci. U.S.A. 87:6353-6357 (1990).  
DR PIR, A36016; A36016.  
DR HSP; P01625; IEK3.  
SQ SEQUENCE 20 AA; 2046 MW; A13201D587F1EBE7 CRC64;

Query Match 28.1%; Score 27; DB 2; Length 20;  
Best Local Similarity 62.5%; Pred. No. 4.8e+03;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 11 TAVSPKG 18  
DB 10 TSVSPRG 17

RESULT 8  
047554\_ECOLI PRELIMINARY; PRT; 19 AA.

ID 047554\_ECOLI PRELIMINARY;  
AC 047554;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Colicin A (Fragment).

OS Escherichia coli.  
OG plasmid pVbP.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

```

OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=93339568; PubMed=7687969; DOI=10.1016/0378-1097(93)90042-Z;
RA Gell V., Lloubes R., Zaai S.A.U., Van Spendonk R.M.L., Rollin C.,
  Benedetti H., Lazdunski C.;
RT "Recognition of the colicin A N-terminal epitope ICI1 in vitro and in
  vivo in Escherichia coli by its cognate monoclonal antibody.";
RL FEMS Microbiol. Lett. 109:335-342(1993).
DR EMBL, X73248; CAA51711.1; -; Genomic_DNA.
KW plasmid.
FT NON TER
SQ SEQUENCE 19 AA; 2082 MW; B1D35A74B858881A CRC64;

Query Match 27.6%; Score 26.5; DB 2; Length 19;
Best Local Similarity 46.7%; Pred. No. 5.5e+03;
Matches 7; Conservative 0; Mismatches 5; Indels 3; Gaps 1;

QY 6 HGVL--TAVSPG 17
DB 2 HGRYLRACVDPG 16

RESULT 9
O53183 RHOSO PRELIMINARY; PRT; 12 AA.
ID O53183;
AC O53183;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Beta-subunit of nitrite hydratase (Fragment).
OS Rhodococcus sp.
OC Bacteria; Actinobacteria; Actinomycetales;
OC Corynebacteriaceae; Rhodococcus.
OX NCBI_TaxID=1831;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=N-774;
RX MEDLINE=95072315; PubMed=7765511;
RA Hashimoto Y., Nishiyama M., Horiuchi S., Beppu T.;
RT "The nitrite hydratase gene from Rhodococcus sp. N-774 requires its
  downstream region for efficient expression.";
RL Biotech. Biochem. 58:1859-1865(1994).
DR EMBL, D30033; BAA06273.1; -; Genomic_DNA.
DR GO; GO:0018822; F:nicotinic hydratase activity; IEA.
DR GO; GO:0006807; P:nitrogen compound metabolism; IEA.
DR InterPro; IPR003168; NHase_beta.
DR Pfam; PF02211; NHase_beta; 1.
FT NON TER
SQ SEQUENCE 12 AA; 1323 MW; 7A5DEF7D993B587B CRC64;

Query Match 27.1%; Score 26; DB 2; Length 12;
Best Local Similarity 61.5%; Pred. No. 4.1e+03;
Matches 8; Conservative 0; Mismatches 3; Indels 2; Gaps 1;

QY 1 DAFPHGYLTAA 13
DB 2 DLFE--GYLEPAA 12

RESULT 10
Q86867 VIRU PRELIMINARY; PRT; 15 AA.
ID Q86867;
AC Q86867;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE S-RNA product protein (Fragment).
GN Name=S-RNA product;
OS Lymphocytic choriomeningitis virus.
OC Viruses; ssRNA negative-strand viruses; Arenaviridae; Arenavirus;
OC Old world arenaviruses.

```

```

OX NCBI_TaxID=11623;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=95190990; PubMed=7533851;
RA Moskopidls D., Zinkernagel R.M.;
RT "Immunobiology of cytotoxic T-cell escape mutants of lymphocytic
  choriomeningitis virus.";
RL J. Virol. 69:2187-2193(1995).
DR EMBL, S75749; AAB33670.1; -; mRNA.
FT NON TER
SQ SEQUENCE 15 AA; 1598 MW; 2D3F82F4F776C1A7 CRC64;

Query Match 27.1%; Score 26; DB 2; Length 15;
Best Local Similarity 71.4%; Pred. No. 5.2e+03;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 PHGYLT 11
DB 7 PGYCLT 13

RESULT 11
Q86869 VIRU PRELIMINARY; PRT; 15 AA.
ID Q86869;
AC Q86869;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE S-RNA product protein (Fragment).
GN Name=S-RNA product;
OS Lymphocytic choriomeningitis virus.
OC Viruses; ssRNA negative-strand viruses; Arenaviridae; Arenavirus;
OC Old world arenaviruses.
OX NCBI_TaxID=11623;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=95190990; PubMed=7533851;
RA Moskopidls D., Zinkernagel R.M.;
RT "Immunobiology of cytotoxic T-cell escape mutants of lymphocytic
  choriomeningitis virus.";
RL J. Virol. 69:2187-2193(1995).
DR EMBL, S75753; AAB33673.1; -; mRNA.
DR InterPro; IPR001535; Arena_glycoprot.
DR Pfam; PF00798; Arena_glycoprot; 1.
FT NON TER
SQ SEQUENCE 15 AA; 1571 MW; 2D25ABF4F776C1A7 CRC64;

Query Match 27.1%; Score 26; DB 2; Length 15;
Best Local Similarity 71.4%; Pred. No. 5.2e+03;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 PHGYLT 11
DB 7 PGYCLT 13

RESULT 12
UC16 MAIZE STANDARD; PRT; 15 AA.
ID UC16 MAIZE;
AC P80622;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Unknown protein from 2D-PAGE of etiolated coleoptile (Spot 308)
  (Fragment).
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP PROTEIN SEQUENCE.
RC TISSUE=Coleoptile;

```

RA Touzet P., Riccardi F., Morin C., Dameraval C., Huet J.-C.,  
 RA Pernotier J.-C., Zivy M., de Vienne D.,  
 RT "The maize two dimensional gel protein database: towards an integrated  
 RT genome analysis program."  
 RU Theor. Appl. Genet. 93:997-1005(1996).  
 CC -1- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown  
 CC protein is: 5.9, its MW is: 18.6 kDa.  
 -----  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 -----  
 CC Malze-2DPRG; P80622; COLEOPTILE.  
 DR Gramene; P80622; -.  
 DR MalzeDB; 123948; -.  
 KW Direct protein sequencing.  
 FT NON TER 1 1  
 FT NON TER 15 15  
 SQ SEQUENCE 15 AA; 1796 MW; D3JA518F7440BE7 CRC64;  
 -----  
 QY Query Match 26.0%; Score 25; DB 1; Length 15;  
 Db Best Local Similarity 62.5%; Pred. No. 7.5e+03;  
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 -----  
 QY 10 LTRAVSPG 17  
 Db 8 VTAFAVEPG 15  
 -----  
 RESULT 13  
 Q71UK9 HALCO  
 ID Q71UK9 HALCO PRELIMINARY; PRT; 15 AA.  
 AC Q71UK9;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Lyalin (Fragment).  
 OS Halictis corrugata (Pink abalone).  
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;  
 OC Vetigastropoda; Halictoidae; Halictidae; Halicti.  
 OX NCBI\_TaxId=6453;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA MEDLINE:98333704; PubMed:9724763; DOI=10.1073/pnas.95.18.10676;  
 RX Metz B.C., Robles-Sikisaka R., Vacquier V.D.;  
 RT "Nonrandom substitution in introns and mitochondrial DNA."  
 RT exceeds substitution in introns and mitochondrial DNA."  
 RL Proc. Natl. Acad. Sci. U.S.A. 95:10676-10681(1998).  
 DR EMBL; AF076830; AAC33932.1; -; Genomic\_DNA.  
 FT NON TER 1 1  
 FT NON TER 15 15  
 SQ SEQUENCE 15 AA; 2083 MW; 3168BDCD2921B6D CRC64;  
 -----  
 QY Query Match 26.0%; Score 25; DB 2; Length 15;  
 Db Best Local Similarity 57.1%; Pred. No. 7.5e+03;  
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 -----  
 QY 3 FBPHGYL 9  
 Db 6 FIPHKYI 12  
 -----  
 RESULT 14  
 Q9JHM3 RAT  
 ID Q9JHM3 RAT PRELIMINARY; PRT; 16 AA.  
 AC Q9JHM3;  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 15, Last annotation update)  
 DE MHC class I antigen (Fragment).  
 GN Name=Rtl;

OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Murinae; Rattus.  
 OX NCBI\_TaxId=10116;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=LEW;  
 RX MEDLINE:20424521; PubMed:10970104; DOI=10.1007/s002510000201;  
 RA Lambrecht-Washington D., Fischer Lindahl K., Womigelt K.;  
 RT "Promoter structures suggest independent translocations of ancestral  
 RT rat Rtl A and mouse H2-K class I genes."  
 RL Immunogenetics 51:873-877(2000).  
 DR EMBL; AF210330; AAF74411.1; -; Genomic\_DNA.  
 FT NON TER 16 16  
 FT NON TER 16 16  
 SQ SEQUENCE 16 AA; 1635 MW; 647FF519E02977D CRC64;  
 -----  
 QY Query Match 26.0%; Score 25; DB 2; Length 16;  
 Db Best Local Similarity 62.5%; Pred. No. 8.1e+03;  
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 -----  
 QY 9 LTRAVSP 16  
 Db 9 LTRAVLAP 16  
 -----  
 RESULT 15  
 Q9HEQ1 PARBR  
 ID Q9HEQ1 PARBR PRELIMINARY; PRT; 17 AA.  
 AC Q9HEQ1;  
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE Alpha-tubulin (Fragment).  
 GN Name=TUB1;  
 OS Paracoccidioides brasiliensis.  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
 OC Oryziales; Microsporid Omygenales; Paracoccidioides.  
 OX NCBI\_TaxId=121759;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=PB18;  
 RA Kasuga T., White T.J., Taylor J.W.;  
 RT "The molecular clock in fungi in the class Plecomycetes."  
 RT Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.  
 RL EMBL; AY013314; AAG40955.1; -; Genomic\_DNA.  
 DR GO: GO:0005874; C:microtubule; IEA.  
 DR GO: GO:0005198; F:structural molecule activity; IEA.  
 DR GO: GO:0007018; F:microtubule-based movement; IEA.  
 DR Interpro; IPR002452; Alpha\_tubulin.  
 DR PANTHER; PTHR11588:SP1; Alpha\_tubulin; 1.  
 FT NON TER 1 1  
 FT NON TER 17 17  
 SQ SEQUENCE 17 AA; 2039 MW; B8E787547655F90A CRC64;  
 -----  
 QY Query Match 26.0%; Score 25; DB 2; Length 17;  
 Db Best Local Similarity 66.7%; Pred. No. 8.6e+03;  
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 -----  
 QY 4 EPHGYL 9  
 Db 12 QPDGYL 17  
 -----  
 RESULT 16  
 Q9HEQ2 AJRDR  
 ID Q9HEQ2 AJRDR PRELIMINARY; PRT; 17 AA.  
 AC Q9HEQ2;  
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE Alpha-tubulin (Fragment).  
 GN Name=TUB1;

```

OS Ajellomyces dermatitidis (Blastomyces dermatitidis).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Ajellomyces; Ajellomyces.
OK NCBT_TaxID=5039;
RN (1)
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC60915;
RA Kaesga T., White T.J., Taylor J.W.;
RT "The molecular clock in fungi in the class Plecomycetes.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY013313; AAG40954.1; -; Genomic_DNA.
DR GO; GO:0005874; C:microtubule; IEA.
DR GO; GO:0005198; P:structural molecule activity; IEA.
DR GO; GO:0007018; P:microtubule-based movement; IEA.
DR InterPro; IPR002452; Alpha_tubulin.
DR PANTHER; PTHR11588:SF1; Alpha_tubulin; 1.
FT NON_TER 1
FT NON_TER 17
SQ SEQUENCE 17 AA; 2039 MW; E8E787547655F90A CRC64;

Query Match
Best Local Similarity 26.0%; Score 25; DB 2; Length 17;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 EPHGYL 9
Db 12 QPDGYL 17

RESULT 17
ID 09HEQ3 AJECA PRELIMINARY; PRT; 17 AA.
AC 09HEQ3;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE Alpha-tubulin (Fragment).
OS Name=TUB1;
OS Ajellomyces capsulata (Histoplasma capsulatum).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Onygenales; Ajellomycetaceae; Ajellomyces.
OX NCBT_TaxID=5037;
RN (1)
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC26032;
RA Kaesga T., White T.J., Taylor J.W.;
RT "The molecular clock in fungi in the class Plecomycetes.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY013312; AAG40953.1; -; Genomic_DNA.
DR GO; GO:0005874; C:microtubule; IEA.
DR GO; GO:0005198; P:structural molecule activity; IEA.
DR GO; GO:0007018; P:microtubule-based movement; IEA.
DR InterPro; IPR002452; Alpha_tubulin.
DR PANTHER; PTHR11588:SF1; Alpha_tubulin; 1.
FT NON_TER 1
FT NON_TER 17
SQ SEQUENCE 17 AA; 2039 MW; E8E787547655F90A CRC64;

Query Match
Best Local Similarity 26.0%; Score 25; DB 2; Length 17;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 EPHGYL 9
Db 12 QPDGYL 17

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DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)
DE Hypothetical protein (Fragment).
GN ORFNames=PB101818.00.0;
OS Plasmodium berghei.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OK NCBT_TaxID=5821;
RN (1)
RP NUCLEOTIDE SEQUENCE.
RA Hall N., Karras M., Raine J.D., Carlson J.M., Kooij T.W.A.,
RA Bertman M., Florens L., Jansen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churche C.,
RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
RA Jance C.J., Barrett B., Turner C.M.R., Waters A.P., Sindén R.S.;
RT "A comprehensive survey of the Plasmodium life cycle by genomic,
transcriptomic, and proteomic analyses."
RL Science 307:82-86(2005).
RC -! CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CA101000743; CAH95036.1; -; Genomic_DNA.
KW Hypothetical protein.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 19 AA; 2375 MW; C416C96CE878PAD3 CRC64;

Query Match
Best Local Similarity 26.0%; Score 25; DB 2; Length 19;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 HGYL 9
Db 2 HGYL 5

RESULT 19
ID WMO2 CHICK STANDARD; PRT; 20 AA.
AC 09P649;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Vitelline membrane outer layer protein II (WMO-II) (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBT_TaxID=9031;
RN (1)
RP PROTEIN SEQUENCE.
RC TISSUE=Egg yolk;
RX MEDLINE=92392273; PubMed=1520265;
RA Kido S., Morimoto A., Kim F., Doi Y.;
RT "Isolation of a novel protein from the outer layer of the vitelline
membrane."
RL Biochem. J. 286:17-22(1992).
CC -! FUNCTION: Exact function not known, component of the outer
CC membrane of the vitelline layer of the egg.
CC -! PTM: All cysteine residues of the mature protein are involved in
CC disulfide bonds.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC PIR; S23981; S23981.
CC Direct protein sequencing.
FT NON_TER 20
FT NON_TER 20
SQ SEQUENCE 20 AA; 2327 MW; 45FC7989AB7527C7 CRC64;

Query Match
Best Local Similarity 26.0%; Score 25; DB 1; Length 20;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```





OY 9 LTTAAVSPGK 18  
: ||| |||  
DB 1 VPSAAKRPCK 10

RESULT 23

O6LC78 RAT PRELIMINARY; PRT; 10 AA.  
AC O6LC78; 05-JUL-2004 (TRENBLREL. 27, Created)  
DT 05-JUL-2004 (TRENBLREL. 27, Last sequence update)  
DE P120/ecto-ATPase (Fragment).  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Murinae; Rattus.  
OX NCBI\_TaxId=10116;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=Sprague-Dawley; TISSUE=Liver;  
RX MEDLINE=96224094; PubMed=8621519; DOI=10.1074/jbc.271.15.8809;  
RA Najjar S.M., Bojicic Y.R., Nabih Z.T., Philippe N., Imai Y.,  
RA Suzuki Y., Suh D.S., Ooi G.T.;  
RT "Cloning and characterization of a functional promoter of the rat  
RT p120 gene, encoding a subunit of the insulin receptor tyrosine  
RT kinase.";  
RL J. Biol. Chem. 271:8809-8817(1996).  
DR EMBL; U27208; AAB05593.1; -; Genomic\_DNA.  
FT NON\_TER 1  
SQ SEQUENCE 10 AA; 1001 MW; 438CBG3BDC1A727 CRC64;

Query Match 25.0%; Score 24; DB 2; Length 10;  
Best Local Similarity 62.5%; Pred. No. 7.2e+03;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 7 GYLTTAAV 14  
: ||| |||  
DB 1 GLLLTAAV 8

RESULT 24  
O05328 9SPHN PRELIMINARY; PRT; 12 AA.  
AC O05328;  
DT 01-JUL-1997 (TRENBLREL. 04, Created)  
DT 01-JUL-1997 (TRENBLREL. 04, Last sequence update)  
DE 01-JUN-2003 (TRENBLREL. 24, Last annotation update)  
DE Catechol 2,3-dioxygenase (Fragment).  
GN Namephne;  
OS Sphingomonas chungbukensis.  
OC Bacteria; Proteobacteria; Alphaproteobacteria; Sphingomonadales;  
OC Sphingomonadaceae; Sphingomonas.  
OX NCBI\_TaxId=56193;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=DJ77;  
RX MEDLINE=97242176; PubMed=9125165; DOI=10.1006/bbrc.1997.6279;  
RA Shin H.J., Kim S.J., Kim Y.C.;  
RT "Sequence analysis of the pnd gene encoding 2-hydroxymuconic  
RT semialdehyde hydrolase in Pseudomonas sp. strain DJ77.";  
RL Biochem. Biophys. Res. Commun. 232:288-291(1997).  
DR EMBL; U83881; AAC45092.1; -; Genomic\_DNA.  
DR GO; GO:0016702; P:oxidoreductase activity, acting on single d. .; IEA.  
FT NON\_TER 12  
SQ SEQUENCE 12 AA; 1277 MW; 2981743DAD0042C8 CRC64;

Query Match 25.0%; Score 24; DB 2; Length 12;  
Best Local Similarity 50.0%; Pred. No. 8.7e+03;  
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 10 LTTAAVSPG 17  
: ||| |||  
DB 3 LTGVIRPG 10

RESULT 25

O47335 ECOLI PRELIMINARY; PRT; 14 AA.  
AC O47335; 01-NOV-1996 (TRENBLREL. 01, Created)  
DT 01-NOV-1996 (TRENBLREL. 01, Last sequence update)  
DE K6ga methyltransferase (kasugamycin sensitivity).  
OS Escherichia coli.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Escherichia.  
OX NCBI\_TaxId=562;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC MEDLINE=88107880; PubMed=3122846; DOI=10.1016/0300-9084(87)90210-0;  
RX van Gemen B., Koels H.J., Plooy C.A.M., Bodlaender J.,  
RA van Knippenberg P.H.;  
RT "Characterization of the k6ga gene of Escherichia coli determining  
RT kasugamycin sensitivity.";  
RL Biochimie 69:841-848(1987).  
DR EMBL; X06536; CAA29785.1; -; Genomic\_DNA.  
DR PIR; S00843; S00843.  
DR GO; GO:0008168; P:methyltransferase activity; IEA.  
DR GO; GO:0016740; P:transferase activity; IEA.  
KW Methyltransferase; Transferase.  
SQ SEQUENCE 14 AA; 1571 MW; 670799ABR3D70D14 CRC64;

Query Match 25.0%; Score 24; DB 2; Length 14;  
Best Local Similarity 50.0%; Pred. No. 1e+04;  
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 9 LTTAAVSPG 18  
: ||| |||  
DB 5 LTRRLSPCK 14

RESULT 26  
O7M2K5 RABIT PRELIMINARY; PRT; 15 AA.  
AC O7M2K5;  
DT 01-MAR-2004 (TRENBLREL. 26, Created)  
DT 01-MAR-2004 (TRENBLREL. 26, Last sequence update)  
DE 01-MAR-2004 (TRENBLREL. 26, Last annotation update)  
DE Phosphoglucosylase (BC 5.4.2.2) (Fragment).  
GN Oryctolagus cuniculus (Rabbit).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae;  
OC Oryctolagus.  
OX NCBI\_TaxId=9986;  
RN [1]  
RP PROTEIN SEQUENCE.  
RX MEDLINE=90282481; PubMed=2162150;  
RA Marchase R.B., Richardson K.L., Strisomasp C., Drake R.R., Haley B.E.;  
RT "Resolution of phosphoglucosylase and the 62-kDa acceptor for the  
RT glucosylphosphotransferase.";  
RL Arch. Biochem. Biophys. 280:122-129(1990).  
DR PIR; S10741; S10741.  
DR GO; GO:0004614; P:phosphoglucosylase activity; IEA.  
FT NON\_TER 15  
SQ SEQUENCE 15 AA; 1452 MW; 8252201C5D34C0C4 CRC64;

Query Match 25.0%; Score 24; DB 2; Length 15;  
Best Local Similarity 50.0%; Pred. No. 1.1e+04;  
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Db 4 GILLTASHMP 13

## RESULT 27

077489\_TUPGL PRELIMINARY; PRT; 16 AA.  
 AC 077489;  
 DT 01-NOV-1998 (TReMBLrel. 08, Created)  
 DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)  
 DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)  
 DE D4 dopamine receptor (D4DR) (Fragment).  
 OS Tupia glis (Tree shrew).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Scandentia; Tupaiidae; Tupia.  
 NCBI\_TaxID=9395;  
 RX NCBI\_TaxID=9395;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Inoue-Murayama M., Takenaka O., Murayama Y.;  
 RT "origin and divergence of tandem repeats of primate D4 dopamine  
 RT receptor genes";  
 RL P-riates 39:217-224 (1998).  
 DR EMBL; AB016198; BAA32036.1; -; Genomic\_DNA.  
 DR GO; GO:0004872; F:receptor activity; IEA.  
 KW Receptor.  
 FT NON\_TER 1 1  
 FT NON\_TER 16 16  
 SQ SEQUENCE 16 AA; 1577 MW; 3865ABE77FB63E09 CRC64;

Query Match 25.0%; Score 24; DB 2; Length 16;  
 Best Local Similarity 66.7%; Pred. No. 1.2e+04;  
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 DAFEPH 6  
 DB 8 DPFGPH 13

## RESULT 28

056385\_9CYAN PRELIMINARY; PRT; 16 AA.  
 AC 056385;  
 DT 10-MAY-2005 (TReMBLrel. 30, Created)  
 DT 10-MAY-2005 (TReMBLrel. 30, Last sequence update)  
 DT 10-MAY-2005 (TReMBLrel. 30, Last annotation update)  
 DE Cpca (Fragment).  
 OS uncultured Cyanobacterium.  
 OC Bacteria; Cyanobacteria; environmental samples.  
 NCBI\_TaxID=1211;  
 RX NCBI\_TaxID=1211;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Kim S.-G., Rhee S.-K., Ahn C.-Y., Bae J.-W., Park Y.-H., Oh H.-M.;  
 RT "Profiling cyanobacterial abundance and diversity based on cpba  
 RT sequences during bloom in Daechung Reservoir, Korea.";  
 RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY942913; AAY82532.1; -; Genomic\_DNA.  
 FT NON\_TER 16 16  
 FT NON\_TER 16 16  
 SQ SEQUENCE 16 AA; 1575 MW; F70724E0948D995A CRC64;

Query Match 25.0%; Score 24; DB 2; Length 16;  
 Best Local Similarity 62.5%; Pred. No. 1.2e+04;  
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 10 LITAAVSPG 17  
 DB 9 VSAADSPG 16

## RESULT 29

086WJ4\_HUMAN PRELIMINARY; PRT; 18 AA.  
 AC 086WJ4;  
 DT 01-JUN-2003 (TReMBLrel. 24, Created)

DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)

DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)

DE Cyclin-dependent kinase inhibitor (Fragment).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;

OC Homo.

NCBI\_TaxID=9606;

RX NCBI\_TaxID=9606;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Heart;

RA Balda G., Pomyskala H., Olopade O.I.;

RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF488410; AA049471.1; -; mRNA.

DR HSSP; P55271; ID95.

DR GO; GO:0016301; F:Kinase activity; IEA.

KW Cyclin; Kinase.

FT NON\_TER 1 1

FT NON\_TER 18 18

SQ SEQUENCE 18 AA; 2003 MW; AD99FCC7D27538E7 CRC64;

Query Match 25.0%; Score 24; DB 2; Length 18;  
 Best Local Similarity 83.3%; Pred. No. 1.3e+04;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GYLTA 12  
 DB 10 GYLTA 15

## RESULT 30

08TDB3\_HUMAN PRELIMINARY; PRT; 19 AA.  
 AC 08TDB3;  
 DT 01-JUN-2002 (TReMBLrel. 21, Created)  
 DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)  
 DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)  
 DE Transhyretin amyloidosis variant A1205 (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;  
 OC Homo.  
 NCBI\_TaxID=9606;  
 RX NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Booth D., Byde A., Peys M., Hawkins P.;  
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF485252; AAL92041.1; -; Genomic\_DNA.  
 DR HSSP; P02766; 1F41.  
 DR GO; GO:0005386; F:carrier activity; IEA.  
 DR GO; GO:0005496; F:steroid binding; IEA.  
 DR GO; GO:0006810; P:transport; IEA.  
 DR InterPro; IPR000895; Transhyretin.  
 DR Pfam; PF00576; Transhyretin; 1.  
 FT NON\_TER 1 1  
 FT NON\_TER 19 19  
 SQ SEQUENCE 19 AA; 1988 MW; F564E31C43209399 CRC64;

Query Match 25.0%; Score 24; DB 2; Length 19;  
 Best Local Similarity 36.4%; Pred. No. 1.4e+04;  
 Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 5 PHGYLTAAVS 15  
 DB 8 PYSYSTSVVT 18

## RESULT 31

09PRY1\_TORCA PRELIMINARY; PRT; 20 AA.  
 AC 09PRY1;  
 DT 01-MAY-2000 (TReMBLrel. 13, Created)  
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)  
 DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)

```

DE AGRIN receptor 190 kDa SUBUNIT=ALPHA-dystroglycan homolog
DE (Fragment)
DE Torpedo californica (Pacific electric ray).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Squalea; Hypnosqualea; Pristigastera; Batoidae;
OC Torpediniformes; Torpedinidae; Torpedo.
OX NCBI_TaxID=787;
(1)
RX PROTEIN SEQUENCE.
RX MEDLINE=94242436; PubMed=8185951; DOI=10.1016/0896-6273(94)90324-7;
RA Bove M.A., Deyat K.A., Leszyk J.D., Fallon J.R.;
RT "Identification and purification of an agrin receptor from Torpedo
RT postsynaptic membranes: a heteromeric complex related to the
RT dystroglycans";
RL Neuron 12:1173-1180 (1994).
FT NON_TER 1 1
FT NON_TER 20 20
SQ SEQUENCE 20 AA; 2239 MW; 038622F02D189F90 CRC64;

Query Match 25.0%; Score 24; DB 2; Length 20;
Best Local Similarity 41.7%; Pred. No. 1.5e+04;
Matches 5; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 6 HGILTAAVSPG 17
DB 1 HEYFMAAAXKGG 12

RESULT 32
Q7M1V9 LYCES PRELIMINARY; PRT; 16 AA.
ID Q7M1V9
AC Q7M1V9
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DE Multicystatin (Fragment).
OS Lycopericon esculentum (Tomato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Solanales; Solanaceae; Solanum; Lycopersicon.
OX NCBI_TaxID=4081;
(1)
RX PROTEIN SEQUENCE.
RX Jactato T., Fernandes K.V.S., Machado O.L.T., Siqueira-Junior C.L.;
RT "Leaves of transgenic tomato plants overexpressing proycetamin
RT accumulate high levels of cystatin.";
RL Plant Sci. 138:35-42 (1998).
DR PIR; A59155; A59155.
FT NON_TER 1 1
FT NON_TER 16 16
SQ SEQUENCE 16 AA; 1789 MW; CAF40110AD660AB9 CRC64;

Query Match 24.5%; Score 23.5; DB 2; Length 16;
Best Local Similarity 50.0%; Pred. No. 1.4e+04;
Matches 6; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

QY 8 YLLT-AAVSPGK 18
DB 1 YITFPAATDAGK 12

RESULT 33
Q9UCG2 HUMAN PRELIMINARY; PRT; 19 AA.
ID Q9UCG2
AC Q9UCG2
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE Pre-alpha 2-plasmin inhibitor (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.

```

```

OX NCBI_TaxID=9606;
(1)
RX PROTEIN SEQUENCE.
RX MEDLINE=93243387; PubMed=8484741;
RA Bangert K., Johnsen A.H., Christensen U., Thorsen S.;
RT "Different N-terminal forms of alpha 2-plasmin inhibitor in human
RT plasma.";
RL Biochem. J. 291:623-625 (1993).
SQ SEQUENCE 19 AA; 2068 MW; 01F3298DD3141992 CRC64;

Query Match 24.5%; Score 23.5; DB 2; Length 19;
Best Local Similarity 44.4%; Pred. No. 1.7e+04;
Matches 8; Conservative 1; Mismatches 4; Indels 5; Gaps 1;

QY 4 EPHGYLTRA----VSP 16
DB 2 EPLGRQLTSGPNOEQVSP 19

RESULT 34
LSK1 LEUMA
ID LSK1 LEUMA STANDARD; PRT; 11 AA.
AC P04428;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Leucosulfakinin-1 (Leucosulfakinin-1) (LSK-1).
OS Leucophaea maderae (Madelra cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberioidea;
OC Blaberidae; Leucophaea.
OX NCBI_TaxID=6988;
(1)
RX PROTEIN SEQUENCE.
RX MEDLINE=86315858; PubMed=3749893;
RA Nachman R.J., Holman G.M., Haddon W.F., Ling N.;
RT "Leucosulfakinin, a sulfated insect neuropeptide with homology to
RT gastrin and cholecystokinin.";
RL Science 234:71-73 (1986).
CC -1- FUNCTION: Changes the frequency and amplitude of contractions of
CC the hinged. Inhibits muscle contraction of hindgut.
CC -1- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR PIR; A01622; GMBOL.
DR InterPro; IPR001651; Gastrin.
DR PROSITE; PS00259; GASTRIN; 1.
KW Amidation; Direct protein sequencing; Hormone; Sulfation.
FT MOD_RES 6 6 Sulfotyrosine.
FT MOD_RES 11 11 Phenylalanine amide.
SQ SEQUENCE 11 AA; 1459 MW; 7E4E0680E8655AAB CRC64;

Query Match 24.0%; Score 23; DB 1; Length 11;
Best Local Similarity 33.3%; Pred. No. 1.2e+04;
Matches 3; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 DAFEPHYGL 9
DB 1 EQFEDYGHM 9

RESULT 35
Q4YEX5 PLAB PRELIMINARY; PRT; 12 AA.
ID Q4YEX5
AC Q4YEX5
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)

```

Hypothetical protein (Fragment).  
 GN ORFNames=PB404919.00.0;  
 OS Plasmodium berghei.  
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
 ON NCBI\_TaxID=5821;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Hall N., Karrae M., Raine J.D., Carlton J.M., Kool J.T.W.A.,  
 Barriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,  
 James K., Rutherford K., Harris B., Harris D., Churcher C.,  
 Quail M.A., Ormond D., Doggett J., Trueman H.B., Mendoza J.,  
 Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,  
 Jense C.J., Barrall B., Turner C.M.R., Waters A.P., Sinden R.S.;  
 RT "A comprehensive survey of the Plasmodium life cycle by genomic,  
 transcriptomic, and proteomic analyses."  
 RL Science 307:82-86(2005).  
 CC -1- CAUTION: The sequence shown here is derived from an  
 EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
 preliminary data.  
 DR EMBL/CAI01005812; CAI03444.1; -, Genomic\_DNA.  
 KW Hypothetical protein.  
 FT NON\_TER 1  
 SQ SEQUENCE 12 AA; 1389 MW; 9843P11441059D1 CRC64;  
 Query Match 24.0%; Score 23; DB 2; Length 12;  
 Best Local Similarity 50.0%; Pred. No. 1.3e+04;  
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 QY 4 EPHGYL 9  
 Db 2 EPHPTI 7  
 RESULT 36  
 ADFB TENMO STANDARD; PRT; 13 AA.  
 ID ADFB TENMO  
 AC P8109;  
 DT 10-OCT-2003 (Rel. 42, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Antidiuretic factor B (ADFB).  
 OS Tenbrilio mollitor (Yellow mealworm).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;  
 OC Tenebrionidae; Tenebriono.  
 ON NCBI\_TaxID=70671;  
 RN [1]  
 RP PROTEIN SEQUENCE, FUNCTION, TISSUE SPECIFICITY, MASS SPECTROMETRY, AND  
 RP SYNTHESIS.  
 RC TISSUE=Head;  
 RX MEDLINE=2245067; PubMed=12576082; DOI=10.1016/S0196-9781(02)00273-5;  
 RA Rigenheer R.A., Wiehart U.M., Nicolson S.W., Schoofs L., Schegg K.M.,  
 Hall J.J., Schooley D.A.;  
 RT "Isolation, identification and localization of a second beetle  
 antidiuretic peptide."  
 RL Peptides 24:27-34(2003).  
 CC -1- FUNCTION: Inhibitor of fluid secretion by Malpighian tubules. Uses  
 GMP as second messenger. May function as an antidiuretic hormone.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: Brain. Appears to be mainly expressed in two  
 pairs of bilaterally symmetrical cells in the protocerebrum.  
 CC -1- MASS SPECTROMETRY: MW=1560.33; METHOD=MALDI; RANGE=1-13;  
 CC NOTE=Ref.1.  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 the European Bioinformatics Institute. There are no restrictions on its  
 use as long as its content is in no way modified and this statement is not  
 removed.  
 CC Direct protein sequencing: Hormone; Neuropeptide.  
 KW EMBL/CAI01001600; CAH96718.1; -, Genomic\_DNA.  
 SQ SEQUENCE 13 AA; 1563 MW; 0240A4504B8A632B CRC64;

Query Match 24.0%; Score 23; DB 1; Length 13;  
 Best Local Similarity 42.9%; Pred. No. 1.4e+04;  
 Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
 QY 2 AFEPHG 8  
 Db 5 SYKPHI 11  
 RESULT 37  
 Q9UDC6 HUMAN  
 ID Q9UDC6 HUMAN PRELIMINARY; PRT; 13 AA.  
 AC Q9UDC6;  
 DT 01-MAY-2000 (TRENBEREL. 13, Created)  
 DT 01-MAY-2000 (TRENBEREL. 13, Last sequence update)  
 DT 01-JUN-2002 (TRENBEREL. 21, Last annotation update)  
 DE ENDOTHELIUM-derived RELATING factor, nitric oxide synthase  
 (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;  
 OC Homo.  
 ON NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=93054573; PubMed=1385404;  
 RA Janssens S.P., Simouchi A., Quettermous T., Bloch D.B., Bloch K.D.;  
 RT "Cloning and expression of a cDNA encoding human endothelium-derived  
 RT relating factor/nitric oxide synthase."  
 RL J. Biol. Chem. 267:22694-22694(1992).  
 FT NON\_TER 1  
 FT NON\_TER 13  
 SQ SEQUENCE 13 AA; 1390 MW; 3231B6DFEC7EB867 CRC64;  
 Query Match 24.0%; Score 23; DB 2; Length 13;  
 Best Local Similarity 66.7%; Pred. No. 1.4e+04;  
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 2 AFEPHG 7  
 Db 2 AFDPGP 7  
 RESULT 38  
 Q4YZ27 PLABE  
 ID Q4YZ27 PLABE PRELIMINARY; PRT; 16 AA.  
 AC Q4YZ27;  
 DT 13-SEP-2005 (TRENBEREL. 31, Created)  
 DT 13-SEP-2005 (TRENBEREL. 31, Last sequence update)  
 DT 13-SEP-2005 (TRENBEREL. 31, Last annotation update)  
 DE Hypothetical protein.  
 GN ORFNames=PB103937.00.0;  
 OS Plasmodium berghei.  
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
 ON NCBI\_TaxID=5821;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Hall N., Karrae M., Raine J.D., Carlton J.M., Kool J.T.W.A.,  
 Barriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,  
 James K., Rutherford K., Harris B., Harris D., Churcher C.,  
 Quail M.A., Ormond D., Doggett J., Trueman H.B., Mendoza J.,  
 Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,  
 Jense C.J., Barrall B., Turner C.M.R., Waters A.P., Sinden R.S.;  
 RT "A comprehensive survey of the Plasmodium life cycle by genomic,  
 transcriptomic, and proteomic analyses."  
 RL Science 307:82-86(2005).  
 CC -1- CAUTION: The sequence shown here is derived from an  
 EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
 preliminary data.  
 DR EMBL/CAI01001600; CAH96718.1; -, Genomic\_DNA.  
 KW Hypothetical protein.  
 SQ SEQUENCE 16 AA; 2063 MW; 22B78003D41CB8FD CRC64;



DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)  
 DE 05-JUL-2004 (TREMBlrel. 27, Last annotation update)  
 DB Thrombopoietin receptor (Fragment).  
 GN Name=Mpl; Synonyms=c-mpl1;  
 OS Mus sp.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Murinae; Mus.  
 NCBI\_TaxID=10095;  
 RX NCBIOTIDE SEQUENCE.  
 RA MEDLINE=5516571; PubMed=7862460;  
 RT Alexander W.S., Dunn A.R.;  
 RT "Structure and transcription of the genomic locus encoding murine c-  
 RT Mpl, a receptor for thrombopoietin."  
 RL Oncogene 10:795-803(1995).  
 DR EMBL; S76842; AAB33462.1; -; mRNA.  
 DR MGI; MGI:97076; Mpl.  
 DR GO; GO:0004872; P:receptor activity; IEA.  
 KM Receptor.  
 FT NON\_TER  
 SQ SEQUENCE 18 AA; 1808 MW; E01CB44E83834E2 CRC64;  
 QY  
 DB 4 EPHG 7  
 ID 1 QPHG 4  
 AC 1 QPHG 4  
 DT 01-JUN-2003 (TREMBlrel. 24, Created)  
 DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)  
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
 DE Truncated p24 protein (Fragment).  
 GN Name=gag;  
 OS Human immunodeficiency virus 1.  
 OC Viruses; Retroviridae; Retroviridae; Lentivirus;  
 OC Primate lentivirus group.  
 NCBI\_TaxID=11676;  
 RX NCBIOTIDE SEQUENCE.  
 RA STRAIN=99TCD.MN044;  
 RA Vidal N., Koyalta D., Richard V., Leclache C., Ndinaromtan T.,  
 RA Djimsingar A., Delaporte E., Peeters M.,  
 RT "High genetic diversity of HIV-1 strains in Chad, West Central  
 RT Africa."  
 RT J. Acquir. Immune Defic. Syndr. 33:139-246(2004).  
 DR EMBL; AJ491020; CAD36428.1; -; Genomic\_DNA.  
 FT NON\_TER  
 SQ SEQUENCE 18 AA; 1978 MW; 1FP3D5BB656A776F CRC64;  
 QY  
 DB 7 GYLLTAAP 16  
 ID 4 GYLLTAAP 16  
 AC 4 GYLLTAAP 16  
 DT 01-DEC-2001 (TREMBlrel. 19, Created)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)

DE ATP-dependent protease subunit (Fragment).  
 OS Abies alba (Edeltanne) (European silver fir).  
 OC Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Abies.  
 NCBI\_TaxID=55372;  
 RX NCBIOTIDE SEQUENCE.  
 RA Liepelt S., Kuhlenskamp V., Anzidei M., Venderamin G.G., Ziegenhagen B.;  
 RL Submitted (Apr-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF367975; AAK53398.1; -; Genomic\_DNA.  
 DR GO; GO:0009507; C:chloroplast; IEA.  
 DR GO; GO:0008233; P:peptidase activity; IEA.  
 KM Chloroplast; Protease.  
 FT NON\_TER  
 SQ SEQUENCE 19 AA; 1958 MW; 7CA63B7278AE394 CRC64;  
 QY  
 DB 2 APEPHGYLLTAAPSPG 17  
 ID 4 APEPHGYLLTAAPSPG 17  
 AC 4 APEPHGYLLTAAPSPG 17  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 01-FEB-2005 (Rel. 46, Last annotation update)  
 DE Protein PR-L1 (Fragment).  
 OS Lupinus luteus (European yellow lupin).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliopsida; eudicotyledons; core eudicotyledons;  
 OC Rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Genisteae;  
 OC Lupinus.  
 NCBI\_TaxID=3873;  
 RX NCBIOTIDE SEQUENCE, AND INDUCTION.  
 RA STRAIN=cv. Ventus; TISSUE=Root tip;  
 RA Przymusiński R., Gwozdz E.A.;  
 RT "Heavy metal-induced polypeptides in lupin roots are similar to  
 RT pathogenesis-related proteins."  
 RT J. Plant Physiol. 154:703-708(1999).  
 CC -1- INDUCTION: BY heavy metal ions.  
 CC -1- SIMILARITY: Belongs to the BetyI family.  
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 DR InterPro; IPR000916; Bet\_v1.  
 DR PROSITE; PS00451; PATHOGENESIS BETVI; PARTIAL.  
 KM Direct protein sequencing; Pathogenesis-related protein;  
 KM Plant defense.  
 FT NON\_TER  
 SQ SEQUENCE 20 AA; 2204 MW; 063D76EB9BD26C85 CRC64;  
 QY  
 DB 11 TAAPSPG 18  
 ID 10 TAAPSPG 18  
 AC 10 TAAPSPG 18  
 DT 01-DEC-2001 (TREMBlrel. 19, Created)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)

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PL6_LUPULU
ID PL6_LUPULU STANDARD; PRT; 20 AA.
AC P83368;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE 01-FEB-2005 (Rel. 46, Last annotation update)
DE Protein PR-L6 (Fragment).
OC Lupinus luteus (European yellow lupin).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliopsida; eudicotyledons; core eudicotyledons;
OC Rosids; eustosids I; Fabales; Fabaceae; Papilionoideae; Genisteae;
OC Lupinus.
OC NCBI_TaxID=3873;
RN [1]
RP NUCLEOTIDE SEQUENCE, AND INDUCTION.
RC STRAIN=cv. Ventus, TISSUE=Root tip;
RA Przybylski R., Gwozdz E.A.;
RT "Heavy metal-induced polypeptides in lupin roots are similar to
pathogenesis-related proteins."
RL J. Plant Physiol. 154:703-708(1999).
CC -1- INDUCTION: By heavy metal ions.
CC -1- SIMILARITY: Belongs to the Betyr family.
-----
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CC removed.
-----
DR InterPro; IPR000916; Bet_v_1.
DR PROSITE; PS00451; PATHOGENESIS BETV1; PARTIAL.
KM Direct protein sequencing; Pathogenesis-related protein;
FT Plant defense.
FT NON_TER 20
SQ SEQUENCE 20 AA; 2190 MW; 063D60824BD26C85 CRC64;

Query Match 24.0%; Score 23; DB 1; Length 20;
Best Local Similarity 50.0%; Pred. No. 2.2e+04;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 11 TAAVSPGK 18
DB 10 TSTVAPAK 17

RESULT 47
Q9BRP3_HUMAN PRELIMINARY; PRT; 20 AA.
ID Q9BRP3;
AC Q9BRP3;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE MAFG protein.
GN Name=MAFG;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OC NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung;
RA MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins B.S., Wagner L., Scheffen C.M., Schuler G.D.,
RA Altshuler S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
RA Brownstein M.J., Ueda T.B., Yoshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullighy S.J.,
RA Bosak S.A., McMan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

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RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kerteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (Apr-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL; BC006143; AA06143.1; -, mRNA.
DR Ensembl; ENSG00000197048; Homo sapiens.
SQ SEQUENCE 20 AA; 2080 MW; DEB42194EE428F84 CRC64;

Query Match 24.0%; Score 23; DB 2; Length 20;
Best Local Similarity 50.0%; Pred. No. 2.2e+04;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 11 TAAVSPGK 18
DB 13 TQQLSPGE 20

RESULT 48
Q9R4U5_STRSL PRELIMINARY; PRT; 20 AA.
ID Q9R4U5_STRSL;
AC Q9R4U5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE Aminopeptidase N (Fragment).
OS Streptococcus salivarius.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OC NCBI_TaxID=1304;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=95081020; PubMed=7989254;
RA Mdwinner R.G., Pritchard G.G.;
RT "Aminopeptidase N from Streptococcus salivarius subsp. thermophilus
RT NCD0 575: purification and properties."
RL J. Appl. Bacteriol. 77:288-295(1994).
SQ SEQUENCE 20 AA; 2328 MW; 55FB0E4BC6EFD2CD CRC64;

Query Match 24.0%; Score 23; DB 2; Length 20;
Best Local Similarity 40.0%; Pred. No. 2.2e+04;
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 DAFEPHGYLL 10
DB 9 ESFIPENTYXL 18

RESULT 49
Q81IS2_MOUSE PRELIMINARY; PRT; 9 AA.
ID Q81IS2_MOUSE;
AC Q81IS2;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DE HCPC1 protein (Fragment).
GN Name=HCPC1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]

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RP NUCLEOTIDE SEQUENCE.  
 RA Reichwald K., Petz U., Rosenthal A., Platzer M.,  
 RL Submitted (NOV-2002) to the EMBL/Genbank/DBJ databases.  
 DR EMBL, AY184361; A024116.1; -; mRNA.  
 FT NON TER 9  
 SQ SEQUENCE 9 AA; 847 MW; CB74C75A2CDC5BD CRC64;

Query Match 22.9%; Score 22; DB 2; Length 9;  
 Best Local Similarity 57.1%; Pred. No. 2.2e+06;  
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 10 LTRAVSP 16  
 : |||||  
 DB 1 MASAVSP 7

RESULT 50  
 Q9MW05\_PODCU PRELIMINARY; PRT; 10 AA.  
 ID Q9MW05\_PODCU  
 AC Q9MW05;  
 DT 01-OCT-2000 (TREMBLrel. 15, Created)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
 DE Cytochrome b (Fragment).  
 GN Name=cytb;  
 OS Podospora curvicollla.  
 OC Mitochondrion.  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 OC Sordariomycetidae; Sordariales; Lasiosphaeriaceae; Podospora.  
 OC NCBI\_TaxId=48157;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=20150243; PubMed=10684923; DOI=10.1093/nar/28.6.1299;  
 RA Saguez C., Lecellier G., Koll F.;  
 RT "intronic G1Y-YIG endonuclease gene in the mitochondrial genome of  
 Podospora curvicollla: evidence for mobility."  
 RL Nucleic Acids Res. 28:1299-1306(2000).  
 DR EMBL, AJ249984; CAB72447.1; -; Genomic\_DNA.  
 DR GO: GO:0005739; C:mitochondrion; IEA.  
 KW Mitochondrion.  
 FT NON TER 1  
 FT NON TER 10  
 SQ SEQUENCE 10 AA; 1200 MW; C31A23B437B0772 CRC64;

Query Match 22.9%; Score 22; DB 2; Length 10;  
 Best Local Similarity 55.6%; Pred. No. 1.5e+04;  
 Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 AFEPHGYLL 10  
 : |||||  
 DB 1 AIVPEWYLL 9

RESULT 51  
 Q9QV21\_9MURI PRELIMINARY; PRT; 10 AA.  
 ID Q9QV21\_9MURI  
 AC Q9QV21;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)  
 DE Neurotrophic factor.  
 GN Ractus sp.;  
 OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Charchonoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Murinae; Ractus.  
 OC NCBI\_TaxId=10118;  
 RN [1]  
 RP PROTEIN SEQUENCE.  
 RX MEDLINE=95056708; PubMed=7967227;  
 RA Yasukura T., Omori K., Mikami T., Inoue M., Uyama M., Inagaki C.;  
 RT "Purification and characterization of neurotrophic factor for retinal  
 cholinergic neurons derived from cultured hippocampal neurons."  
 Jpn. J. Pharmacol. 65:153-162(1994).

SQ SEQUENCE 10 AA; 1145 MW; 58922952D6DDC767 CRC64;  
 Query Match 22.9%; Score 22; DB 2; Length 10;  
 Best Local Similarity 62.5%; Pred. No. 1.5e+04;  
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 8 YLTPAAS 15  
 : |||||  
 DB 1 YLTPAQVN 8

RESULT 52  
 Q86D31\_TRYCR PRELIMINARY; PRT; 11 AA.  
 ID Q86D31\_TRYCR  
 AC Q86D31;  
 DT 01-JUN-2003 (TREMBLrel. 24, Created)  
 DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)  
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)  
 DE Histone H1 (Fragment).  
 OS Trypanosoma cruzi.  
 OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma;  
 OC Schizotrypanum.  
 OC NCBI\_TaxId=5693;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=22557728; PubMed=12670512; DOI=10.1016/S0020-7519(02)00264-3;  
 RA Sturm N.R., Vargas N.S., Westendorp S.J., Zingales B.,  
 RA Campbell D.A.;  
 RT "Evidence for multiple hybrid groups in Trypanosoma cruzi."  
 RL Int. J. Parasitol. 33:269-279(2003).  
 DR EMBL, AF545076; AAP21506.1; -; Genomic\_DNA.  
 FT NON TER 11  
 FT NON TER 11  
 SQ SEQUENCE 11 AA; 1174 MW; CCD1B21E7772CDD CRC64;

Query Match 22.9%; Score 22; DB 2; Length 11;  
 Best Local Similarity 50.0%; Pred. No. 1.7e+04;  
 Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 9 LTRAVSPGK 18  
 : |||||  
 DB 1 MPDAVAPPK 10

RESULT 53  
 Q9MW03\_PODCU PRELIMINARY; PRT; 14 AA.  
 ID Q9MW03\_PODCU  
 AC Q9MW03;  
 DT 01-OCT-2000 (TREMBLrel. 15, Created)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
 DE Cytochrome b (Fragment).  
 GN Name=cytb;  
 OS Podospora curvicollla.  
 OC Mitochondrion.  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 OC Sordariomycetidae; Sordariales; Lasiosphaeriaceae; Podospora.  
 OC NCBI\_TaxId=48157;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=20150243; PubMed=10684923; DOI=10.1093/nar/28.6.1299;  
 RA Saguez C., Lecellier G., Koll F.;  
 RT "intronic G1Y-YIG endonuclease gene in the mitochondrial genome of  
 Podospora curvicollla: evidence for mobility."  
 RL Nucleic Acids Res. 28:1299-1306(2000).  
 DR EMBL, AJ249985; CAB72449.1; -; Genomic\_DNA.  
 DR GO: GO:0005739; C:mitochondrion; IEA.  
 KW Mitochondrion.  
 FT NON TER 1  
 FT NON TER 14  
 SQ SEQUENCE 14 AA; 1603 MW; 2972D7731A723B43 CRC64;

Query Match 22.9%; Score 22; DB 2; Length 14;  
 Best Local Similarity 55.6%; Pred. No. 2.2e+04;

Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 APEPHGYL 10  
| | | |  
DB 2 AIVPEWYLL 10

RESULT 54  
Q5OSJ7 TRIMA

ID Q5OSJ7 TRIMA PRELIMINARY; PRT; 14 AA.

AC Q5OSJ7;

DT 01-FEB-2005 (TrEMBLrel. 29, Created)

DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)

DE 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)

DE HspB2 protein (Fragment).

GN Name=mkbp;

OS Trichechus manatus (Caribbean manatee) (West Indian manatee).

OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Afrotheria; Sirenia; Trichechidae; Trichechus.

NCBI\_TaxID=9778;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RA Doerwald L., van Rieede T., Dirks R.P., Madsen O., Rexwinkel R.,

van Geneen S.T., Martens G.J., de Jong W.W., Lubsen N.H.;

RT "Sequence and functional conservation of the intergenic region between

RT the head-to-head genes encoding the small heat shock proteins alphaB-

RT cryofallin and HspB2 in the mammalian lineage."

RL J. Mol. Evol. 59:674-686(2004).

DR EMBL; AJ617824; CAB9475.1; -; Genomic\_DNA.

FT NON\_TER 14

SO SEQUENCE 14 AA; 1419 MW; 2F09350ABC6DE8F7 CRC64;

Query Match 22.9%; Score 22; DB 2; Length 14;  
Best Local Similarity 50.0%; Pred. No. 2.2e+04;  
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 5 PHGYLTA 12  
| | | |  
DB 7 PHAHPATA 14

RESULT 55  
Q5OSJ5 CYCDI

ID Q5OSJ5 CYCDI PRELIMINARY; PRT; 14 AA.

AC Q5OSJ5;

DT 01-FEB-2005 (TrEMBLrel. 29, Created)

DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)

DE 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)

DE HspB2 protein (Fragment).

GN Name=mkbp;

OS Cyclops didactylus (Silky anteater).

OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Xenarthra; Myrmecophagidae; Cyclopes.

NCBI\_TaxID=84074;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RA Doerwald L., van Rieede T., Dirks R.P., Madsen O., Rexwinkel R.,

van Geneen S.T., Martens G.J., de Jong W.W., Lubsen N.H.;

RT "Sequence and functional conservation of the intergenic region between

RT the head-to-head genes encoding the small heat shock proteins alphaB-

RT cryofallin and HspB2 in the mammalian lineage."

RL J. Mol. Evol. 59:674-686(2004).

DR EMBL; AJ617820; CAB9454.1; -; Genomic\_DNA.

FT NON\_TER 14

SO SEQUENCE 14 AA; 1419 MW; 2F09350ABC6DE8F7 CRC64;

Query Match 22.9%; Score 22; DB 2; Length 14;  
Best Local Similarity 50.0%; Pred. No. 2.2e+04;  
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 5 PHGYLTA 12  
| | | |  
DB 7 PHAHPATA 14

RESULT 56  
Q5OSJ7 SPAEH

ID Q5OSJ7 SPAEH PRELIMINARY; PRT; 14 AA.

AC Q5OSJ7;

DT 01-FEB-2005 (TrEMBLrel. 29, Created)

DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)

DE 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)

DE HspB2 protein (Fragment).

GN Name=mkbp;

OS Spalax leucodon ehrenbergi (Ehrenberg's mole rat).

OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muridae; Spalacinae; Nannospalax.

NCBI\_TaxID=30637;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RA Doerwald L., van Rieede T., Dirks R.P., Madsen O., Rexwinkel R.,

van Geneen S.T., Martens G.J., de Jong W.W., Lubsen N.H.;

RT "Sequence and functional conservation of the intergenic region between

RT the head-to-head genes encoding the small heat shock proteins alphaB-

RT cryofallin and HspB2 in the mammalian lineage."

RL J. Mol. Evol. 59:674-686(2004).

DR EMBL; AJ617819; CAB9448.1; -; Genomic\_DNA.

FT NON\_TER 14

SO SEQUENCE 14 AA; 1449 MW; 2F09351BF86DE8F7 CRC64;

Query Match 22.9%; Score 22; DB 2; Length 14;  
Best Local Similarity 50.0%; Pred. No. 2.2e+04;  
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 5 PHGYLTA 12  
| | | |  
DB 7 PHAHPATA 14

RESULT 57  
GSTB1\_PSEUO

ID GSTB1\_PSEUO STANDARD; PRT; 15 AA.

AC P82999;

DT 05-JUL-2004 (Rel. 44, Created)

DT 05-JUL-2004 (Rel. 44, Last sequence update)

DT 10-MAY-2005 (Rel. 47, Last annotation update)

DE Glutathione S-transferase (BC 2.5.1.18) (Fragment).

OS Pseudomonas sp. (Strain M1).

OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;

OC Pseudomonadaceae; Pseudomonas.

NCBI\_TaxID=95619;

RN [1]

RP PROTEIN SEQUENCE, FUNCTION, CATALYTIC ACTIVITY, SUBUNIT, AND

RP SUBCELLULAR LOCATION.

RX MEDLINE=21896940; PubMed=11900268; DOI=10.1016/S0923-2508(01)01293-1;

RA Santos P.M., Mignogna G., Heidegger H.J., Zennaro E.;

RT "Occurrence and properties of glutathione S-transferases in phenol-

RT degrading Pseudomonas strains";

Res. Microbiol. 153:89-98(2002).

CC -1- FUNCTION: Conjugation of reduced glutathione to a wide number of

CC exogenous and endogenous hydrophobic electrophiles.

CC -1- CATALYTIC ACTIVITY: RX + glutathione = HX + R-S-glutathione.

CC -1- SUBUNIT: Monomer and homodimer.

CC -1- SUBCELLULAR LOCATION: Cytoplasmic.

CC -1- SIMILARITY: Belongs to the GST superfamily.

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CC removed.

DR GO; GO:0005737; C:cytoplasm; NAS.

DR GO; GO:0004364; F:glutathione transferase activity; NAS.

DR GO; GO:0008152; P:metabolism; IC.

KM Direct protein sequencing; Transferase.

FT NCN TER 15 15  
SQ SEQUENCE 15 AA; 1817 MW; 0E2A0FCSF55CBAC2 CRC64;

Query Match 22.9%; Score 22; DB 1; Length 15;  
Best Local Similarity 55.6%; Pred. No. 2.3e+04;  
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 8 YLTPAVSP 16  
| | | | |  
DB 3 YLTPVHSP 11

RESULT 58

005694 MOUSE  
ID 005694\_MOUSE PRELIMINARY; PRT; 15 AA.

AC 005694;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)

DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

DE Proline-rich protein (Fragment).  
GN Name=Mp61

OC Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Murinae; Mus.

OC NCBI\_TaxID=10090;  
RN [1]

NP NUCLEOTIDE SEQUENCE.  
RP STRAIN=BALB/C;

RX MEDLINE=92030206; PubMed=1747160;  
RA Roberts S.G.B., Layfield R., McDonald C.J.;

RT "The mouse proline-rich protein Mp6 promoter binds isoprenaline-  
inducible peroxid nuclear proteins via a highly conserved NFkB/rel-

like site."  
RL Nucleic Acids Res. 19:5205-5211 (1991).

DR EMBL; X61126; CAA43438.1; -; Genomic\_DNA.  
FT NCN TER 15 15

SQ SEQUENCE 15 AA; 1557 MW; C0FF9514A8F70BE4 CRC64;

Query Match 22.9%; Score 22; DB 2; Length 15;  
Best Local Similarity 83.3%; Pred. No. 2.3e+04;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 9 LTPAAV 14  
| | | | |  
DB 5 LTPAAL 10

RESULT 59

069353\_HHV2  
ID 069353\_HHV2 PRELIMINARY; PRT; 15 AA.

AC 069353;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)

DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

DE HSV-2 (333) N terminus of 17.8 kd protein gene (0.642 mu).  
DB (Fragment).

OS Human herpesvirus 2 (HHV-2) (Human herpes simplex virus 2).  
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;

OC Alphaherpesvirinae; Simplexvirinae;  
OC NCBI\_TaxID=10310;

RN [1]  
NP NUCLEOTIDE SEQUENCE.

RA MEDLINE=5033906; PubMed=6092683;  
RA Draper K.G., Frink R.J., Devl G.B., Swain M., Galloway D.,

RT "Herpes simplex virus types 1 and 2 homology in the region between  
0.58 and 0.68 map units."

RL EMBL; X03360; AAA45840.1; -; Genomic\_DNA.  
FT NCN TER 15 15

SQ SEQUENCE 15 AA; 1603 MW; 20B04DC0BA4507FE CRC64;

Query Match 22.9%; Score 22; DB 2; Length 15;

Best Local Similarity 66.7%; Pred. No. 2.3e+04;  
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 AFRPHG 7  
| | | | |  
DB 2 AFRPSG 7

RESULT 60

09TRR1\_RABIT  
ID 09TRR1\_RABIT PRELIMINARY; PRT; 16 AA.

AC 09TRR1;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)

DE Fibronectin 47 kDa fragment (Fragment).  
OS Oryctolagus cuniculus (Rabbit).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae;

OC Oryctolagus.  
OC NCBI\_TaxID=9986;

RN [1]  
NP PROTEIN SEQUENCE.

RX MEDLINE=92283375; PubMed=1597256;  
RA Lesot H., Faussier J.L., Akiyama S.K., Staub A., Black D., Kubler M.D.,

RA Ruch J.V.;"The carboxy-terminal extension of the collagen binding domain of  
RT fibronectin mediates interaction with a 165 kDa membrane protein

involved in odontoblast differentiation."  
RL Differentiation 49:109-118 (1992).

FT NCN TER 1 1  
FT NCN TER 16 16

SQ SEQUENCE 16 AA; 1764 MW; B196CAAC53F5739 CRC64;

Query Match 22.9%; Score 22; DB 2; Length 16;  
Best Local Similarity 42.9%; Pred. No. 2.5e+04;  
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 5 PHGYLVT 11  
| | | | |  
DB 10 PYGHXYT 16

RESULT 61

09QZY3\_MOUSE  
ID 09QZY3\_MOUSE PRELIMINARY; PRT; 16 AA.

AC 09QZY3;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)

DE R29144/1 (Fragment).  
GN Name=R29144/1;

OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Murinae; Mus.

OC NCBI\_TaxID=10090;  
RN [1]

NP NUCLEOTIDE SEQUENCE.  
RC STRAIN=129;

RX MEDLINE=99330555; PubMed=10400995; DOI=10.1093/nmg/8.8.1479;  
RA Smith D.P., Spicer J., Smith A., Swift S., Ashworth A.;

RT "The mouse Peutz-Jeghers syndrome gene lkb1 encodes a nuclear protein  
kinase."

RL Hum. Mol. Genet. 8:1479-1485 (1999).  
DR EMBL; AF145697; AAD5370.1; -; Genomic\_DNA.

FT NCN TER 1 1  
SQ SEQUENCE 16 AA; 1518 MW; D6C720E4BF0A1D2 CRC64;

Query Match 22.9%; Score 22; DB 2; Length 16;  
Best Local Similarity 50.0%; Pred. No. 2.5e+04;

Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 9 LITAAVSP 16  
|:|:|  
RT 1 LIVAAAP 8

RESULT 62  
ID 06LC11\_HUMAN PRELIMINARY; PRT; 17 AA.  
AC 06LC11;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Na<sup>+</sup>-phosphate cotransporter type II (Fragment).  
GN Name=NPRT2;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=93317607; PubMed=8327470;  
RA Mageruin S., Werner A., Markovich D., Sorribas V., Stange G.,  
RA Biber U., Murer H.;  
RT "Expression cloning of human and rat renal cortex Na/Pi cotransport.";  
RL Proc. Natl. Acad. Sci. U.S.A. 90:5979-5983 (1993).  
RN [2]  
RN NUCLEOTIDE SEQUENCE.  
RX MEDLINE=96393539; PubMed=8693007; DOI=10.1073/pnas.93.14.7409;  
RA Hartman C.M., Hewson A.S., Kos C.H., Hilleker H., Soumounou Y.,  
RA Murer H., Tenenhouse H.S.;  
RT "Structure of murine and human renal type II Na<sup>+</sup>-phosphate  
cotransporter genes (NPCT and NPRT2).";  
RL Proc. Natl. Acad. Sci. U.S.A. 93:7409-7414 (1996).  
DR EMBL; U56692; AAD14864.1; -; Genomic\_DNA.  
FT NON\_TER 1 1  
FT NON\_TER 17 17  
SQ SEQUENCE 17 AA; 1796 MW; 20ECDFE839C6D26D CRC64;

Query Match 22.9%; Score 22; DB 2; Length 17;  
Best Local Similarity 37.5%; Pred. No. 2.7e+04;  
Matches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 9 LITAAVSP 16  
|:|:|:|  
DB 8 VFTSALT 15

RESULT 63  
ID 07MOD8\_MOUSE PRELIMINARY; PRT; 17 AA.  
AC 07MOD8;  
DT 01-MAR-2004 (TrEMBLrel. 26, Created)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Probable integrin alpha3 beta1 (Fragment).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RN PROTEIN SEQUENCE.  
RA McCormick J.I., Johnstone R.M.;  
RT "Identification of the integrin alpha(3)beta(1) as a component of a  
partially purified A-system amino acid transporter from Ehrlich cell  
RT plasma membranes.";  
RL Biochem. J. 311:743-751 (1995).  
RN [2]  
RN PROTEIN SEQUENCE.  
RX PubMed=7487928;

RA McCormick J.I., Johnstone R.M.;  
RT "Identification of the integrin alpha 3 beta 1 as a component of a  
RT partially purified A-system amino acid transporter from Ehrlich cell  
RT plasma membranes.";  
RL Biochem. J. 311 ( Pt 3):743-751 (1995).  
DR PIR; S59512; S59512.  
FT NON\_TER 1 1  
FT NON\_TER 17 17  
SQ SEQUENCE 17 AA; 1917 MW; 2A106ECB15011902 CRC64;

Query Match 22.9%; Score 22; DB 2; Length 17;  
Best Local Similarity 80.0%; Pred. No. 2.7e+04;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 13 AVSPG 17  
|:|:|  
DB 13 AVNPG 17

RESULT 64  
ID 075MP5\_HUMAN PRELIMINARY; PRT; 18 AA.  
AC 075MP5;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Hypothetical protein UBR2H (Fragment).  
GN Name=UBR2H;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RN NUCLEOTIDE SEQUENCE.  
RX MEDLINE=22737999; PubMed=12853948; DOI=10.1038/nature01782;  
RA Hillier L.W., Fulton R.S., Fulton L.A., Graves T.A., Pepin K.H.,  
RA Wagner-McPherson C., Layman D., Maas J., Jaeger S., Walker R.,  
RA Wyllie K., Sekhon M., Becker M.C., O'Laughlin M.D., Schaller M.E.,  
RA Fewell G.A., Delahunty K.D., Miner T.L., Nash W.E., Cordes M., Du H.,  
RA Sun H., Edwards J., Bradshaw-Cordum H., Ali J., Andrews S., Isak A.,  
RA Vandrunt A., Nguyen C., Du F., Lamar B., Courtney L., Kalicki J.,  
RA Ozerzky P., Bielicki L., Scott K., Holmes A., Harkins R., Harris A.,  
RA Strong C.M., Hou S., Tomlinson C., Dauphin-Kohlberg S.,  
RA Kozlowski-Reilly A., Leonard S., Rohlfing T., Rock S.M.,  
RA Tiro-Wollam A.M., Abbott A., Mink P., Maupin R., Stromatt C.,  
RA Latreille P., Miller N., Johnson D., Murray J., Woessner J.P.,  
RA Wendl M.C., Yang S.-P., Schultz B.R., Wallis J.W., Spieth J.,  
RA Bieri T.A., Nelson J.O., Berkowicz N., Wohlmann P.E., Cook L.L.,  
RA Hickenbotham M.T., Bidler J., Williams D., Bedell J.A., Mardis E.R.,  
RA Clifton S.W., Chisose S.L., Marra M.A., Raymond C., Haugen E.,  
RA Gillett W., Zhou Y., James R., Phelps K., Iadonato S., Bubb K.,  
RA Simme B., Levy R., Clendinning J., Kaul R., Kent W.J., Porey T.S.,  
RA Baertsch R.A., Brent M.R., Keibler E., Flicker P., Bork P., Suyama M.,  
RA Bailey J.A., Portnoy M.B., Torrents D., Chimwalia A.T., Gish W.R.,  
RA Eddy S.R., McPherson J.D., Olson M.V., Bichter E.B., Green E.D.,  
RA Waterston R.H., Wilson R.K.;  
RT "The DNA sequence of human chromosome 7.";  
RL Nature 424:157-164 (2003).  
RN [2]  
RN NUCLEOTIDE SEQUENCE.  
RA Haakenson W., Kyung K.;  
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RN NUCLEOTIDE SEQUENCE.  
RA Waterston R.;  
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RN NUCLEOTIDE SEQUENCE.  
RA Wilson R.;  
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AC073320; AAS07548.1; -; Genomic\_DNA.  
KW Hypothetical protein.

FT NON TER 18 18  
SQ SEQUENCE 18 AA; 2004 MW; 7616C1121A8730F0 CRC64;

Query Match 22.9%; Score 22; DB 2; Length 18;  
Best Local Similarity 100.0%; Pred. No. 2.8e+04;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 SPQK 18  
DB 5 SPQK 8

## RESULT 65

05C123\_SCHUA PRELIMINARY; PRT; 19 AA.

AC 05C123;  
DT 10-MAY-2005 (TrEMBLrel. 30, Created)  
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)  
DE 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)  
DS Hypothetical protein.  
OS Schistosoma japonicum (Blood fluke).  
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Scrigelidae;  
OC Schistosomatoidea; Schistosomatidae; Schistosoma.  
OX NCBI\_TaxID=6182;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Han Z.  
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY610763; AX26652.1; -; mRNA.  
KM Hypothetical protein.  
SQ SEQUENCE 19 AA; 2259 MW; FE2492FB8464550 CRC64;

Query Match 22.9%; Score 22; DB 2; Length 19;  
Best Local Similarity 42.9%; Pred. No. 3e+04;  
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 6 HGYLTRA 12  
DB 12 HNTLVSS 18

## RESULT 66

04YGN5\_PLABE PRELIMINARY; PRT; 19 AA.

AC 04YGN5;  
DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
DE 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
DS Hypothetical protein (Fragment).  
GN ORName=PB403349.00.0;  
OS Plasmodium berghel.  
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
OX NCBI\_TaxID=5821;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Hall N., Katras M., Raine J.D., Carlton J.M., Kool J.T.W.A.,  
RA Bertrman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,  
RA James K., Rutherford K., Harris B., Harris D., Churcher C.,  
RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,  
RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,  
RA Janse C.J., Barrrell B., Turner C.M.R., Waters A.P., Sinden R.S.,  
RT "A comprehensive survey of the Plasmodium life cycle by genomic,  
transcriptomic, and proteomic analyses."  
RL Science 307:82-86(2005).  
CC -1- CAUTION: The sequence shown here is derived from an  
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
preliminary data.

CC EMBL; CAI01005269; CAI02832.1; -; Genomic\_DNA.  
DR Hypothetical protein.  
FT NON TER 1  
SQ SEQUENCE 19 AA; 2184 MW; 9014FEFF1869BD28 CRC64;

Query Match 22.9%; Score 22; DB 2; Length 19;

Best Local Similarity 44.4%; Pred. No. 3e+04;  
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 6 HGYLTRA 14  
DB 11 NGYILAAI 19

## RESULT 67

04W2E7\_SEUTH PRELIMINARY; PRT; 19 AA.

AC 04W2E7;  
DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
DE Putative Signal Transducer and Activator of Transcription  
DE (Fragment).  
GN Name=stat5A;  
OS Manis temminckii (ground pangolin).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Laurasiatheria; Pholidota; Manidae; Manis.  
OX NCBI\_TaxID=302418;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Bick G.N., Jacobs D.S., Matchee C.R.;  
RT "A phylogenetic perspective of the evolution of echolocation and  
RT historical biogeography of extant bats (Chiroptera)."  
RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AJ865445; CA126367.1; -; Genomic\_DNA.  
FT NON TER 1  
SQ SEQUENCE 19 AA; 1910 MW; 8B83C620FC87B5C8 CRC64;

Query Match 22.9%; Score 22; DB 2; Length 19;  
Best Local Similarity 62.5%; Pred. No. 3e+04;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 10 LTAVSPG 17  
DB 8 LGASPSPG 15

## RESULT 68

07TBG5\_ADE08 PRELIMINARY; PRT; 19 AA.

AC 07TBG5;  
DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DS Fiber (Fragment).  
OS Human adenovirus 8 (HAdV-8).  
OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.  
OX NCBI\_TaxID=31545;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA STRAIN=H16;  
RC PubMed=12560390; DOI=10.1136/jcp.56.2.120;  
RA Adhikary A.K., Nunaga J., Kaburaki T., Kawashima H., Araie M.,  
RA Ikeda Y., Ogino T., Suzuki E., Ushijima H., Mukoyama A., Matsuno S.,  
RA Inada T., Okabe N.;  
RT "Genetic Characterization of Adenovirus Type 8 Isolated in Hiroshima  
RT City over a 15-year Period."  
RL J. Clin. Pathol. 56:120-125(2003).  
DR EMBL; AB102672; BAC78838.1; -; Genomic\_DNA.  
FT NON TER 19  
SQ SEQUENCE 19 AA; 2364 MW; AC340337188B135F CRC64;

Query Match 22.9%; Score 22; DB 2; Length 19;  
Best Local Similarity 75.0%; Pred. No. 3e+04;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 PHGY 8  
DB 1

Db 16 PYGY 19

RESULT 69  
ID PL3\_LUPLU STANDARD; PRT; 20 AA.  
AC P83365;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 01-FEB-2005 (Rel. 46, Last annotation update)  
DE Protein PR-L3 (Fragment).  
OS Lupinus luteus (European yellow lupin).  
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
OC rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Genisteae;  
OC Lupinus.  
OX NCBI\_TaxID=3873;  
RN [1]  
RP PROTEIN SEQUENCE, AND INDUCTION.  
RC STRAIN=cv. Ventus; TISSUE=Root tip;  
RA Przytusinski R., Gwozdz B.A.;  
RT "Heavy metal-induced polypeptides in lupin roots are similar to  
pathogenesis-related proteins.";  
RL J. Plant Physiol. 154:703-708 (1999).  
CC -1- INDUCTION: By heavy metal ions.  
CC -1- SIMILARITY: Belongs to the Betyr family.  
-----  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
between the Swiss Institute of Bioinformatics and the EMBL outstation -  
the European Bioinformatics Institute. There are no restrictions on its  
use as long as its content is in no way modified and this statement is not  
removed.  
-----  
DR InterPro; IPR000916; Bet v 1.  
DR PROSITE; PS00451; PATHOGENESIS\_BETV1, PARTIAL.  
KW Direct protein sequencing; Pathogenesis-related protein;  
KW Plant defense.  
FT NON TER 20 20  
SQ SEQUENCE 20 AA; 2218 MW; 063BADEB9BD26C85 CRC64;

Query Match 22.9%; Score 22; DB 1; Length 20;  
Best Local Similarity 50.0%; Pred. No. 3.1e+04;  
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 11 TAAVSPK 18  
| | | | |  
Db 10 TTTVAPAK 17

RESULT 70  
ID Q8NFW3\_HUMAN PRELIMINARY; PRT; 20 AA.  
AC Q8NFW3;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
DE Synovial sarcoma SYT/SSX1 fusion protein (Fragment).  
GN Name=SYT/SSX1 fusion;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Tamborini E., Ague V., Pierotti M.A., Piliotti S., Rosal J.;  
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF402619; AAM95901.1; -, mRNA.  
FT NON TER 1 20  
SQ SEQUENCE 20 AA; 2377 MW; F1534C73F9108E83 CRC64;

Query Match 22.9%; Score 22; DB 2; Length 20;

Best Local Similarity 75.0%; Pred. No. 3.1e+04;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PHGYL 8  
| | | | |  
Db 4 PYGY 7

RESULT 71  
ID Q6UCN3\_ECOLI PRELIMINARY; PRT; 20 AA.  
AC Q6UCN3;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)  
DE Afac (Fragment).  
OS Escherichia coli.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Escherichia.  
OX NCBI\_TaxID=562;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=DABCT18, DABCT19, DABCT13, DABCT14, DABCT7, DABCT5, DABCT20,  
RC DABCT162, DABCT2a, DABCT2b, DABCT1a, DABCT1b, DABCT18, DABCT19, BC7372,  
RC ECOR37, DABCT9, ECOR50, IH1128, C1845, and ECOR64;  
RX PubMed=15014151; DOI=10.1093/molbev/mnh118;  
RA Bacchar-Paramo P., Clermont O., Blanc-Potard A.B., But H.,  
le Bougenec C., Denamur E.;  
RT "A Specific Genetic Background Is Required for Acquisition and  
Expression of Virulence Factors in Escherichia coli.";  
RL Mol. Biol. Evol. 21:1085-1094 (2004).  
DR EMBL; AY525515; AAT00550.1; -, Genomic DNA.  
DR EMBL; AY525516; AAT00552.1; -, Genomic DNA.  
DR EMBL; AY525517; AAT00554.1; -, Genomic DNA.  
DR EMBL; AY525518; AAT00556.1; -, Genomic DNA.  
DR EMBL; AY525519; AAT00558.1; -, Genomic DNA.  
DR EMBL; AY525520; AAT00560.1; -, Genomic DNA.  
DR EMBL; AY525521; AAT00562.1; -, Genomic DNA.  
DR EMBL; AY525522; AAT00564.1; -, Genomic DNA.  
DR EMBL; AY525523; AAT00566.1; -, Genomic DNA.  
DR EMBL; AY525524; AAT00568.1; -, Genomic DNA.  
DR EMBL; AY525525; AAT00570.1; -, Genomic DNA.  
DR EMBL; AY525526; AAT00572.1; -, Genomic DNA.  
DR EMBL; AY525527; AAT00574.1; -, Genomic DNA.  
DR EMBL; AY525528; AAT00576.1; -, Genomic DNA.  
DR EMBL; AY525529; AAT00578.1; -, Genomic DNA.  
DR EMBL; AY525530; AAT00580.1; -, Genomic DNA.  
DR EMBL; AY525531; AAT00582.1; -, Genomic DNA.  
DR EMBL; AY525532; AAT00584.1; -, Genomic DNA.  
DR EMBL; AY525533; AAT00586.1; -, Genomic DNA.  
DR EMBL; AY525534; AAT00588.1; -, Genomic DNA.  
DR EMBL; AY525514; AAT00548.1; -, Genomic DNA.  
FT NON TER 1 1  
SQ SEQUENCE 20 AA; 2282 MW; A3406B687822556D CRC64;

Query Match 22.9%; Score 22; DB 2; Length 20;  
Best Local Similarity 50.0%; Pred. No. 3.1e+04;  
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 5 PHGYLTAAY 14  
| | | | |  
Db 9 PAGIFLTQTV 18

RESULT 72  
ID Q9PRR9\_YAVES PRELIMINARY; PRT; 16 AA.  
AC Q9PRR9;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)  
DE NA/K adenosine triphosphatase alpha subunit (Fragment).  
OS Anas (ducks).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Aves; Neognathae; Anseriformes; Anatidae.  
 OX NCBI\_TaxID=8835;  
 RN [1]  
 RP PROTEIN SEQUENCE.  
 RX MEDLINE=96074588; PubMed=7488178;  
 RA Bol'dyrev A.A., Lopina O.D., Kenney M., Johnson P.;  
 RT "Characterization of the subunit isoforms of duck salt gland Na/K  
 RT adenosine triphosphatase.";  
 RL Biochem. Biophys. Res. Commun. 216:1048-1053(1995).  
 SO SEQUENCE 16 AA; 1784 MW; 1A338D2CE6B820 CRC64;

Query Match 22.4%; Score 21.5; DB 2; Length 16;  
 Best Local Similarity 41.7%; Pred. No. 3e+04;  
 Matches 5; Conservative 1; Mismatches 1; Indels 5; Gaps 1;

QY 1 DAFEP----HG 7  
 DB 3 DKYEPTXSHHG 14

RESULT 73  
 OSGK34\_COXBU  
 ID OSGK34\_COXBU PRELIMINARY; PRT; 18 AA.  
 AC OSGK34;  
 DT 10-MAY-2005 (TrEMBLrel. 30, Created)  
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)  
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)  
 DE Malate oxidoreductase (Fragment).  
 OS Coxifella burnetii.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;  
 OC Coxifellaceae; Coxifella.  
 OX NCBI\_TaxID=777;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Roux V., glazunova O., Raoult D.;  
 RT "Multiplex Sequence Typing (MST): a New Method for Coxifella Isolates  
 RT Characterization."  
 RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY502662; AM586373.1; -, genomic\_DNA.  
 FT NON TER 1  
 SQ SEQUENCE 18 AA; 2356 MW; 4660304A2F63A47 CRC64;

Query Match 22.4%; Score 21.5; DB 2; Length 18;  
 Best Local Similarity 71.4%; Pred. No. 3.4e+04;  
 Matches 5; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 3 FEPHGYL 9  
 DB 8 WEPH-YL 13

RESULT 74  
 O8AM46\_BRARE  
 ID O8AM46\_BRARE PRELIMINARY; PRT; 20 AA.  
 AC O8AM46;  
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Activated leukocyte cell adhesion molecule (Fragment).  
 GN Name=alcam; ORNames=alcam-001;  
 OS Brachydanio rerio (Zebrafish) (Danio rerio).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
 OC Cyprinidae; Danio.  
 OX NCBI\_TaxID=7955;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Skuce C.;  
 RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AL645788; CAD58771.1; -, Genomic DNA.  
 DR Ensembl; ENSDARG0000029359; Danio rerio.

DR ZFIN; ZDB-GENE-990415-30; alcam.  
 FT NON TER 20  
 SQ SEQUENCE 20 AA; 2022 MW; 9435BD622E7DF308 CRC64;

Query Match 22.4%; Score 21.5; DB 2; Length 20;  
 Best Local Similarity 50.0%; Pred. No. 3.8e+04;  
 Matches 6; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

QY 7 GYLITAAV-SPG 17  
 DB 9 GAFIAAAVAPFG 20

RESULT 75  
 O84U84\_SOYBN  
 ID O84U84\_SOYBN PRELIMINARY; PRT; 9 AA.  
 AC O84U84;  
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Flavonoid 3'-hydroxylase (Fragment).  
 OS Glycine max (Soybean).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC euroside I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.  
 OX NCBI\_TaxID=3847;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=22474238; PubMed=12586717;  
 RA Zebala G., Vodkin L.;  
 RT "Cloning of the pleiotropic T locus in soybean and two recessive  
 RT alleles that differentially affect structure and expression of the  
 RT encoded flavonoid 3'-hydroxylase."  
 RL Genetics 163:295-309(2003).  
 DR EMBL; AF499732; AA047848.1; -, mRNA.  
 FT NON TER 1  
 SQ SEQUENCE 9 AA; 978 MW; 25A0B685AB42C1F7 CRC64;

Query Match 21.9%; Score 21; DB 2; Length 9;  
 Best Local Similarity 37.5%; Pred. No. 2.2e+06;  
 Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 5 PHGYLTA 12  
 DB 2 PHVYSMS 9

RESULT 76  
 O7M4X1\_9ZYGO  
 ID O7M4X1\_9ZYGO PRELIMINARY; PRT; 10 AA.  
 AC O7M4X1;  
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Nuclease Bhl (BC 3.1.-.-) (Fragment).  
 OS Basidiobolus haplosporius.  
 OC Basidiobolaceae; Basidiobolus.  
 OC Eukaryota; Fungi; Zygomycota; Zygomycetes; Entomophthorales;  
 OC Basidiobolaceae; Basidiobolus.  
 OX NCBI\_TaxID=90248;  
 RN [1]  
 RP PROTEIN SEQUENCE.  
 RA Desai N., Shankar V.;  
 RL Submitted (FEB-2000) to the PIR data bank.  
 DR PIR; A59173; A59173.  
 FT NON TER 1  
 FT NON TER 10  
 SQ SEQUENCE 10 AA; 1066 MW; 53B96C2721B87727 CRC64;

Query Match 21.9%; Score 21; DB 2; Length 10;  
 Best Local Similarity 80.0%; Pred. No. 2.2e+04;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 GYLIT 11

Db 5 GHLLT 9

## RESULT 77

07KZ15 HUMAN  
ID 07KZ15 HUMAN PRELIMINARY; PRT; 10 AA.

AC 07KZ15;

DT 05-JUL-2004 (TrEMBLrel. 27, Created)

DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

DE Collagen alpha 2(I) (Fragment).

GN Name=collagen alpha 2(I);

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;

OC Homo.

OC NCBI\_TaxID=9606;

OX [1]

RP NUCLEOTIDE SEQUENCE.

RX MEDLINE=91291136; PubMed=2064612;

RA Bateman J.F., Hamagun M., Chan D., Cole W.G.;

RT "Characterization of a type I collagen alpha 2(I) glycine-586 to

valine substitution in osteogenesis imperfecta type IV. Detection of

the mutation and prenatal diagnosis by a chemical cleavage method.";

RL Biochem. J. 276:765-770(1991).

DR EMBL, 839878; AAB19314.1; -; mRNA.

KW Collagen.

FT NON\_TER 1 10

FT SEQUENCE 10 AA; 912 MW; D002867DCD2D40D CRC64;

Query Match Best Local Similarity 21.9%; Score 21; DB 2; Length 10;

Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 12 AAVSPG 17

Db 3 AAVAPG 8

## RESULT 78

09R7J8 HELPY  
ID 09R7J8 HELPY PRELIMINARY; PRT; 10 AA.

AC 09R7J8;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-JUN-2000 (TrEMBLrel. 13, Last sequence update)

DE Vacuolating cytolysin (Fragment).

GN Name=vaca;

OS Helicobacter pylori (Campylobacter pylori).

OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;

OC Helicobacteraceae; Helicobacter.

OC NCBI\_TaxID=210;

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=Kobe 500;

RA Shitazaka D.;

RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.

DR EMBL, AB017599; BAA33412.1; -; Genomic\_DNA.

FT NON\_TER 1 10

FT SEQUENCE 10 AA; 1018 MW; 414390C76879CDD7 CRC64;

Query Match Best Local Similarity 21.9%; Score 21; DB 2; Length 10;

Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 AAPPNG 7

Db 4 AFGPG 9

## RESULT 79

06ED32 TRYCR  
ID 06ED32 TRYCR PRELIMINARY; PRT; 11 AA.

AC 06ED32;

DT 01-JUN-2003 (TrEMBLrel. 24, Created)

DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)

DE 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)

GN Histone H1 (Fragment).

OS Trypanosoma cruzi.

OC Eukaryota; Eukaryota; Kinetoplastida; Trypanosomatidae; Trypanosoma;

OC Schizotrypanum.

OC NCBI\_TaxID=5693;

OX [1]

RP NUCLEOTIDE SEQUENCE.

RX MEDLINE=22557728; PubMed=12670512; DOI=10.1016/S0020-7519(02)00264-3;

RA Sturm N.R., Vargas N.S., Westenderger S.J., Zingales B.,

RT "Evidence for multiple hybrid groups in Trypanosoma cruzi.";

RL Int. J. Parasitol. 33:269-279(2003).

RN [2]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=NR c13, SC43 c11, Tulahuen c12, CM17, M5631, CB8 c13, and

RC M4167;

RA Westenderger S.J., Sturm N.R., Campbell D.A.;

RT "Extensive heterozygosity of hybrid groups of Trypanosoma cruzi.";

RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.

DR EMBL, AF545075; AAF21903.1; -; Genomic\_DNA.

DR EMBL, AY540674; AAX92650.1; -; Genomic\_DNA.

DR EMBL, AY540676; AAX92654.1; -; Genomic\_DNA.

DR EMBL, AY540677; AAX92655.1; -; Genomic\_DNA.

DR EMBL, AY540678; AAX92658.1; -; Genomic\_DNA.

DR EMBL, AY540679; AAX92660.1; -; Genomic\_DNA.

DR EMBL, AY540680; AAX92662.1; -; Genomic\_DNA.

DR EMBL, AY540672; AAX92647.1; -; Genomic\_DNA.

FT NON\_TER 11 11

FT SEQUENCE 11 AA; 1114 MW; CCCLB31E772CDD CRC64;

QY 12 AAVSPG 18

Db 4 AAVPPK 10

## RESULT 80

09TRW5 BOVIN  
ID 09TRW5 BOVIN PRELIMINARY; PRT; 11 AA.

AC 09TRW5;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DE 25 kDa protein P25, peptide P4 (Fragment).

GN Bos taurus (Bovine).

OS Bos taurus; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;

OC Pecora; Bovidae; Bovinae; Bos.

OC NCBI\_TaxID=9913;

OX [1]

RP PROTEIN SEQUENCE.

RX MEDLINE=91372400; PubMed=1909972; DOI=10.1016/0014-5793(91)80903-G;

RA Takahashi M., Tomizawa K., Ishiguro K., Sato K., Onori A., Sato S.,

RT "A novel brain-specific 25 kDa protein (p25) is phosphorylated by a

ser/Thr-Pro kinase (TPK II) from tau protein kinase fractions.";

RL FEBS Lett. 289:37-43(1991).

FT NON\_TER 1 11

FT SEQUENCE 11 AA; 1276 MW; CAF72DAF65A76AA9 CRC64;

Query Match Best Local Similarity 21.9%; Score 21; DB 2; Length 11;

Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;



Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 DAFPHG 7  
: | |  
Db 2 ERDPSC 8

RESULT 81  
09K670\_BACHD  
ID 09K670\_BACHD PRELIMINARY; PRT; 12 AA.  
AC 09K670;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE BH3662 protein.  
GN OrderedLocuNames=BH3662;  
OS Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
OC Bacillus halodurans.  
OX NCBI\_TaxID=86665;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C-125 / JCM 9153;  
RX MEDLINE=20512582; PubMed=11058132; DOI=10.1093/nar/28.21.4317;  
RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,  
RA Fujii F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,  
RA Horikoshi K.,  
RT "Complete genome sequence of the alkaliphilic bacterium Bacillus  
halodurans and genomic sequence comparison with Bacillus subtilis.";  
RL EMBL/ BA000004/ BAB07581.1; -; Genomic\_DNA.  
DR F84132; F84132.  
KM Complete proteome.  
SQ SEQUENCE 12 AA; 1463 MW; 44B501F695321A7 CRC64;

Query Match 21.9%; Score 21; DB 2; Length 12;  
Best Local Similarity 57.1%; Pred. No. 2.7e+04;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 8 YLITAAV 14  
: | | | |  
: | | | |  
Db 3 YLITKII 9

RESULT 82  
088575\_9PICO  
ID 088575\_9PICO PRELIMINARY; PRT; 12 AA.  
AC 088575;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Theiler's murine encephalomyelitis virus 5' flank and 5' end cds.  
DE (fragment).  
OS Theiler's encephalomyelitis virus.  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;  
OC Cardiovirus.  
OX NCBI\_TaxID=12124;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=FA;  
RX MEDLINE=92194426; PubMed=1548749;  
RA Pritchard A.E., Calenoff M.A., Simpson S., Jensen K., Lipton H.L.,  
RT "A single base deletion in the 5' noncoding region of Theiler's virus  
attenuates neurovirulence.";  
RL J. Virol. 66:1951-1958(1992).  
DR EMBL/ M80883; AAA73154.1; -; mRNA.  
FT NON TER 12  
SQ SEQUENCE 12 AA; 1321 MW; F79B7D908E7B5871 CRC64;

Query Match 21.9%; Score 21; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 2.7e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 HGY 8

Db 5 HGY 7

RESULT 83  
088576\_9PICO  
ID 088576\_9PICO PRELIMINARY; PRT; 12 AA.  
AC 088576;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Theiler's murine encephalomyelitis virus 5' flank and 5' end cds.  
DE (fragment).  
OS Theiler's encephalomyelitis virus.  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;  
OC Cardiovirus.  
OX NCBI\_TaxID=12124;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=MHG;  
RX MEDLINE=92194426; PubMed=1548749;  
RA Pritchard A.E., Calenoff M.A., Simpson S., Jensen K., Lipton H.L.,  
RT "A single base deletion in the 5' noncoding region of Theiler's virus  
attenuates neurovirulence.";  
RL J. Virol. 66:1951-1958(1992).  
DR EMBL/ M80884; AAA73155.1; -; mRNA.  
FT NON TER 12  
SQ SEQUENCE 12 AA; 1321 MW; F79B7D908E7B5871 CRC64;

Query Match 21.9%; Score 21; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 2.7e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 HGY 8  
: | | |  
: | | |  
Db 5 HGY 7

RESULT 84  
088577\_9PICO  
ID 088577\_9PICO PRELIMINARY; PRT; 12 AA.  
AC 088577;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Theiler's murine encephalomyelitis virus 5' flank and 5' end cds.  
DE (fragment).  
OS Theiler's encephalomyelitis virus.  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;  
OC Cardiovirus.  
OX NCBI\_TaxID=12124;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=NO;  
RX MEDLINE=92194426; PubMed=1548749;  
RA Pritchard A.E., Calenoff M.A., Simpson S., Jensen K., Lipton H.L.,  
RT "A single base deletion in the 5' noncoding region of Theiler's virus  
attenuates neurovirulence.";  
RL J. Virol. 66:1951-1958(1992).  
DR EMBL/ M80885; AAA73156.1; -; mRNA.  
FT NON TER 12  
SQ SEQUENCE 12 AA; 1321 MW; F79B7D908E7B5871 CRC64;

Query Match 21.9%; Score 21; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 2.7e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 HGY 8  
: | | |  
: | | |  
Db 5 HGY 7

RESULT 85

088578\_9PICO  
ID 088578\_9PICO PRELIMINARY; PRT; 12 AA.  
AC 088578;  
DT 01-NOV-1996 (TReMBLrel. 01, Created)  
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)  
DE Theiler's murine encephalomyelitis virus 5' flank and 5' end cds.  
DE (Fragment).  
OS Theiler's encephalomyelitis virus.  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;  
OC Cardiovirus.  
OX NCBI\_TaxID=12124;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=NO;  
RX MEDLINE=92194426; PubMed=1548749;  
RA Pritchard A.E., Calenoff M.A., Simpson S., Jensen K., Lipton H.L.;  
RT "A single base deletion in the 5' noncoding region of Theiler's virus  
attenuates neurovirulence.";  
RL J. Virol. 66:1951-1958(1992).  
DR EMBL; M80886; AAA73157.1; -; mRNA.  
FT NON\_TER 12 12  
SQ SEQUENCE 12 AA; 1321 MW; F79B7D908E7B5871 CRC64;  
  
Query Match 21.9%; Score 21; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 2.7e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 6 HGY 8  
DB 5 HGY 7  
  
RESULT 86  
ID 088579\_9PICO PRELIMINARY; PRT; 12 AA.  
AC 088579;  
DT 01-NOV-1996 (TReMBLrel. 01, Created)  
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)  
DE Theiler's murine encephalomyelitis virus 5' flank and 5' end cds.  
DE (Fragment).  
OS Theiler's encephalomyelitis virus.  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;  
OC Cardiovirus.  
OX NCBI\_TaxID=12124;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=VL;  
RX MEDLINE=92194426; PubMed=1548749;  
RA Pritchard A.E., Calenoff M.A., Simpson S., Jensen K., Lipton H.L.;  
RT "A single base deletion in the 5' noncoding region of Theiler's virus  
attenuates neurovirulence.";  
RL J. Virol. 66:1951-1958(1992).  
DR EMBL; M80887; AAA73158.1; -; mRNA.  
FT NON\_TER 12 12  
SQ SEQUENCE 12 AA; 1321 MW; F79B7D908E7B5871 CRC64;  
  
Query Match 21.9%; Score 21; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 2.7e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 6 HGY 8  
DB 5 HGY 7  
  
RESULT 87  
ID 088580\_9PICO PRELIMINARY; PRT; 12 AA.  
AC 088580;  
DT 01-NOV-1996 (TReMBLrel. 01, Created)  
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)

DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)  
DE Theiler's murine encephalomyelitis virus 5' flank and 5' end cds.  
DE (Fragment).  
OS Theiler's encephalomyelitis virus.  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;  
OC Cardiovirus.  
OX NCBI\_TaxID=12124;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=Vilyusk;  
RX MEDLINE=92194426; PubMed=1548749;  
RA Pritchard A.E., Calenoff M.A., Simpson S., Jensen K., Lipton H.L.;  
RT "A single base deletion in the 5' noncoding region of Theiler's virus  
attenuates neurovirulence.";  
RL J. Virol. 66:1951-1958(1992).  
DR EMBL; M80888; AAA73159.1; -; mRNA.  
FT NON\_TER 12 12  
SQ SEQUENCE 12 AA; 1321 MW; F79B7D908E7B5871 CRC64;  
  
Query Match 21.9%; Score 21; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 2.7e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 6 HGY 8  
DB 5 HGY 7  
  
RESULT 88  
ID 088581\_9PICO PRELIMINARY; PRT; 12 AA.  
AC 088581;  
DT 01-NOV-1996 (TReMBLrel. 01, Created)  
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)  
DE Theiler's murine encephalomyelitis virus 5' flank and 5' end cds.  
DE (Fragment).  
OS Theiler's encephalomyelitis virus.  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;  
OC Cardiovirus.  
OX NCBI\_TaxID=12124;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=MW;  
RX MEDLINE=92194426; PubMed=1548749;  
RA Pritchard A.E., Calenoff M.A., Simpson S., Jensen K., Lipton H.L.;  
RT "A single base deletion in the 5' noncoding region of Theiler's virus  
attenuates neurovirulence.";  
RL J. Virol. 66:1951-1958(1992).  
DR EMBL; M80889; AAA73160.1; -; mRNA.  
FT NON\_TER 12 12  
SQ SEQUENCE 12 AA; 1321 MW; F79B7D908E7B5871 CRC64;  
  
Query Match 21.9%; Score 21; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 2.7e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 6 HGY 8  
DB 5 HGY 7  
  
RESULT 89  
ID 088582\_9PICO PRELIMINARY; PRT; 12 AA.  
AC 088582;  
DT 01-NOV-1996 (TReMBLrel. 01, Created)  
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)  
DE Theiler's murine encephalomyelitis virus 5' flank and 5' end cds.  
DE (Fragment).  
OS Theiler's encephalomyelitis virus.  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;

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OC Cardiolavinus.
OX NCBI_TaxID=12124;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=TO;
RX MEDLINE=2194426; PubMed=1548749;
RA Pritchard A.B., Calenoff M.A., Simpson S., Jensen K., Lipton H.L.;
RT "A single base deletion in the 5' noncoding region of Theiler's virus
RT attenuates neurovirulence.";
RL J Virol 66:1951-1958(1992).
DR EMBL; M80890; AAA73161.1; -; mRNA.
FT NON_TER
SQ SEQUENCE 12 AA; 1321 MW; F79B7D908B7B5871 CRC64;

Query Match
Best Local Similarity 21.9%; Score 21; DB 2; Length 12;
Pred. No. 2.7e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 HGY 8
Db 5 HGY 7

RESULT 90
O18890 ATBBE
ID 018890_ATBBE PRELIMINARY; PRT; 13 AA.
AC 018890
DT 01-JUN-1998 (TrEMBLrel. 05, Created)
DT 01-JUN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Gransyme B (Fragment).
OS Ateles belzebuth chamek (Chamek spider monkey).
OC Bakayotea; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Platyrrhini; Cebidae;
OC Aellinae; Ateles.
OX NCBI_TaxID=118643;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98267189; PubMed=9601975; DOI=10.1007/s004120050282;
RA Canavez F., Moreira M.A.M., Bonvicino C.R., Parham P., Senanez H.N.;
RT "Comparative gene assignment in Ateles paniscus chamek (Platyrrhini,
RT Primates) and man: association of three separate human syntenic groups
RT and evolutionary considerations.";
RL Chromosoma 107:73-79(1998).
DR EMBL; AF029165; AAB84196.1; -; Genomic_DNA.
DR InterPro; IPR001254; Peptidase_S1_S6.
DR PROSITE; PS00134; TRYPsin_HIS; UNKNOWN_1.
FT NON_TER
SQ SEQUENCE 13 AA; 1394 MW; C0FF86BFAE5EDDD CRC64;

Query Match
Best Local Similarity 21.9%; Score 21; DB 2; Length 13;
Pred. No. 2.9e+04;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 8 YLTAA 13
Db 2 YLTAA 7

RESULT 91
O7M1A2 BACNO
ID 07M1A2_BACNO PRELIMINARY; PRT; 13 AA.
AC 07M1A2
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE 40X extracellular proteinase (Fragment).
OS Bacteroides nodosus (Dichelobacter nodosus).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Cardiobacteriales;
OC Cardiobacteriaceae; Dichelobacter.
OX NCBI_TaxID=870;
RN [1]

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RP PROTEIN SEQUENCE.
RX MEDLINE=92263812; PubMed=1814046;
RA Gong Y.H., Moses E.;
RT "Overexpression of an extracellular bacteroides nodosus protease in
RT E.coli and isolation and characterization of its promoter.";
RL Acta Microbiol. Sin. 31:433-437(1991).
DR PIR; PC1008; PC1008.
FT NON_TER
SQ SEQUENCE 13 AA; 1483 MW; 158DA695392221E4 CRC64;

Query Match
Best Local Similarity 21.9%; Score 21; DB 2; Length 13;
Pred. No. 2.9e+04;
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 2 AFPHGYLTAA 13
Db 1 AFNIRNHLTSLA 12

RESULT 92
O6ZYT7 GCARY
ID 06ZYT7_GCARY PRELIMINARY; PRT; 14 AA.
AC 06ZYT7
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Cytochrome b6/f complex subunit VI (Fragment).
GN Name=petL;
OS Silene acaulis.
OC Chloroplast.
OC Bakayotea; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllales; Caryophyllaceae; Silene.
OX NCBI_TaxID=269082;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=leaf;
RA Popp M.;
RT "Disentangling the reticulate history of polyploids in Silene
RT (Caryophyllaceae).";
RL Thees (2004), Department of Evolutionary Biology, Systematic Botany,
RL Uppsala university, Uppsala, Sweden.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=leaf;
RA Popp M., Erikson P., Beggans F., Oxelman B.;
RT Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
RL EMBL; AJ634219; CAG24647.1; -; Genomic_DNA.
DR GO; GO:0009507; Chloroplast; IEA.
DR GO; GO:0009512; Cytochrome b6f complex; IEA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005489; P:electron transporter activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR007802; PetL.
DR Pfam; PF05115; PetL; 1.
KW Chloroplast.
FT NON_TER
SQ SEQUENCE 14 AA; 1532 MW; 06428D1B688740DB CRC64;

Query Match
Best Local Similarity 21.9%; Score 21; DB 2; Length 14;
Pred. No. 3.2e+04;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GYLTAA 12
Db 9 GYLTAA 14

RESULT 93
O7L222 ANAPL
ID 07L222_ANAPL PRELIMINARY; PRT; 14 AA.
AC 07L222

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DT 01-MAR-2004 (TrEMBLrel. 26, Created)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Ovarstatin (Fragment).  
 OS Anas platyrhynchos (Domestic duck).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anas.  
 NCBI\_TaxID=8839;  
 RN [1]  
 RP PROTEIN SEQUENCE.  
 RX MEDLINE=86111792; PubMed=3511043;  
 RA Nagase H., Harris Jr., E.D., Brew K.;  
 RT "Evidence for a thiol ester in duck ovarstatin (ovomacroglobulin).";  
 RL J. Biol. Chem. 261:1421-1426(1986).  
 DR PIR: S00150; S00150.  
 FT NON\_TER 1  
 FT NON\_TER 14  
 FT NON\_TER 14  
 SQ SEQUENCE 14 AA; 1600 MW; 1BDD822683DE95DB CRC64;

Query Match 21.9%; Score 21; DB 2; Length 14;  
 Best Local Similarity 45.5%; Pred. No. 3.4e+04;  
 Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 4 EPHGYLITRAV 14  
 ||| : |||  
 Db 4 EPOYVLMVPAV 14

RESULT 94  
 Q6ZYT6\_9CARY PRELIMINARY; PRT; 15 AA.  
 ID Q6ZYT6;  
 AC 06ZYT6;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Cytochrome b6/f complex subunit VI (Fragment).  
 GN Name=petl;  
 OS Silene aurlensis.  
 OC Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Caryophyllales; Caryophyllaceae; Silene.  
 NCBI\_TaxID=269082;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=leaf;  
 RA Popl M.;  
 RT "Disentangling the reticulate history of polyploids in Silene (Caryophyllaceae).";  
 RL Thesis (2004), Department of Evolutionary Biology, Systematic Botany, Uppsala university, Uppsala, Sweden.  
 RN [2]  
 RN NUCLEOTIDE SEQUENCE.  
 RC TISSUE=leaf;  
 RA Popl M.;  
 RT Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: A7634220; CAG24649.1; -; Genomic\_DNA.  
 DR GO: GO:0009507; Chloroplast; IEA.  
 DR GO: GO:0009512; Cytochrome b6f complex; IEA.  
 DR GO: GO:0016021; Integral to membrane; IEA.  
 DR GO: GO:0005489; Electon transporter activity; IEA.  
 DR GO: GO:0006118; Electon transport; IEA.  
 DR InterPro: IPR007802; Petl.  
 DR Pfam: PF05115; Petl; 1.  
 DR Chloroplast.  
 FT NON\_TER 15  
 FT NON\_TER 15  
 SQ SEQUENCE 15 AA; 1645 MW; C716428D1B688740 CRC64;

Query Match 21.9%; Score 21; DB 2; Length 15;  
 Best Local Similarity 66.7%; Pred. No. 3.4e+04;  
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 Qy 7 GYLITRA 12

Db 9 GYLITRA 14  
 ||| : |||

RESULT 95  
 Q9SQ16\_ORYSA PRELIMINARY; PRT; 15 AA.  
 ID Q9SQ16\_ORYSA  
 AC Q9SQ16;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Translation elongation factor (Fragment).  
 OS Oryza sativa (Rice).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC Ehrhartoideae; Oryzaceae; Oryza.  
 NCBI\_TaxID=4530;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Li Z.-Y., Chen S.-Y.;  
 RT "Inducible expression of translation elongation factor 1A gene in rice seedlings in response to environmental stresses.";  
 RL Acta Bot. Sin. 41:800-806(1999).  
 RN [2]  
 RN NUCLEOTIDE SEQUENCE.  
 RA Li Z.-Y., Chen S.-Y.;  
 RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF067195; AAC79991.1; -; mRNA.  
 DR Gramene; Q9SQ16; -;  
 DR GO: GO:0003746; F:translation elongation factor activity; IEA.  
 FT NON\_TER 1  
 FT NON\_TER 1  
 SQ SEQUENCE 15 AA; 1514 MW; 95B5C4F069C9775 CRC64;

Query Match 21.9%; Score 21; DB 2; Length 15;  
 Best Local Similarity 33.3%; Pred. No. 3.4e+04;  
 Matches 5; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

Qy 4 EPHGYLITRAVSPK 18  
 ||| : ||| : |||  
 Db 1 DPTGAKVTKAAKK 15

RESULT 96  
 Q9QV62\_9MURI PRELIMINARY; PRT; 15 AA.  
 ID Q9QV62\_9MURI  
 AC Q9QV62;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE Differentiation enhancing factor, DEF (Fragment).  
 OS Mus sp.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Murinae; Mus.  
 NCBI\_TaxID=10095;  
 RN [1]  
 RP PROTEIN SEQUENCE.  
 RX MEDLINE=93312351; PubMed=8323566;  
 RA Sparall B., Patrone M., Passalacqua M., Pessino A., Falchetto R., Melloni B., Pontremoli S.;  
 RT "Characterization of the biological role of murine erythroleukemia cells 'differentiation enhancing factor' using antisense oligodeoxynucleotides.";  
 RT Biochem. Biophys. Res. Commun. 193:941-947(1993).  
 RL Biochem. Biophys. Res. Commun. 193:941-947(1993).  
 FT NON\_TER 1  
 FT NON\_TER 1  
 FT NON\_TER 15  
 FT NON\_TER 15  
 SQ SEQUENCE 15 AA; 1706 MW; 53329477F40FB99 CRC64;

Query Match 21.9%; Score 21; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 3.4e+04;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GYLL 10  
 ||||  
 DB 11 GYLL 14

## RESULT 97

KTIC AREMA STANDARD; PRT; 16 AA.

ID KTIC AREMA  
 AC P11917;  
 DT 01-OCT-1989 (Rel. 12, Created)  
 DT 01-OCT-1989 (Rel. 12, Last sequence update)  
 DT 10-MAY-2005 (Rel. 47, Last annotation update)  
 DE taurocyamine kinase (EC 2.7.3.4) (Fragment).  
 OS Arenicola marina (lugworm) (Rock worm).  
 OC Eukaryota; Metazoa; Annelida; Polychaeta; Scolecida; Capitellida;  
 OC Arenicolidae; Arenicola.  
 OK NCBI\_TaxId=6344;  
 RN (1)  
 RP PROTEIN SEQUENCE.  
 RX MEDLINE=75184095; PubMed=166684;  
 RA Brevet A., Zetoun Y., Pradel L.A.;  
 RT "Comparative structural studies of the active site of ATP: guanidine  
 phosphotransferases. The essential cysteine tryptic peptide of  
 taurocyamine kinase from Arenicola marina.";  
 RL Biochim. Biophys. Acta 393:1-9(1975).  
 CC -1- CATALYTIC ACTIVITY: ATP + taurocyamine = ADP + N-  
 phosphotaurocyamine.  
 CC -1- SIMILARITY: Belongs to the ATP:guanido phosphotransferase family.  
 CC -----  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.

DR PIR; A11488; A11488.  
 DR InterPro; IPR000749; ATP-Gua\_Pyrans.  
 DR PROSITE; PS00112; GUNNID\_KINASE; 1.  
 KM Direct protein sequencing; Kinase; Transferase.  
 FT ACT\_SITE 7 7  
 FT NON\_TER 1 1  
 FT NON\_TER 16 16  
 SQ SEQUENCE 16 AA; 1636 MW; CF05E7326D427E94 CRC64;

Query Match 21.9%; Score 21; DB 1; Length 16;  
 Best Local Similarity 45.5%; Pred. No. 3.6e+04;  
 Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;  
 QY 7 GYLLTAAVAPG 17  
 |||||  
 DB 2 GYLLGTCPNIG 12

## RESULT 98

Q44543 ANAVA PRELIMINARY; PRT; 16 AA.

ID Q44543 ANAVA PRELIMINARY; PRT; 16 AA.  
 AC Q44543;  
 DT 01-NOV-1996 (TRMBLrel. 01, Created)  
 DT 01-JAN-1999 (TRMBLrel. 09, Last sequence update)  
 DT 01-MAR-2003 (TRMBLrel. 23, Last annotation update)  
 DE Recombled functional n1fd gene encoding alpha nitrogenase, partial  
 DE cds. (Fragment).  
 OS Anabaena variabilis.  
 OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Anabaena.  
 OK NCBI\_TaxId=11172;  
 RN (1)  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=89327123; PubMed=2502534;  
 RA Brueca J.S., Hale M.A., Carrasco C.D., Golden J.W.,  
 RT "Extension of an 11-kilobase-pair DNA element from within the n1fd gene  
 in anabaena variabilis heterocysts.";  
 RL J. Bacteriol. 171:4138-4145(1989).  
 DR EMBL; M29073; AAAA2009.1; -; Genomic\_DNA.

DR HSP; P00466; 1GU.  
 FT NON\_TER 1 1  
 FT NON\_TER 16 16  
 SQ SEQUENCE 16 AA; 1999 MW; 46724FFC7F701577 CRC64;

Query Match 21.9%; Score 21; DB 2; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 3.6e+04;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 HGY 8  
 ||||  
 DB 13 HGY 15

## RESULT 99

Q14316 HUMAN PRELIMINARY; PRT; 17 AA.

ID Q14316 HUMAN PRELIMINARY; PRT; 17 AA.  
 AC Q14316;  
 DT 01-NOV-1996 (TRMBLrel. 01, Created)  
 DT 01-JUN-2003 (TRMBLrel. 24, Last sequence update)  
 DT 01-MAR-2004 (TRMBLrel. 26, Last annotation update)  
 DE Factor IX protein (Fragment).  
 GN Name-factor IX;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;  
 OC Homo.  
 OK NCBI\_TaxId=9606;  
 RN (1)  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=88327116; PubMed=3416069;  
 RA Reitema P.A., Bertina R.M., Ploos van Amstel J.K., Riemens A.,  
 RA Brier E.;  
 RT "The putative factor IX gene promoter in hemophilia B Leyden.";  
 RL Blood 72:1074-1076(1988).  
 DR EMBL; X55008; CAB38245.2; -; Genomic\_DNA.  
 DR HSP; P00734; 1UMA.  
 FT NON\_TER 17 17  
 SQ SEQUENCE 17 AA; 1807 MW; 73B87873A971A4F1 CRC64;

Query Match 21.9%; Score 21; DB 2; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 3.9e+04;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 7 GYLL 10  
 ||||  
 DB 14 GYLL 17

## RESULT 100

Q7R0U2 PLAYO PRELIMINARY; PRT; 17 AA.

ID Q7R0U2 PLAYO PRELIMINARY; PRT; 17 AA.  
 AC Q7R0U2;  
 DT 01-MAR-2004 (TRMBLrel. 26, Created)  
 DT 01-MAR-2004 (TRMBLrel. 26, Last sequence update)  
 DT 01-MAR-2004 (TRMBLrel. 26, Last annotation update)  
 DE Hypothetical protein.  
 GN Name=PY00998;  
 OS Plasmodium yoelii yoelii.  
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
 OK NCBI\_TaxId=73239;  
 RN (1)  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=17XNL;  
 RX MEDLINE=22255706; PubMed=12368865; DOI=10.1038/nature01099;  
 RA Carlton J.M., Anguolli S.V., Suh B.B., Kooij T.W., Pertea M.,  
 RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,  
 RA Peterson J.D., Pop M., Kosack D.S., Stumway M.F., Bidwell S.L.,  
 RA Shalton S.J., van Aken S.B., Riedmiller S.B., Feldblum T.V.,  
 RA Cho J.K., Quackenbush J., Sedegah M., Shoat A., Cummings L.M.,  
 RA Florens L., Yates J.R. III, Raine J.D., Sinden R.B., Harris M.A.,  
 RA Cunningham D.A., Preiser P.R., Bergman L.W., Valdivia A.B.,  
 RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,

RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,  
 RA Carucci D.J.;  
 RT "Genome sequence and comparative analysis of the model rodent malaria  
 RT parasite Plasmodium yoelii yoelii.";  
 RL Nature 419:512-519 (2002).  
 CC -!- CAUTION: The sequence shown here is derived from an  
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
 CC preliminary data.  
 DR EMBL; AABL01000269; EAA19799.1; -; Genomic\_DNA.  
 KW Hypothetical protein.  
 SQ SEQUENCE 17 AA; 2102 MW; CF0CCD41BA198092 CRC64;

Query Match 21.9%; Score 21; DB 2; Length 17;  
 Best Local Similarity 60.0%; Pred. No. 3.9e+04;  
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 FEPRG 7  
 | : | | |  
 Db 11 FDPRG 15

Search completed: January 20, 2006, 19:11:12  
 Job time : 61.8846 secs